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OM protein - protein search, using sw model

Run on: November 14, 2004, 13:32:59 ; Search time 27 Seconds
(without alignments)
34.387 Million cell updates/sec

Title: US-09-831-253F-6

Perfect score: 71
Sequence: 1 TSLDASIIWAMQGN 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 145874

Minimum DB seq length: 0
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2.6/prodata/1/iaa/5A COMB.pep.*
2: /cgn2.6/prodata/1/iaa/5B COMB.pep.*
3: /cgn2.6/prodata/1/iaa/6A COMB.pep.*
4: /cgn2.6/prodata/1/iaa/6B COMB.pep.*
5: /cgn2.6/prodata/1/iaa/PCUS COMB.pep.*
6: /cgn2.6/prodata/1/iaa/backfilesi.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	39.4	12	1	US-08-241-054-34
2	28	39.4	12	1	US-08-241-054-50
3	28	39.4	12	1	US-08-390-156A-14
4	28	39.4	12	1	US-08-390-156A-22
5	28	39.4	12	1	US-08-439-817-14
6	28	39.4	12	1	US-08-439-817-30
7	28	39.4	12	1	US-08-485-508-34
8	28	39.4	12	1	US-08-485-508-50
9	26	36.6	12	1	US-08-241-054-5
10	26	36.6	12	1	US-08-390-156A-76
11	26	36.6	12	1	US-08-439-817-4
12	26	36.6	12	1	US-08-485-508-5
13	26	36.6	12	4	US-09-428-082B-149
14	25	35.2	12	4	US-09-842-164A-10
15	25	35.2	14	4	US-09-053-611-29
16	24	33.8	6	1	US-08-133-020-3
17	24	33.8	8	3	US-08-444-818-563
18	24	33.8	8	3	US-08-444-818-564
19	24	33.8	8	3	US-08-160-604-112
20	24	33.8	9	3	US-09-171-705-76
21	24	33.8	10	2	US-08-617-929-24
22	24	33.8	10	4	US-08-388-852B-6
23	24	33.8	10	4	US-08-234-784B-77
24	24	33.8	12	1	US-08-241-054-7
25	24	33.8	12	1	US-08-241-054-68
26	24	33.8	12	1	US-08-241-054-100
27	24	33.8	12	1	US-08-241-054-117

28	24	33.8	12	1	US-08-390-156A-10
29	24	33.8	12	1	US-08-390-156A-64
30	24	33.8	12	1	US-08-390-156A-88
31	24	33.8	12	1	US-08-390-156A-103
32	24	33.8	12	1	US-08-439-817-6
33	24	33.8	12	1	US-08-439-817-48
34	24	33.8	12	1	US-08-439-817-80
35	24	33.8	12	1	US-08-439-817-99
36	24	33.8	12	1	US-08-439-817-209
37	24	33.8	12	1	US-08-485-508-7
38	24	33.8	12	1	US-08-485-508-68
39	24	33.8	12	1	US-08-485-508-100
40	24	33.8	12	1	US-08-485-508-117
41	24	33.8	12	2	US-08-461-990B-27
42	24	33.8	12	3	US-08-817-869-5
43	24	33.8	12	3	US-08-160-604-109
44	24	33.8	12	4	US-09-205-258-304
45	24	33.8	12	4	US-09-428-082B-150

ALIGNMENTS

RESULT 1
US-08-241-054-34
; Sequence 34, Application US/08241054
; Patent No. 5643873
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Cwirla, Steven E.
; APPLICANT: Dower, William J.
; APPLICANT: Koller, Kerry J.
; APPLICANT: Lee, Jung
; APPLICANT: Martens, Christine L.
; APPLICANT: Ruhland-Fritsch, Beatrice
; TITLE OF INVENTION: Peptides and Compounds That Bind
; TITLE OF INVENTION: Selectins Including Endothelium Leukocyte Adhesion
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/241,054
; FILING DATE: 11-MAY-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,295
; FILING DATE: 05-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/881,395
; FILING DATE: 06-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Gerald F. Swiss
; REGISTRATION NUMBER: 30,113
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-7400
; TELEFAX: 415-854-8275
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-241-054-34

Query Match 39.4%; Score 28; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. NO. 1.3e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 IWMWQ 13
Db 7 LWMWQ 12

RESULT 2

US-08-241-054-50
; Sequence 50, Application US/08241054
; Patent No. 5643873
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Cwiria, Steven E.
; APPLICANT: Dower, William J.
; APPLICANT: Koller, Kerry J.
; APPLICANT: Lee, Jung
; APPLICANT: Martens, Christine L.
; APPLICANT: Ruhland-Fritsch, Beatrice
; TITLE OF INVENTION: Peptides and Compounds That Bind
; TITLE OF INVENTION: Selectins Including Endothellum Leukocyte Adhesion
; TITLE OF INVENTION: Molecule 1
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/241,054
FILING DATE: 11-MAY-1994
CLASSIFICATION: 520

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,295
FILING DATE: 05-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/881,395
FILING DATE: 06-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gerald F. Swiss
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 000324-002
TELEPHONE: 415-854-7400
TELEFAX: 415-854-8275
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-241-054-50

Query Match 39.4%; Score 28; DB 1; Length 12;
Best Local Similarity 50.0%; Pred. NO. 1.3e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 SIWMWQ 13
:::| |

Db 5 NMLWNMMQ 12

RESULT 3

US-08-390-156A-14
; Sequence 14, Application US/08390156A
; Patent No. 5648458
; GENERAL INFORMATION:
; APPLICANT: Cwiria, Steven E.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Dower, William J.
; APPLICANT: Martens, Christine L.
; TITLE OF INVENTION: Peptides and Compounds That Bind to
; TITLE OF INVENTION: ELAM-1
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies, N.V.
; STREET: 4001 Miranda Ave.
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,156A
FILING DATE: 16-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,295
FILING DATE: 05-MAY-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/881,395
FILING DATE: 06-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Swiss, Gerald F.
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 1023.1A
TELEPHONE: 415-496-2300
TELEFAX: 415-424-0832

INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-390-156A-14

Query Match 39.4%; Score 28; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. NO. 1.3e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 IWMWQ 13
Db 7 LWMWQ 12

RESULT 4

US-08-390-156A-22
; Sequence 22, Application US/08390156A
; Patent No. 5648458
; GENERAL INFORMATION:
; APPLICANT: Cwiria, Steven E.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Dower, William J.
; APPLICANT: Martens, Christine L.
; TITLE OF INVENTION: Peptides and Compounds That Bind to
; TITLE OF INVENTION: ELAM-1
; NUMBER OF SEQUENCES: 113

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Affymax Technologies, N.V.
;; STREET: 4001 Miranda Ave.
;; CITY: Palo Alto
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94304
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/390,156A
;; FILING DATE: 16-FEB-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/057,295
;; FILING DATE: 05-MAY-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/881,395
;; FILING DATE: 06-MAY-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Swiss, Gerald F.
;; REGISTRATION NUMBER: 30,113
;; REFERENCE/DOCKET NUMBER: 1023.1A
;; TELEPHONE: 415-496-2300
;; TELEFAX: 415-424-0832
;; INFORMATION FOR SEQ ID NO: 22:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 12 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-390-156A-22

Query Match 39.4%; Score 28; DB 1; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 SIWMMQ 13
Db 5 NMLWMMQ 12

RESULT 5
US-08-439-817-14
; Sequence 14, Application US/08439817
; Patent No. 5728802
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Cwiria, Steven E.
; APPLICANT: Dower, William J.
; APPLICANT: Koller, Kerry J.
; APPLICANT: Lee, Jung
; APPLICANT: Martens, Christine L.
; APPLICANT: Ruhland-Fritsch, Beatrice
; TITLE OF INVENTION: Peptides and Compounds That Bind
; TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion
; TITLE OF INVENTION: Molecule I (ELAM-1)
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies, NV
; STREET: 4001 Miranda Ave.
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/439,817
;; FILING DATE: 12-MAY-1995
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/241,054
;; FILING DATE: 11-MAY-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/057,295
;; FILING DATE: 05-MAY-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/881,395
;; FILING DATE: 06-MAY-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Stevens, Lauren L.
;; REGISTRATION NUMBER: 36,691
;; REFERENCE/DOCKET NUMBER: 000324-046/1056.1
;; TELEPHONE: 415-496-2300
;; TELEFAX: 415-424-0832
;; INFORMATION FOR SEQ ID NO: 14:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 12 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-439-817-14

Query Match 39.4%; Score 28; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 IWMMQ 13
Db 7 LWMMQ 12

RESULT 6
US-08-439-817-30
; Sequence 30, Application US/08439817
; Patent No. 5728802
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Cwiria, Steven E.
; APPLICANT: Dower, William J.
; APPLICANT: Koller, Kerry J.
; APPLICANT: Lee, Jung
; APPLICANT: Martens, Christine L.
; APPLICANT: Ruhland-Fritsch, Beatrice
; TITLE OF INVENTION: Peptides and Compounds That Bind
; TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion
; TITLE OF INVENTION: Molecule I (ELAM-1)
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies, NV
; STREET: 4001 Miranda Ave.
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/439,817
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/241,054

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/ FILING DATE: 11-MAY-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/057,295
/ FILING DATE: 05-MAY-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/881,395
/ FILING DATE: 06-MAY-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Stevens, Lauren L.
/ REGISTRATION NUMBER: 36,691
/ REFERENCE/DOCKET NUMBER: 000324-046/1056.1
/ TELEPHONE: 415-496-2300
/ TELEFAX: 415-424-0832
/ INFORMATION FOR SEQ ID NO: 30:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 12 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-439-817-30

Query Match 39.4%; Score 28; DB 1; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 SIWMMQ 13
DB 5 NMLWMMQ 12

RESULT 7
US-08-485-508-34
/ Sequence 34, Application US/08485508
/ Patent No. 5786322
/ GENERAL INFORMATION:
/ APPLICANT: Barrett, Ronald W.
/ APPLICANT: Cwiria, Steven E.
/ APPLICANT: Dower, William J.
/ APPLICANT: Koller, Kerry J.
/ APPLICANT: Lee, Jung
/ APPLICANT: Martens, Christine L.
/ APPLICANT: Ruhland-Fritsch, Beatrice
/ TITLE OF INVENTION: Peptides and Compounds That Bind
/ TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion
/ TITLE OF INVENTION: Molecule 1
/ NUMBER OF SEQUENCES: 162
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Affymax Technologies, NV
/ STREET: 4001 Miranda Ave.
/ CITY: Palo Alto
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/485,508
/ FILING DATE: Herewith
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/241,054
/ FILING DATE: 11-MAY-1994
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/057,295
/ FILING DATE: 05-MAY-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/881,395
/ FILING DATE: 06-MAY-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Stevens, Lauren L.
/ REGISTRATION NUMBER: 36,691
/ REFERENCE/DOCKET NUMBER: 000324-002/1056
/ TELECOMMUNICATION INFORMATION:
```

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/ FILING DATE: 06-MAY-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Stevens, Lauren L.
/ REGISTRATION NUMBER: 36,691
/ REFERENCE/DOCKET NUMBER: 000324-002/1056
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-496-2300
/ TELEFAX: 415-424-0832
/ INFORMATION FOR SEQ ID NO: 34:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 12 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-485-508-34

Query Match 39.4%; Score 28; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 IWMQM 13
DB 7 LWVMMQ 12

RESULT 8
US-08-485-508-50
/ Sequence 50, Application US/08485508
/ Patent No. 5786322
/ GENERAL INFORMATION:
/ APPLICANT: Barrett, Ronald W.
/ APPLICANT: Cwiria, Steven E.
/ APPLICANT: Dower, William J.
/ APPLICANT: Koller, Kerry J.
/ APPLICANT: Lee, Jung
/ APPLICANT: Martens, Christine L.
/ APPLICANT: Ruhland-Fritsch, Beatrice
/ TITLE OF INVENTION: Peptides and Compounds That Bind
/ TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion
/ TITLE OF INVENTION: Molecule 1
/ NUMBER OF SEQUENCES: 162
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Affymax Technologies, NV
/ STREET: 4001 Miranda Ave.
/ CITY: Palo Alto
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/485,508
/ FILING DATE: Herewith
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/241,054
/ FILING DATE: 11-MAY-1994
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/057,295
/ FILING DATE: 05-MAY-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/881,395
/ FILING DATE: 06-MAY-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Stevens, Lauren L.
/ REGISTRATION NUMBER: 36,691
/ REFERENCE/DOCKET NUMBER: 000324-002/1056
/ TELECOMMUNICATION INFORMATION:
```

DT 17-MAY-2001 (first entry)
XX
DE CD66 peptide CD66f (11)-10.
XX
KW CD66; CEACAM; adhesion molecule; antiviral; antibacterial;
KW antiinflammatory; cytostatic; neutrophil activation; proliferation;
KW differentiation; cancer; angiogenesis.
XX
OS Unidentified.
XX
XX WO200113937-A1.
PN
PD 01-MAR-2001.
XX
PF 25-AUG-2000; 2000WO-US023482.
XX
XX 26-AUG-1999; 99US-0150791P.
PR
PR 02-SEP-1999; 99US-0152501P.
XX
XX (SKUB/). SKUBITZ K M.
PA (SKUB/). SKUBITZ A P N.
PA
XX Skubitz KM, Skubitz APN;
XX
XX WPI; 2001-234981/24.
DR
XX
XX Novel peptides useful for activating neutrophils or blocking activation
XX of neutrophils, modulating homotypic or heterotypic adhesion of CD66
XX polypeptides, and modulating immune cell activation.
XX
PS Claim 1; Page 54; 102pp; English.
XX
XX The present sequence is an isolated peptide that was tested for its
CC ability to modulate the function of CD66 family polypeptides and CD66
CC ligands. 106 sequences of 13 or 14 amino acids in length, and their
CC analogues, were identified that modulate the function of at least one
CC CD66 family polypeptide and/or at least one ligand of the polypeptide.
CC The peptides are capable of modulating activation of neutrophils,
CC activation or inhibition, proliferation and/or differentiation of T-
CC cells, B-cells, NK cells, LAK cells, dendritic cells, or other immune
CC system cells, proliferation and/or differentiation of epithelial cells,
CC homotypic and/or heterotypic adhesion among CD66 family polypeptides and
CC adhesion of CD66 family polypeptides to other ligands. The peptides are
CC useful for delivering a therapeutically active agent to a patient, for
CC modifying the metastasis of malignant cells, for altering bacterial or
CC viral binding to cells or a biomaterial, for altering cell adhesion to a
CC biomaterial, for detecting tumours, for detecting inflammation, for
CC detecting a CD66 protein or its ligand, for altering angiogenesis by
CC contacting endothelial cells, tumour cells or immune cells, for altering
CC an immune response, and for altering keratinocyte proliferation
XX
XX Sequence 14 AA;
SQ
Query Match 46.5%; Score 33; DB 4; Length 14;
Best Local Similarity 60.0%; Pred. No. 55;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 SLDASIIWAM 11
Db :|||||:
3 TLDASYLWMM 12
RESULT 10
ADM73036
XX ADM73036 standard; peptide; 9 AA.
ID
XX ADM73036;
AC
XX
DT 03-JUN-2004 (first entry)
XX
DE Human GAGE-1 epitope SEQ ID NO:295.
XX
XX epitope; epitope cluster; virucide; cytostatic; vaccine; viral infection;

KW cancer; tumour; human; GAGE-1.
XX
OS Homo sapiens.
OS Synthetic.
PN WO2004022709-A2.
XX
XX 18-MAR-2004.
XX
XX 05-SEP-2003; 2003WO-US027706.
XX
XX 06-SEP-2002; 2002US-0409123P.
PR (MANN-) MANNKIND CORP.
XX
XX Simard J.L., Diamond DC, Liu L, Liu Z;
XX WPI; 2004-315564/29.
DR
XX
XX New polypeptides and encoding nucleic acids that are useful epitopes of
PT target-associated antigens, useful for diagnosing and/or treating viral
PT infections, cancers and tumors.
XX
XX Claim 1; SEQ ID NO 295; 357pp; English.
XX
XX The present invention describes a polypeptide (I) comprising a component
CC selected from: (a) a polypeptide epitope having any of the 503 fully
CC defined sequences of 8-33 amino acids (SEQ ID NO:108-610); (b) an epitope
CC cluster comprising the polypeptide of (a); (c) a polypeptide having
CC substantial similarity to (a) or (b); (d) a polypeptide having functional
CC similarity to any of (a)-(c); or (e) a nucleic acid encoding the
CC polypeptide of (a)-(d). (I) has virucide and cytostatic activities, and
CC can be used in vaccines. The methods and compositions of the present
CC invention are useful for the diagnosis and/or treatment of viral
CC infections, cancers and tumors. The present sequence is used in the
CC exemplification of the present invention.
XX
XX Sequence 9 AA;
SQ
Query Match 40.8%; Score 29; DB 8; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 7 IIVAMQON 14
Db 1 ILWLLMNN 8
RESULT 11
ADM73041
ID ADM73041 standard; peptide; 9 AA.
XX
XX ADM73041;
AC
XX
XX 03-JUN-2004 (first entry)
DT
XX
XX Human GAGE-1 epitope SEQ ID NO:300.
DE
XX
XX epitope; epitope cluster; virucide; cytostatic; vaccine; viral infection;
KW cancer; tumour; human; GAGE-1.
XX
OS Homo sapiens.
OS Synthetic.
PN WO2004022709-A2.
XX
XX 18-MAR-2004.
XX
XX 05-SEP-2003; 2003WO-US027706.
PF
XX
XX 06-SEP-2002; 2002US-0409123P.
PR (MANN-) MANNKIND CORP.
XX
XX

QY 7 IIWAMMON 14
 Db 1 ILWLLMNN 8

RESULT 14
 ADM73035
 ID ADM73035 standard; peptide; 10 AA.
 XX
 AC ADM73035;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE Human GAGE-1 epitope SEQ ID NO:294.
 XX
 KW epitope; epitope cluster; virucide; cytostatic; vaccine; viral infection;
 KW cancer; tumour; human; GAGE-1.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO2004022709-A2.
 XX
 PD 18-MAR-2004.
 XX
 PF 05-SEP-2003; 2003WO-US027706.
 XX
 PR 06-SEP-2002; 2002US-0409123P.
 XX
 PA (MANN-) MANNKIND CORP.
 XX
 PI Simard JUL, Diamond DC, Liu L, Liu Z;
 XX
 DR WPI; 2004-315564/29.
 XX
 PT New polypeptides and encoding nucleic acids that are useful epitopes of
 PT target-associated antigens, useful for diagnosing and/or treating viral
 PT infections, cancers and tumors.
 XX
 PS Claim 1; SEQ ID NO 294; 357pp; English.
 XX
 CC The present invention describes a polypeptide (I) comprising a component
 CC selected from: (a) a polypeptide epitope having any of the 503 fully
 CC defined sequences of 8-33 amino acids (SEQ ID NO:108-610); (b) an epitope
 CC cluster comprising the polypeptide of (a); (c) a polypeptide having
 CC substantial similarity to (a) or (b); (d) a polypeptide having functional
 CC similarity to any of (a)-(c); or (e) a nucleic acid encoding the
 CC polypeptide of (a)-(d). (I) has virucide and cytostatic activities, and
 CC can be used in vaccines. The methods and compositions of the present
 CC invention are useful for the diagnosis and/or treatment of viral
 CC infections, cancers and tumors. The present sequence is used in the
 CC exemplification of the present invention.

QY 7 IIWAMMON 14
 Db 2 ILWLLMNN 9

RESULT 15
 AAY93007
 ID AAY93007 standard; peptide; 12 AA.
 XX
 AC AAY93007;
 XX
 DT 08-NOV-2000 (first entry)
 XX

Query Match 40.8%; Score 29; DB 8; Length 10;
 Best Local Similarity 50.0%; Pred. No. 2e+02;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 IIWAMMON 14
 Db 2 ILWLLMNN 9

Query Match 40.8%; Score 29; DB 3; Length 12;
 Best Local Similarity 75.0%; Pred. No. 2.4e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLDASII 8
 Db 5 TSLDATMI 12

Search completed: November 14, 2004, 13:44:57
 Job time : 112.5 secs

DE Transforming growth factor inhibitory peptide P53.
 XX
 KW Hepatotropic; antagonist; transforming growth factor betaf; TGF-b1;
 KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
 KW extracellular matrix degradation inhibitor; mimotope; cirrhosis.
 XX
 OS Rattus sp.
 XX
 PN WO200031135-A1.
 XX
 PD 02-JUN-2000.
 XX
 PF 23-NOV-1999; 99WO-ES000375.
 XX
 PR 24-NOV-1998; 98ES-00002465.
 XX
 PA (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
 XX
 PI Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
 PI Borrás Cuesta F;
 XX
 DR WPI; 2000-411935/35.
 XX
 PT Peptides that antagonize binding of transforming growth factor betaf,
 PT useful for treatment of liver disease, especially cirrhosis, are partial
 PT sequences of the factor or its receptors.
 XX
 PS Disclosure; Page 27; 86pp; Spanish.
 XX
 CC The invention relates to synthetic peptides that antagonise the binding
 CC of transforming growth (TGF) factor betaf (TGF-b1) to its receptor in
 CC vivo which have partial amino acid sequences identical, or similar, with
 CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
 CC examples of the peptides of the invention. The peptides act by
 CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
 CC they are inhibitors of stimulation of collagen synthesis in liver cells
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
 CC expression systems) encoding the peptides are used for treatment of liver
 CC disease, specifically cirrhosis
 XX
 SQ Sequence 12 AA;

Query Match 40.8%; Score 29; DB 3; Length 12;
 Best Local Similarity 75.0%; Pred. No. 2.4e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLDASII 8
 Db 5 TSLDATMI 12

Search completed: November 14, 2004, 13:44:57
 Job time : 112.5 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2004, 13:18:48 ; Search time 110.5 Seconds
(without alignments)
45.450 Million cell updates/sec

Title: US-09-831-253F-6

Perfect score: 71
Sequence: 1 TSLDASIIWMMQN 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 543373

Minimum DB seq length: 0
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003s:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	71	100.0	14	3 AAY93098	Aay93098 Transform
2	71	100.0	14	3 AAY92950	Aay92950 Transform
3	50	70.4	12	3 AAY93009	Aay93009 Transform
4	50	70.4	12	3 AAY92947	Aay92947 Transform
5	50	70.4	12	3 AAY93008	Aay93008 Transform
6	40	56.3	12	3 AAY93093	Aay93093 Transform
7	37	52.1	11	3 AAY93094	Aay93094 Transform
8	37	52.1	12	3 AAY93010	Aay93010 Transform
9	33	46.5	14	4 AAB88161	Aab88161 CD66 pept
10	29	40.8	9	4 ADM73036	Adm73036 Human GAG
11	29	40.8	9	8 ADM73041	Adm73041 Human GAG
12	29	40.8	10	8 ADM73042	Adm73042 Human GAG
13	29	40.8	10	8 ADM73040	Adm73040 Human GAG
14	29	40.8	10	8 ADM73035	Adm73035 Human GAG
15	29	40.8	12	3 AAY93007	Aay93007 Transform
16	28	39.4	12	2 AAR86049	Aar86049 Anti-ELAM
17	28	39.4	12	2 AAR86065	Aar86065 Anti-ELAM
18	28	39.4	12	2 AAW26857	Aaw26857 ELAM-1 bi
19	28	39.4	12	2 AAW26865	Aaw26865 ELAM-1 bi
20	28	39.4	12	2 AAW63875	Aaw63875 ELAM-1 pe
21	28	39.4	12	2 AAW63859	Aaw63859 ELAM-1 pe
22	27.5	38.7	9	3 AAY93096	Aay93096 Transform
23	27.5	38.7	9	3 AAY92949	Aay92949 Transform
24	27	38.0	7	3 AAW46010	Aaw46010 Peptide #
25	27	38.0	7	3 AAY93095	Aay93095 Transform

26	27	38.0	11	5 ABB05301	Abb05301 Polyureth
27	27	38.0	12	2 AAR83343	Aar83343 K5-bindin
28	27	38.0	14	4 ABB56643	Abb56643 Human SNP
29	26	36.6	9	5 AAO14709	Aao14709 Human cri
30	26	36.6	9	5 AAG80179	Aag80179 HER-2 mim
31	26	36.6	10	5 AAO14645	Aao14645 Human cri
32	26	36.6	11	5 ABR52334	Abr52334 Peptide r
33	26	36.6	11	5 ABJ07364	Abj07364 Hepatitis
34	26	36.6	12	2 AAR72136	Aar72136 Endotheli
35	26	36.6	12	2 AAR86025	Aar86025 Anti-ELAM
36	26	36.6	12	2 AAR86041	Aar86041 Anti-ELAM
37	26	36.6	12	2 AAW26845	Aaw26845 ELAM-1 bi
38	26	36.6	12	2 AAW63849	Aaw63849 ELAM-1 pe
39	26	36.6	12	3 AAB17093	Aab17093 Selectin
40	26	36.6	12	5 AAU81139	Aau81139 Selectin
41	26	36.6	12	5 ABB72976	Abb72976 Selectin
42	26	36.6	12	7 ADJ73130	Adj73130 Integrin
43	26	36.6	12	8 ADJ52765	Adj52765 CHI delet
44	26	36.6	12	8 ADJ51726	Adj51726 CHI delet
45	26	36.6	13	2 AAR86115	Aar86115 Anti-ELAM

ALIGNMENTS

RESULT 1

AAY93098
ID AAY93098 standard; peptide; 14 AA.

XX AC AAY93098;

XX DT 08-NOV-2000 (first entry)

XX DE Transforming growth factor inhibitory peptide PI44.

XX KW Hepatotropic; antagonist; transforming growth factor beta1; TGF-beta1; competitive inhibition; collagen synthesis stimulation inhibitor; liver; extracellular matrix degradation inhibitor; mimetope; cirrhosis.

XX OS Homo sapiens.

XX PN WO200031135-A1.

XX PD 02-JUN-2000.

XX PF 23-NOV-1999; 99WO-ES000375.

XX PR 24-NOV-1998; 98ES-0002465.

XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.

XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J; Borras Cuesta F;

XX WPI; 2000-411935/35.

XX PT Peptides that antagonize binding of transforming growth factor beta1, useful for treatment of liver disease, especially cirrhosis, are partial sequences of the factor or its receptors.

XX PS Disclosure; Page 31; 86pp; Spanish.

XX CC The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor beta1 (TGF-beta1) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-beta1 and/or its receptors. Peptides AAY92945-Y93133 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-beta1 to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver disease, specifically cirrhosis

CC those of TGF- β 1 and/or its receptors. Peptides AAY92945-Y93133 represent
 CC examples of the peptides of the invention. The peptides act by
 CC competitive inhibition of the binding of TGF- β 1 to its receptors, e.g.
 CC they are inhibitors of stimulation of collagen synthesis in liver cells
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
 CC expression systems) encoding the peptides are used for treatment of liver
 CC disease, specifically cirrhosis
 XX
 SQ Sequence 12 AA;

Query Match 56.3%; Score 40; DB 3; Length 12;
 Best Local Similarity 77.8%; Pred. No. 2.7;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLDASIIW 9
 DB 1 TSLDATMIW 9
 |||||:|

RESULT 7
 AAY93094
 ID AAY93094 standard; peptide; 11 AA.
 XX
 AC AAY93094;

XX
 DT 08-NOV-2000 (first entry)
 XX

DE Transforming growth factor inhibitory peptide P140.

XX Hepatotropic; antagonist; transforming growth factor beta1; TGF- β 1;
 KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
 KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.

XX Homo sapiens.

XX WO200031135-A1.

XX 02-JUN-2000.

XX 23-NOV-1999; 99WO-ES000375.

XX 24-NOV-1998; 98ES-00002465.

XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.

XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
 PI Borras Cuesta F;

XX WPI; 2000-411935/35.

XX Peptides that antagonize binding of transforming growth factor beta1,
 PT useful for treatment of liver disease, especially cirrhosis, are partial
 PT sequences of the factor or its receptors.

XX Disclosure; Page 31; 86pp; Spanish.

XX The invention relates to synthetic peptides that antagonise the binding
 CC of transforming growth (TGF) factor beta1 (TGF- β 1) to its receptor in
 CC vivo which have partial amino acid sequences identical, or similar, with
 CC those of TGF- β 1 and/or its receptors. Peptides AAY92945-Y93133 represent
 CC examples of the peptides of the invention. The peptides act by
 CC competitive inhibition of the binding of TGF- β 1 to its receptors, e.g.
 CC they are inhibitors of stimulation of collagen synthesis in liver cells
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
 CC expression systems) encoding the peptides are used for treatment of liver
 CC disease, specifically cirrhosis
 XX

SQ Sequence 11 AA;

Query Match 52.1%; Score 37; DB 3; Length 11;
 Best Local Similarity 66.7%; Pred. No. 8.4;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 4 DASIIWMM 12
 ||:| |
 DB 3 DATMIWTMM 11

RESULT 8
 AAY93010
 ID AAY93010 standard; peptide; 12 AA.
 XX
 AC AAY93010;

XX
 DT 08-NOV-2000 (first entry)
 XX

DE Transforming growth factor inhibitory peptide P56.

XX Hepatotropic; antagonist; transforming growth factor beta1; TGF- β 1;
 KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
 KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.

XX Rattus sp.

XX WO200031135-A1.

XX 02-JUN-2000.

XX 23-NOV-1999; 99WO-ES000375.

XX 24-NOV-1998; 98ES-00002465.

XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.

XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
 PI Borras Cuesta F;

XX WPI; 2000-411935/35.

XX Peptides that antagonize binding of transforming growth factor beta1,
 PT useful for treatment of liver disease, especially cirrhosis, are partial
 PT sequences of the factor or its receptors.

XX Disclosure; Page 27; 86pp; Spanish.

XX The invention relates to synthetic peptides that antagonise the binding
 CC of transforming growth (TGF) factor beta1 (TGF- β 1) to its receptor in
 CC vivo which have partial amino acid sequences identical, or similar, with
 CC those of TGF- β 1 and/or its receptors. Peptides AAY92945-Y93133 represent
 CC examples of the peptides of the invention. The peptides act by
 CC competitive inhibition of the binding of TGF- β 1 to its receptors, e.g.
 CC they are inhibitors of stimulation of collagen synthesis in liver cells
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
 CC expression systems) encoding the peptides are used for treatment of liver
 CC disease, specifically cirrhosis
 XX

SQ Sequence 12 AA;

Query Match 52.1%; Score 37; DB 3; Length 12;
 Best Local Similarity 75.0%; Pred. No. 9.2;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 IIVWMMQN 14
 ||:| |
 DB 1 MIWTMMQN 8

RESULT 9
 AAB88161
 ID AAB88161 standard; peptide; 14 AA.
 XX
 AC AAB88161;

XX

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```

RN  SEQUENCE FROM N.A.
RP  MEDLINE=22404279; PubMed=12516573;
RA  Kurth J., Pernik A., Schmitz R., Iking-Konert C., Chiorazzi N.,
RT  Thompson K.M., Winkler T., Rajewsky K., Kueppers R.;
RT  "Lack of deleterious somatic mutations in the CD95 gene of
RT  plasmablasts from systemic lupus erythematosus patients and
RT  autoantibody-producing cell lines.";
RL  Eur. J. Immunol. 32:3785-3792(2002).
DR  EMBL; D31968; BAA28850.1; -
DR  EMBL; AJ279011; CAC35539.1; -
DR  EMBL; AJ279012; CAC35540.1; -
DR  EMBL; AJ279013; CAC35541.1; -
DR  EMBL; AJ509179; CAD48929.1; -
DR  EMBL; AJ509180; CAD48930.1; -
FT  NON_TER
SQ  SEQUENCE 11 AA; 1256 MW; 0802145E2731B370 CRC64;

Query Match      26.8%; Score 19; DB 2; Length 11;
Best Local Similarity 40.0%; Pred. No. 1.4e+04;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy  8 IWMM 12
Db  4 IWTL 8

RESULT 15
Q9TWX6
ID  Q9TWX6      PRELIMINARY;      PRT;      11 AA.
AC  Q9TWX6;
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DT  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT  01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE  Juvenile hormone binding protein, JHBP=12.5 kDa CNBR peptide
DE  (Fragment).
OS  Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC  Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingioidea;
OC  Spingidae; Sphinginae; Manduca.
OX  NCBI_TaxID=7130;
RN  [1]
RP  SEQUENCE.
RX  MEDLINE=92134256; PubMed=1734862;
RA  Touhara K.; Prestwich G.D.;
RT  "Binding site mapping of a photoaffinity-labeled juvenile hormone
RT  binding protein.";
RL  Biochem. Biophys. Res. Commun. 182:466-473(1992).
FT  NON_TER 1 1
FT  NON_TER 11 11
SQ  SEQUENCE 11 AA; 1071 MW; D232A98E705045BD CRC64;

Query Match      26.8%; Score 19; DB 2; Length 11;
Best Local Similarity 57.1%; Pred. No. 1.4e+04;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy  2 SLDASII 8
Db  1 NIQASII 7

```

Search completed: November 14, 2004, 13:41:10
 Job time : 124.5 secs

FT NON TER 1 1
 FT NON TER 14 14
 SQ SEQUENCE 14 AA; 1544 MW; OBC0478DB855A33B CRC64;

Query Match 29.6%; Score 21; DB 2; Length 14;
 Best Local Similarity 50.0%; Pred. No. 7.5e+03;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 TSLDASII 8
 Db 1 TSLESSYL 8

RESULT 11

Q841R8 PRELIMINARY; PRT; 13 AA.
 AC Q841R8; 2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Ccch (Fragment).
 GN Name-cpH;
 OS Synchococcus sp. (strain PCC 6301) (Anacystis nidulans).
 OC Bacteria; Cyanobacteria; Chroococcales; Synchococcus.
 OX NCBI_TaxID=1139;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9321540; PubMed=7682531;
 RA Kalla R., Bhalarao R.P., Gustafsson P.;
 RT "Regulation of phycoobilisome rod proteins and mRNA at different light
 intensities in the cyanobacterium Synchococcus 6301.";
 RL Gene 126:77-83(1993).
 DR EMBL; S58974; RAP13908.1; -.
 FT NON TER 13 13
 SQ SEQUENCE 13 AA; 1439 MW; D58F2E86F2D0DDD CRC64;

Query Match 28.2%; Score 20; DB 2; Length 13;
 Best Local Similarity 66.7%; Pred. No. 1.1e+04;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLDAS 6
 Db 2 TSLEAA 7

RESULT 12

P82383 PRELIMINARY; PRT; 10 AA.
 AC P82383;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Larval cuticle LCP2A protein (Minor band protein) (Fragment).
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=OREGON-R; TISSUE=LARVA;
 RA Chihara C.J.;
 RT "Third instar cuticle proteins.";
 RL Submitted (XXX-2000) to Swiss-Prot.
 CC -1- FUNCTION: COMPONENT OF THE CUTICLE OF THE LARVA OF FRUIT FLY.
 DR Flybase; FBgn0061208; Lcp2a.
 DR GO; GO:0042302; F:structural constituent of cuticle; IEA.
 DR InterPro; IPR000618; Insect cuticle.
 DR PROSITE; PS00233; CUTICLE; PARTIAL.
 KW Cuticle; Structural protein.
 FT NON TER 10 10
 SQ SEQUENCE 10 AA; 1100 MW; 9DCF320732C44DDA CRC64;

Query Match 26.8%; Score 19; DB 2; Length 10;
 Best Local Similarity 33.3%; Pred. No. 1.3e+04;
 Matches 3; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2 SLDASIIWA 10
 Db 1 NVDANVLRA 9

RESULT 13

Q25356 PRELIMINARY; PRT; 10 AA.
 ID Q25356;
 AC Q25356;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
 DE Vitellogenin B (Fragment).
 OS Locusta migratoria (Migratory locust).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.
 OX NCBI_TaxID=7004;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88003971; PubMed=2820677;
 RA Locke J., White B.N., Wyatt G.R.;
 RT "Cloning and 5' end nucleotide sequences of two juvenile hormone-
 inducible vitellogenin genes of the African migratory locust.";
 RL DNA 6:331-342(1987).
 DR EMBL; M17334; AAA29285.1; -.
 FT NON TER 10 10
 SQ SEQUENCE 10 AA; 1116 MW; D1B31165B720572D CRC64;

Query Match 26.8%; Score 19; DB 2; Length 10;
 Best Local Similarity 40.0%; Pred. No. 1.3e+04;
 Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 IWAMM 12
 Db 1 MWALI 5

RESULT 14

Q9UEL0 PRELIMINARY; PRT; 11 AA.
 ID Q9UEL0;
 AC Q9UEL0;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Fas antigen (CD95 antigen) (Fragment).
 GN Name-CD95;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=95355401; PubMed=7543095;
 RA Wada N., Matsumura M., Ohba Y., Kobayashi N., Takizawa T.,
 RA Nakanishi Y.;
 RT "Transcription Stimulation of the Fas-encoding gene by nuclear factor
 for interleukin-6 expression upon influenza virus infection.";
 RL J. Biol. Chem. 270:18007-18012(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Muschen M., Re D., Brauning A., Wolf J., Hansmann M.L., Diehl V.,
 RA Kuppers R., Rajewsky K.;
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Muschen M., Re D., Jungnickel B., Diehl V., Rajewsky K., Kuppers R.;
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.

```

DR EMBL; AY128666; AAM96953.1; -.
FT NON TER 8
SQ SEQUENCE 8 AA; 965 MW; F99DC37B1046D876 CRC64;

Query Match          29.6%; Score 21; DB 2; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 IIVAM 11
| |||
Db 4 IEWAM 8

RESULT 7
APE_CAPGI STANDARD; PRT; 10 AA.
AC P80474;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Aminopeptidase (EC 3.4.11.-) (Fragment).
OS Capnocytophaga gingivalis.
OC Bacteria; Bacteroidetes; Flavobacteriales;
OC Flavobacteriaceae; Capnocytophaga.
OX NCBI_TaxID=1017;
RN [1]
RP SEQUENCE.
RC STRAIN=ATCC 33624;
RX MEDLINE=96118234; PubMed=8574402;
RA Spratt D.A., Greenman J., Schaffer A.G.;
RT "Capnocytophaga gingivalis aminopeptidase: a potential virulence
factor.";
RL Microbiology 141:3087-3093(1995).
CC -1- FUNCTION: Aminopeptidase which hydrolyzes substrates with free N-
terminal amino acid residues but not N-terminal blocked ones.
CC Optimum activity is measured at pH 7.5. May be important in the
CC nutrition and pathogenesis of the organism in the human oral
CC cavity.
CC -1- COFACTOR: Requires magnesium or calcium.
KW Aminopeptidase; Calcium; Direct protein sequencing; Hydrolase;
KW Magnesium.
FT NON TER 1 1
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1306 MW; 00C0A6DB43772694 CRC64;

Query Match          29.6%; Score 21; DB 1; Length 10;
Best Local Similarity 33.3%; Pred. No. 5.2e+03;
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 DASIIW 9
| : : |
Db 1 DVNMLW 6

RESULT 8
Q7MLJ3 PRELIMINARY; PRT; 10 AA.
AC Q7MLJ3;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cystathionine gamma-synthase (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Amaranthaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE.
RX MEDLINE=95142682; PubMed=7840669;
RA Ravanel S., Droux M., Douce R.;
RT "Methionine biosynthesis in higher plants. I. Purification and
RT characterization of cystathionine gamma-synthase from spinach

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RT chloroplasts.";
RL Arch. Biochem. Biophys. 316:572-584(1995).
DR PIR; S69159; S69159. 1
FT NON TER 1
FT NON TER 10 10
SQ SEQUENCE 10 AA; 873 MW; D88458DDDDAB2CD CRC64;

Query Match          29.6%; Score 21; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 5.2e+03;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 TSLDASII 8
| : : |
Db 2 TAVDAAA 9

RESULT 9
O77895 PRELIMINARY; PRT; 11 AA.
AC O77895;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II B locus 12 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidaei;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid MHC
RT class II B loci.";
RL Genetics 149:1527-1537(1998).
DR EMBL; AF050005; AAC41344.1; -.
FT NON TER 1 1
FT NON TER 11 11
SQ SEQUENCE 11 AA; 1367 MW; 3F47C9EA772045A3 CRC64;

Query Match          29.6%; Score 21; DB 2; Length 11;
Best Local Similarity 75.0%; Pred. No. 5.8e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 SIIV 9
| : : |
Db 5 SIIV 8

RESULT 10
Q9R5Q6 PRELIMINARY; PRT; 14 AA.
AC Q9R5Q6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE 2-HALOGENOATE 1,2-dioxygenase component A beta subunit
DE (Fragment).
OS Burkholderia cepacia (Pseudomonas cepacia).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia.
OX NCBI_TaxID=292;
RN [1]
RP SEQUENCE.
RX MEDLINE=92104974; PubMed=1370284;
RA Fetzner S., Muller R., Lingens F.;
RT "Purification and some properties of 2-halobenzoate 1,2-dioxygenase, a
RT two-component enzyme system from Pseudomonas cepacia 2CBS.";
RL J. Bacteriol. 174:279-290(1992).
DR PIR; A44920; A44920.

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RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
 RA Figueroa F., Sultmann H., Klein J.,
 RT "Linkage relationships and haplotype polymorphism among cichlid MHC
 class II B loci.",
 RL Genetics 149:1527-1537(1998).
 DR EMBL; AF050004; AAC41343.1; -.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1367 MW; 3F47DCOA62C045A3 CRC64;

Query Match 31.0%; Score 22; DB 2; Length 11;
 Best Local Similarity 75.0%; Pred. No. 3.7e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 SIIV 9
 ||:|
 Db 5 SIVW 8

RESULT 3
 O77898 PRELIMINARY; PRT; 11 AA.
 AC O77898;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MHC class II B locus 12 (Fragment).
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;
 OC Cichlidae; Oreochromis.
 OX NCBI_TaxID=8128;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98315113; PubMed=9649539;
 RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
 RA Figueroa F., Sultmann H., Klein J.,
 RT "Linkage relationships and haplotype polymorphism among cichlid MHC
 class II B loci.",
 RL Genetics 149:1527-1537(1998).
 DR EMBL; AF050008; AAC41347.1; -.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1367 MW; 3F47DCOA62C045A3 CRC64;

Query Match 31.0%; Score 22; DB 2; Length 11;
 Best Local Similarity 75.0%; Pred. No. 3.7e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 SIIV 9
 ||:|
 Db 5 SIVW 8

RESULT 4
 Q7M1U2 PRELIMINARY; PRT; 11 AA.
 AC Q7M1U2;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Unidentified 5.7/35k protein (Fragment).
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE.
 RA Komatsu S., Kajiwarra H., Hirano H.;
 RT "A rice protein library; a data-file of rice proteins separated by
 RT two-dimensional electrophoresis.";

RL Theor. Appl. Genet. 86:935-942(1993).
 DR PIR; P00731; P00731.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1319 MW; CBE97F0E53277362 CRC64;

Query Match 31.0%; Score 22; DB 2; Length 11;
 Best Local Similarity 40.0%; Pred. No. 3.7e+03;
 Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 5 ASIIV 9
 ||:|
 Db 1 ATVW 5

RESULT 5
 Q99902 PRELIMINARY; PRT; 14 AA.
 AC Q99902;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
 DE ERG/EWS protein (Fragment).
 GN Name=ERG/EWS;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Liver;
 RX MEDLINE=96321017; PubMed=8707406;
 RA Peter M., Mugneret F., Aurias A., Thomas G., Magdelenat H.,
 RA Delattre O.,
 RT "An EWS/ERG fusion with a truncated N-terminal domain of EWS in a
 RT Ewing's tumor.";
 RL Int. J. Cancer 67:339-342(1996).
 DR EMBL; S82338; AAD15010.2; -.
 FT NON_TER 1 1
 FT NON_TER 14 14
 SQ SEQUENCE 14 AA; 1624 MW; D8808FFB7C07C61D CRC64;

Query Match 31.0%; Score 22; DB 2; Length 14;
 Best Local Similarity 50.0%; Pred. No. 4.8e+03;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 LDASIWA 10
 ||:|
 Db 5 LSAEHLWA 12

RESULT 6
 Q86SL0 PRELIMINARY; PRT; 8 AA.
 AC Q86SL0;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Flavocytochrome b-558 alpha polypeptide (fragment).
 GN Name=CYBA;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22615572; PubMed=12729892;
 RA Moreno M.U., San Jose G., Orbe J., Pizarro J.A., Belouqui O., Diez J.,
 RA Zalba G.;
 RT "Preliminary characterisation of the promoter of the human p22phox
 RT gene: identification of a new polymorphism associated with
 RT hypertension.";
 RL FEBS Lett. 542:27-31(2003).

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OM protein - protein search, using sw model

Run on: November 14, 2004, 13:17:28 ; Search time 122.5 Seconds
(without alignments)
65.757 Million cell updates/sec

Title: US-09-831-253F-6

Perfect score: 71

Sequence: 1 TSLDASIWAMQMN 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 6764

Minimum DB seq length: 0

Maximum DB seq length: 14

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	31.0	10	2 Q9ESU5	Q9esU5 mus musculus
2	22	31.0	11	2 Q77894	Q77894 oreochromis
3	22	31.0	11	2 Q77898	Q77898 oreochromis
4	22	31.0	11	2 Q7MIU2	Q7mlU2 oryza sativ
5	22	31.0	14	2 Q99902	Q99902 homo sapien
6	21	29.6	8	2 Q86SL0	Q86SL0 homo sapien
7	21	29.6	10	1 APE_CAPGI	P80474 capnocytoph
8	21	29.6	10	2 Q7MLJ3	Q7mlJ3 spinacia ol
9	21	29.6	11	2 Q77895	Q77895 oreochromis
10	21	29.6	14	2 Q9RS06	Q9rs06 burkholderi
11	20	28.2	13	2 Q841R8	Q841R8 synechococc
12	19	26.8	10	2 P82383	P82383 drosophila
13	19	26.8	10	2 Q25356	Q25356 locusta mig
14	19	26.8	11	2 Q9UELO	Q9ueL0 homo sapien
15	19	26.8	11	2 Q9TWX6	Q9twX6 manduca sex
16	19	26.8	11	2 Q77896	Q77896 oreochromis
17	19	26.8	12	2 Q9UCR3	Q9ucR3 homo sapien
18	19	26.8	12	2 Q6X7V1	Q6x7V1 canis fam
19	19	26.8	12	2 AAP79619	AP79619 canis fam
20	19	26.8	13	2 Q7RFA9	Q7rfA9 plasmodium
21	19	26.8	14	2 Q9SAP8	Q9sAP8 plasmodium
22	18	25.4	8	2 Q70V57	Q70V57 fuerstia af
23	18	25.4	8	2 CAD45547	CAD4547 fuerstia
24	18	25.4	9	2 Q85DB0	Q85db0 lepilemur s
25	18	25.4	9	2 Q85DB8	Q85db8 lepilemur e
26	18	25.4	9	2 Q94NR9	Q94nr9 daubentonia
27	18	25.4	9	2 Q94NB0	Q94nb0 microcebus
28	18	25.4	9	2 Q94NB1	Q94nb1 microcebus
29	18	25.4	9	2 Q94NB2	Q94nb2 microcebus
30	18	25.4	10	2 Q7M501	Q7m501 aspergillus
31	18	25.4	10	2 Q6EEZ7	Q6eeZ7 homo sapien

32	18	25.4	10	2 Q25355	Q25355 locusta mig
33	18	25.4	10	2 Q7ZZJ2	Q7zzJ2 motacilla f
34	18	25.4	11	2 Q78118	Q78118 oreochromis
35	18	25.4	11	2 Q78120	Q78120 oreochromis
36	18	25.4	11	2 Q56972	Q56972 yersinia pe
37	18	25.4	11	2 Q7LZ10	Q7Lz10 gadus sp. a
38	18	25.4	11	2 Q7ZZI6	Q7zzI6 motacilla f
39	18	25.4	11	2 Q7ZZI9	Q7zzI9 motacilla f
40	18	25.4	11	2 Q8ADI8	Q8adi8 human immun
41	18	25.4	12	2 Q7M348	Q7m348 pan troglod
42	18	25.4	12	2 Q7M350	Q7m350 callithrix
43	18	25.4	12	2 Q7M351	Q7m351 macaca fusc
44	18	25.4	12	2 Q7M352	Q7m352 hylobates l
45	18	25.4	12	2 Q7M353	Q7m353 pongo pygma

ALIGNMENTS

RESULT 1

Q9ESU5 PRELIMINARY; PRT; 10 AA.
AC Q9ESU5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Fas death receptor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/He;
RX MEDLINE=20127858; PubMed=10660538;
RA Munsch D., Watanabe-Fukunaga R., Bourdon J.C., Nagata S., May E.,
RA Yonish-Rouach E., Reisdorf P.;
RT "Human and mouse Fas (APO-1/CD95) death receptor genes each contain a
RT p53-responsive element that is activated by p53 mutants unable to
RT induce apoptosis.";
RL J. Biol. Chem. 275:3867-3872(2000).
DR EMBL; AF282865; AAG02410.1; -;
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1242 MW; 22145E32CDC37043 CRC64;
Query Match 31.0%; Score 22; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 IWAMM 12
DB 4 IWAVL 8

RESULT 2

O77894 PRELIMINARY; PRT; 11 AA.
AC O77894;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II B locus 12 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;

A;Reference number: PH1754; MUID:93301585; PMID:8391057
A;Accession: PH1768
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-14 <POR>

Query Match 26.8%; Score 19; DB 2; Length 14;
Best Local Similarity 33.3%; Pred. No. 2.3e+03;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TSLDASIIW 9
| : : :
Db 5 TDSNYQLIW 13

RESULT 15

S66195
alcohol dehydrogenase (EC 1.1.1.1) class III low affinity form - cod (Gadus sp.) (fragment)
C;Species: Gadus sp. (cod)
C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 12-Jun-1998
C;Accession: S66195
R;Hjelmqvist, L.; Hackett, M.; Shafqat, J.; Danielsson, O.; Iida, J.; Hendrickson, R.C.;
FEBS Lett 367, 237-240, 1995
A;Title: Multiplicity of N-terminal structures of medium-chain alcohol dehydrogenases. M
nzyme.

A;Reference number: S66191; MUID:95331382; PMID:7607314
A;Accession: S66195
A;Molecule type: protein
A;Residues: 1-6 <HJE>
C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
C;Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match 25.4%; Score 18; DB 2; Length 6;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 5 ASIIW 9
| : :
Db 1 AAVAW 5

Search completed: November 14, 2004, 13:45:47
Job time : 22.5 secs

A;Note: sequence extracted from NCBI backbone (NCBIP:75379)

Query Match 29.6%; Score 21; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 9.6e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 TSLDASII 8
| | | | |
Dy 1 TSLESSYL 8

RESULT 9

PH1769

T cell receptor alpha chain V region (clone 2V alpha 7.2-4) - human (fragment)

C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C;Accession: PH1769
R;Porcelli, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 178, 1-16, 1993

A;Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A;Reference number: PH1754; MUID:93301585; PMID:8391057

A;Accession: PH1769

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-14 <PDR>

Query Match 28.2%; Score 20; DB 2; Length 14;
Best Local Similarity 40.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 4; Mismatches 0; Indels 2; Gaps 1;

QY 2 SLDAS--IIW 9
| | | | |
Dy 4 SMDSNYQLIW 13

RESULT 10

PT0519

T-cell receptor beta chain V-D-J region (100-4C) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C;Accession: PT0519

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0519

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-6 <FEE>

A;Experimental source: adult thymus, strain BALB/c

C;Keywords: T-cell receptor

Query Match 26.8%; Score 19; DB 2; Length 6;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 ASIIW 9
| | | | |
Dy 1 ASSLW 5

RESULT 11

S09652

hypothetical protein (aacC2 3' region) - Enterobacter cloacae (fragment)

C;Species: Enterobacter cloacae

C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 08-Oct-1999

C;Accession: S09652

R;Vliegthart, J.S.; Ketelaar-van Gaalen, P.A.G.; van de Klundert, J.A.M.

Antimicrob. Agents Chemother. 33, 1153-1159, 1989

A;Title: Nucleotide sequence of the aacC2 gene, a gentamicin resistance determinant inv

A;Reference number: S09651; MUID:90024972; PMID:2552900

A;Accession: S09652

A;Molecule type: DNA

A;Residues: 1-7 <VLI>

A;Cross-references: EMBL:X51534; NID:940878; PIDN:CAA35914.1; PID:9581034

Query Match 26.8%; Score 19; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 IIW 9
| | | | |
Dy 2 IIW 4

RESULT 12

PH1602

Ig H chain V-D-J region (wild-type clone 313) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999

C;Accession: PH1602

R;Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mic

A;Reference number: PH1580; MUID:93301609; PMID:8315387

A;Accession: PH1602

A;Molecule type: DNA

A;Residues: 1-7 <LEV>

A;Experimental source: bone marrow pre-B lymphocyte

C;Keywords: immunoglobulin

Query Match 26.8%; Score 19; DB 2; Length 7;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 ASIIW 9
| | | | |
Dy 2 ASSLW 6

RESULT 13

S66248

processing enzyme, 33K - black gram (fragment)

C;Species: Vigna mungo (black gram)

C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

C;Accession: S66248

R;Okamoto, T.; Minamikawa, T.

Eur. J. Biochem. 231, 300-305, 1995

A;Title: Purification of a processing enzyme (VmPE-1) that is involved in post-translat

A;Reference number: S66248; MUID:95361851; PMID:7635141

A;Accession: S66248

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 <OKA>

A;Cross-references: UNIPROT:Q9XFZ4

Query Match 26.8%; Score 19; DB 2; Length 10;
Best Local Similarity 33.3%; Pred. No. 1.8e+03;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 DASIIWAM 12
| | | | |
Dy 1 DEGTWAVL 9

RESULT 14

PH1768

T cell receptor alpha chain V region (clone 2V alpha 7.2-3) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999

C;Accession: PH1768

R;Porcelli, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.

J. Exp. Med. 178, 1-16, 1993

A;Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

Db 2 TAVDAAAI 9

RESULT 3
S69123
proton-translocating transhydrogenase - Rhodospirillum rubrum (fragment)
C;Species: Rhodospirillum rubrum
C;Date: 10-Mar-1998 #sequence_revision 24-Apr-1998 #text_change 24-Apr-1998
C;Accession: S69123
R;Diggle, C.; Hutton, M.; Jones, G.R.; Thomas, C.M.; Jackson, J.B.
Eur. J. Biochem. 228, 719-726, 1995
A;Title: Properties of the soluble polypeptide of the proton-translocating transhydrogenase
A;Reference number: S69123; MUID:95255277; PMID:7737169
A;Accession: S69123
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-12 <DIG>

Query Match 31.0%; Score 22; DB 2; Length 12;
Best Local Similarity 22.2%; Pred. No. 5.2e+02;
Matches 2; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 5 ASIIWAMQ 13
| : : : :
Db 2 ADVVWKVQR 10

RESULT 4
PT0586
T-cell receptor beta chain V-D-J region (141-1CN) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0586; PT0592
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0586
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-7 <FEE>
A;Experimental source: day 19 fetal thymus, strain BALB/c (clones 141-1CN and 141-1CD)
C;Keywords: T-cell receptor

Query Match 29.6%; Score 21; DB 2; Length 7;
Best Local Similarity 80.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ASIIW 9
| : : : :
Db 1 ASSIW 5

RESULT 5
S69159
cystathionine gamma-synthase - spinach (fragment)
C;Species: Spinacia oleracea (spinach)
C;Date: 12-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
C;Accession: S69159
R;Ravanel, S.; Droux, M.; Douce, R.
Arch. Biochem. Biophys. 316, 572-584, 1995
A;Title: Methionine biosynthesis in higher plants. I. Purification and characterization
A;Reference number: S69159; MUID:95142682; PMID:7840669
A;Accession: S69159
A;Molecule type: protein
A;Residues: 1-10 <RAV>
A;Cross-references: UNIPROT:Q7M1J3
C;Keywords: chloroplast

Query Match 29.6%; Score 21; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 TSLDASII 8
| : : : : |

Db 2 TAVDAAAI 9

RESULT 6
I64829
gene HEXA protein - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C;Accession: I64829
R;Boles, D.J.; Proia, R.L.
Am. J. Hum. Genet. 56, 716-724, 1995
A;Title: The molecular basis of HEXA mRNA deficiency caused by the most common Tay-Sachs
A;Reference number: I51882; MUID:95193801; PMID:7887427
A;Accession: I64829
A;Status: preliminary; translated from GB/EMBL/DBBJ
A;Molecule type: mRNA
A;Residues: 1-12 <RES>
A;Cross-references: GB:S76984; NID:9912781; PIDN:AAD14243.1; PID:94261943
C;Genetics:
A;Gene: GDB:HEXA
A;Cross-references: GDB:120040; OMIM:272800
A;Map position: 15q23-15q24
C;Superfamily: beta-hexosaminidase

Query Match 29.6%; Score 21; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 8.1e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 SIIW 9
| : : : :
Db 8 SILW 11

RESULT 7
PHI327
Ig heavy chain DJ region (clone C113-105) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PHI327
R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A;Title: Predominance of fetal type DJH joining in young children with B precursor lymphoma
A;Reference number: PHI302; MUID:93094761; PMID:1460419
A;Accession: PHI327
A;Molecule type: DNA
A;Residues: 1-14 <WAS>
C;Keywords: heterotetramer; immunoglobulin

Query Match 29.6%; Score 21; DB 2; Length 14;
Best Local Similarity 75.0%; Pred. No. 9.6e+02;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 WAMM 12
| : : : :
Db 2 WYMM 5

RESULT 8
A44920
2-halobenzoate 1,2-dioxygenase component A beta chain - Pseudomonas cepacia (fragment)
C;Species: Pseudomonas cepacia
C;Date: 01-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A44920
R;Fetner, S.; Muller, R.; Lingens, F.
J. Bacteriol. 174, 279-290, 1992
A;Title: Purification and some properties of 2-halobenzoate 1,2-dioxygenase, a two-component
A;Reference number: A44920; MUID:92104974; PMID:1370284
A;Contents: 2CBS
A;Accession: A44920
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-14 <FET>
A;Cross-references: UNIPROT:Q9RSQ6

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2004, 13:32:33 ; Search time 22.5 Seconds
(without alignments)
59.868 Million cell updates/sec

Title: US-09-831-253F-6

Perfect score: 71

Sequence: 1 TSLDASIWMQMN 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2096

Minimum DB seq length: 0

Maximum DB seq length: 14

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: Pir1:*

2: Pir2:*

3: Pir3:*

4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	36.6	14	2 A35105	hypothetical prote
2	22	31.0	11	2 PQ0731	unidentified 5.7/3
3	22	31.0	12	2 S69123	proton-translocati
4	21	29.6	7	2 PT0586	T-cell receptor be
5	21	29.6	10	2 S69159	cystathionine gamm
6	21	29.6	12	2 I64829	gene HEXA protein
7	21	29.6	14	2 PH1327	Ig heavy chain DJ
8	21	29.6	14	2 A44920	2-halobenzoate 1,2
9	20	28.2	14	2 PH1769	T cell receptor al
10	19	26.8	6	2 PT0519	T-cell receptor be
11	19	26.8	7	2 S09652	hypothetical prote
12	19	26.8	7	2 PH1802	Ig H chain V-D-J r
13	19	26.8	10	2 S66248	processing enzyme,
14	19	26.8	14	2 PH1768	T cell receptor al
15	18	25.4	6	2 S66195	alcohol dehydrogen
16	18	25.4	9	2 S13889	phosphoenolpyruvat
17	18	25.4	10	2 D61440	polygalacturonase
18	18	25.4	11	2 S66196	alcohol dehydrogen
19	18	25.4	12	2 PN0581	tyrosine 3-monooxy
20	18	25.4	12	2 PN0580	tyrosine 3-monooxy
21	18	25.4	12	2 PN0579	tyrosine 3-monooxy
22	18	25.4	12	2 PN0577	tyrosine 3-monooxy
23	18	25.4	12	2 PN0576	tyrosine 3-monooxy
24	18	25.4	12	2 PN0578	tyrosine 3-monooxy
25	18	25.4	13	2 I54984	aeg-46.5 protein -
26	18	25.4	14	2 PH1758	T cell receptor al
27	18	25.4	14	2 PH1766	T cell receptor al
28	18	25.4	14	2 S14336	mastoparan B - hor
29	17	23.9	9	2 S07241	litorin - Rohde's

30 17 23.9 9 2 I58350
31 17 23.9 10 2 S48182
32 17 23.9 10 2 A35556
33 17 23.9 10 2 B33143
34 17 23.9 10 2 A33143
35 17 23.9 12 2 A29169
36 17 23.9 13 2 S57567
37 17 23.9 14 2 PH1757
38 17 23.9 14 2 PH1759
39 17 23.9 14 2 PH1767
40 16 22.5 7 2 PX0008
41 16 22.5 8 2 A39308
42 16 22.5 9 2 S07205
43 16 22.5 9 2 S07204
44 16 22.5 10 2 A60647
45 16 22.5 10 2 PQ0177

ALIGNMENTS

RESULT 1

A35105

hypothetical protein - Neurospora crassa mitochondrion (fragment)

C;Species: mitochondrion Neurospora crassa

C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 07-Dec-1999

C;Accession: A35105

R;Saville, B.J.; Collins, R.A.

Cell 61, 685-696, 1990

A;Title: A site-specific self-cleavage reaction performed by a novel RNA in neurospora

A;Reference number: A35105; MUID:90263093; PMID:2160856

A;Accession: A35105

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-14 <SAV>

C;Genetics:

A;Genome: mitochondrion

A;Genetic code: SGC3

C;Keywords: mitochondrion

Query Match 36.6%; Score 26; DB 2; Length 14;
Best Local Similarity 37.5%; Pred. No. 1.1e+02;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 6 SIWMMQ 13

Db 2 SFLWTLQ 9

RESULT 2

PQ0731

unidentified 5.7/35K protein [imported] - rice (fragment)

C;Species: Oryza sativa (rice)

C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004

C;Accession: PQ0731

R;Komatsu, S.; Kajiwara, H.; Hirano, H.

Theor. Appl. Genet. 86, 935-942, 1993

A;Title: A rice protein library; a data-file of rice proteins separated by two-dimensio

A;Reference number: PQ0696

A;Accession: PQ0731

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <KOM>

A;Cross-references: UNIPROT:Q7M1U2

Query Match 31.0%; Score 22; DB 2; Length 11;
Best Local Similarity 40.0%; Pred. No. 4.7e+02;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 5 ASIIV 9

Db 1 ATVWV 5

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ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,141A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 174611B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)-594-6734
TELEFAX: (908)-594-4720
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-469-141A-32

Query Match 38.0%; Score 27; DB 3; Length 15;
Best Local Similarity 71.4%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 DASIWA 10
|
Db 7 DNGIWA 13

Search completed: November 14, 2004, 12:08:49
Job time : 12.0213 secs

REFERENCE/DOCKET NUMBER: 0233 US
TELEPHONE: (515) 245-3594
TELEFAX: (515) 245-3634
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-179-632-15

Query Match 39.4%; Score 28; DB 1; Length 23;
Best Local Similarity 66.7%; Pred. No. 2.5e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 IIWMM 12
Db 12 LIWALM 17

RESULT 13
US-08-440-174A-15
Sequence 15, Application US/08440174A
Patent No. 5717061
GENERAL INFORMATION:
APPLICANT: Rao, Gururaj A.
APPLICANT: Zhong, Lingxiu
TITLE OF INVENTION: SYNTHETIC ANTIMICROBIAL PEPTIDES
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC.
STREET: 7100 N.W. 62nd Avenue
CITY: Johnston
STATE: Iowa
COUNTRY: USA
ZIP: 50131
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,174A
FILING DATE: 12-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/079,512
FILING DATE: 18-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bobrowicz, Donna
REGISTRATION NUMBER: 32,196
REFERENCE/DOCKET NUMBER: 0234R2D-US
TELEPHONE: (515) 334-6883
TELEFAX: (515) 334-6883
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-440-174A-15

Query Match 39.4%; Score 28; DB 1; Length 23;
Best Local Similarity 66.7%; Pred. No. 2.5e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 IIWMM 12
Db 12 LIWALM 17

RESULT 14
PCT-US95-00062-15
Sequence 15, Application PC/TUS9500062
GENERAL INFORMATION:
APPLICANT: Pioneer Hi-Bred International, Inc.
TITLE OF INVENTION: SYNTHETIC ANTIMICROBIAL PEPTIDES
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pioneer Hi-Bred International, Inc.
STREET: 700 Capital Square, 400 Locust Street
CITY: Des Moines
STATE: Iowa
COUNTRY: United States
ZIP: 50309
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS/Microsoft Windows
SOFTWARE: Microsoft Windows Notepad
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00062
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Yates, Michael E.; Sweeney, Patricia A.;
NAME: Roth, Michael J.; & Simon, Soma G.
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 234R2-PCT
TELEPHONE: (515) 248-4800
TELEFAX: (515) 248-4844
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-00062-15

Query Match 39.4%; Score 28; DB 5; Length 23;
Best Local Similarity 66.7%; Pred. No. 2.5e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 IIWMM 12
Db 12 LIWALM 17

RESULT 15
US-08-469-141A-32
Sequence 32, Application US/08469141A
Patent No. 6124107
GENERAL INFORMATION:
APPLICANT: MUMFORD, RICHARD A.
APPLICANT: DAVIES, D.T. PHILIP
APPLICANT: DAHLGREN, MARY E.
APPLICANT: BOGER, JOSHUA S.
APPLICANT: HUMES, JOHN L.
TITLE OF INVENTION: ASSAY FOR MARKER OF HUMAN
TITLE OF INVENTION: POLYMORPHONUCLEAR LEUKOCYTE ELASTASE ACTIVITY
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: DR. CHRISTINE E. CARTY
STREET: 126 E. LINCOLN AVENUE., P.O. BOX 2000
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: USA

; SEQUENCE CHARACTERISTICS:

; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-485-508-34

Query Match 39.4%; Score 28; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 IWAMMQ 13
:| |||
Db 7 LWVMMQ 12

RESULT 10

US-08-485-508-50
; Sequence 50, Application US/08485508
; Patent No. 5786322

; GENERAL INFORMATION:

; APPLICANT: Barrett, Ronald W.
; APPLICANT: Cwiria, Steven E.
; APPLICANT: Dower, William J.
; APPLICANT: Koller, Kerry J.
; APPLICANT: Lee, Jung
; APPLICANT: Martens, Christine L.
; APPLICANT: Ruhland-Fritsch, Beatrice
; TITLE OF INVENTION: Peptides and Compounds That Bind
; TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion
; TITLE OF INVENTION: Molecule I
; NUMBER OF SEQUENCES: 162
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies, NV
; STREET: 4001 Miranda Ave.
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION NUMBER: US/08/485,508
; FILING DATE: Herewith

; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/241,054
; FILING DATE: 11-MAY-1994

; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/057,295
; FILING DATE: 05-MAY-1993

; APPLICATION DATA:
; APPLICATION NUMBER: US 07/881,395
; FILING DATE: 06-MAY-1992

; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.

; REGISTRATION NUMBER: 35,691

; REFERENCE/DOCKET NUMBER: 000324-002/1056

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300

; TELEFAX: 415-424-0832

; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 12 amino acids
; TYPE: amino acid

; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-485-508-50

Query Match 39.4%; Score 28; DB 1; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 SIWAMMQ 13
:| |||
Db 5 NMLWNMQ 12

RESULT 11

US-09-255-501-108
; Sequence 108, Application US/09255501
; Patent No. 6596525

; GENERAL INFORMATION:

; APPLICANT: Estell, David
; APPLICANT: Harding, Fiona
; TITLE OF INVENTION: MUTANT PROTEINS HAVING LOWER ALLERGENIC RESPONSE IN
; TITLE OF INVENTION: HUMANS AND METHODS FOR CONSTRUCTING, IDENTIFYING AND
; TITLE OF INVENTION: PRODUCING SUCH PROTEINS
; FILE REFERENCE: GC527
; CURRENT APPLICATION NUMBER: US/09/255,501
; CURRENT FILING DATE: 1999-02-23
; NUMBER OF SEQ ID NOS: 211
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 108
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; US-09-255-501-108

Query Match 39.4%; Score 28; DB 4; Length 15;
Best Local Similarity 44.4%; Pred. No. 1.6e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 LDASIIWAM 11
:| |||
Db 1 LQADVLWQM 9

RESULT 12

US-08-179-632-15
; Sequence 15, Application US/08179632
; Patent No. 5607914

; GENERAL INFORMATION:

; APPLICANT: Rao, A. Gururaj; Zhong, Lingxiu
; TITLE OF INVENTION: SYNTHETIC ANTIMICROBIAL PEPTIDES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pioneer Hi-Bred International, Inc.
; STREET: 700 Capital Square, 400 Locust Street
; CITY: Des Moines
; STATE: Iowa
; COUNTRY: United States
; ZIP: 50309

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS/Microsoft Windows
; SOFTWARE: Microsoft Windows No. 5607914epad

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/179,632
; FILING DATE: 07-JAN-1994

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/079,512
; FILING DATE: 06/18/93

; ATTORNEY/AGENT INFORMATION:
; NAME: Roth, Michael J.

; REGISTRATION NUMBER: 29,342

APPLICATION NUMBER: US 08/057,295
FILING DATE: 05-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/881,395
FILING DATE: 06-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Stevens, Lauren L.
REGISTRATION NUMBER: 36,691
REFERENCE/DOCKET NUMBER: 000324-046/1056.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-496-2300
TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-439-817-14

Query Match 39.4%; Score 28; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 IWAMMQ 13
Db 7 LWVMMQ 12

RESULT 8
US-08-439-817-30
Sequence 30, Application US/08439817
Patent No. 5728802
GENERAL INFORMATION:
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Dower, William J.
APPLICANT: Koller, Kerry J.
APPLICANT: Lee, Jung
APPLICANT: Martens, Christine L.
APPLICANT: Ruhland-Fritsch, Beatrice
TITLE OF INVENTION: Peptides and Compounds That Bind
TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion
TITLE OF INVENTION: Molecule I (ELAM-1)
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: Affymax Technologies, NV
STREET: 4001 Miranda Ave.
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,817
FILING DATE: 12-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/241,054
FILING DATE: 11-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,295
FILING DATE: 05-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/881,395
FILING DATE: 06-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Stevens, Lauren L.

REGISTRATION NUMBER: 36,691
REFERENCE/DOCKET NUMBER: 000324-046/1056.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-496-2300
TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-439-817-30

Query Match 39.4%; Score 28; DB 1; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 SIWAMMQ 13
Db 5 NMLWNMQ 12

RESULT 9
US-08-485-508-34
Sequence 34, Application US/08485508
Patent No. 5786322
GENERAL INFORMATION:
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Dower, William J.
APPLICANT: Koller, Kerry J.
APPLICANT: Lee, Jung
APPLICANT: Martens, Christine L.
APPLICANT: Ruhland-Fritsch, Beatrice
TITLE OF INVENTION: Peptides and Compounds That Bind
TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion
TITLE OF INVENTION: Molecule I
NUMBER OF SEQUENCES: 162
CORRESPONDENCE ADDRESS:
ADDRESSEE: Affymax Technologies, NV
STREET: 4001 Miranda Ave.
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,508
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/241,054
FILING DATE: 11-MAY-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,295
FILING DATE: 05-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/881,395
FILING DATE: 06-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Stevens, Lauren L.
REGISTRATION NUMBER: 36,691
REFERENCE/DOCKET NUMBER: 000324-002/1056
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-496-2300
TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO: 34:

APPLICANT: Barrett, Ronald W.
APPLICANT: Dower, William J.
APPLICANT: Martens, Christine L.
TITLE OF INVENTION: Peptides and Compounds That Bind to
TITLE OF INVENTION: ELAM-1
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Affymax Technologies, N.V.
STREET: 4001 Miranda Ave.
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,156A
FILING DATE: 16-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,295
FILING DATE: 05-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Swiss, Gerald F.
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 1023.1A
TELEPHONE: 415-496-2300
TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-390-156A-14

Query Match 39.4%; Score 28; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 8 IWAMMQ 13
Db 7 LWVMMQ 12

RESULT 6
US-08-390-156A-22
Sequence 22, Application US/08390156A
Patent No. 5648458
GENERAL INFORMATION:
APPLICANT: Cwirla, Steven E.
APPLICANT: Barrett, Ronald W.
APPLICANT: Dower, William J.
APPLICANT: Martens, Christine L.
TITLE OF INVENTION: Peptides and Compounds That Bind to
TITLE OF INVENTION: ELAM-1
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Affymax Technologies, N.V.
STREET: 4001 Miranda Ave.
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,156A
FILING DATE: 16-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,295
FILING DATE: 05-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/881,395
FILING DATE: 06-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Swiss, Gerald F.
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 1023.1A
TELEPHONE: 415-496-2300
TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-390-156A-22

Query Match 39.4%; Score 28; DB 1; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 6 SIWAMMQ 13
Db 5 NMLWNMMQ 12

RESULT 7
US-08-439-817-14
Sequence 14, Application US/08439817
Patent No. 5728802
GENERAL INFORMATION:
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Dower, William J.
APPLICANT: Koller, Kerry J.
APPLICANT: Lee, Jung
APPLICANT: Martens, Christine L.
APPLICANT: Ruhland-Fritsch, Beatrice
TITLE OF INVENTION: Peptides and Compounds That Bind
TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion
TITLE OF INVENTION: Molecule 1 (ELAM-1)
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: Affymax Technologies, NV
STREET: 4001 Miranda Ave.
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,817
FILING DATE: 12-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/241,054
FILING DATE: 11-MAY-1994
PRIOR APPLICATION DATA:

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-255-501-107

Query Match 40.8%; Score 29; DB 4; Length 15;
Best Local Similarity 40.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 SLDASIIWAM 11

Db 3 TLQADVLMQM 12

RESULT 3

US-08-241-054-34
; Sequence 34, Application US/08241054
; Patent No. 5643873
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Cwirla, Steven E.
; APPLICANT: Dower, William J.
; APPLICANT: Koller, Kerry J.
; APPLICANT: Lee, Jung
; APPLICANT: Martens, Christine L.
; APPLICANT: Ruhland-Fritsch, Beatrice
; TITLE OF INVENTION: Peptides and Compounds That Bind
; TITLE OF INVENTION: Selectins Including Endothelium Leukocyte Adhesion
; TITLE OF INVENTION: Molecule 1
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/241,054
; FILING DATE: 11-MAY-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,295
; FILING DATE: 05-MAY-1993
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/241,054
; FILING DATE: 11-MAY-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,295
; FILING DATE: 05-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/881,395
; FILING DATE: 06-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Gerald F. Swiss
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 000324-002
; TELEPHONE: 415-854-7400
; TELEFAX: 415-854-8275
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-241-054-34

Query Match 39.4%; Score 28; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 IWAMQM 13

Db 7 LWMQM 12

RESULT 4

US-08-241-054-50
; Sequence 50, Application US/08241054
; Patent No. 5643873
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Cwirla, Steven E.
; APPLICANT: Dower, William J.
; APPLICANT: Koller, Kerry J.
; APPLICANT: Lee, Jung
; APPLICANT: Martens, Christine L.
; APPLICANT: Ruhland-Fritsch, Beatrice
; TITLE OF INVENTION: Peptides and Compounds That Bind
; TITLE OF INVENTION: Selectins Including Endothelium Leukocyte Adhesion
; TITLE OF INVENTION: Molecule 1
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/241,054
; FILING DATE: 11-MAY-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,295
; FILING DATE: 05-MAY-1993
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/241,054
; FILING DATE: 11-MAY-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,295
; FILING DATE: 05-MAY-1993
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 07/881,395
; FILING DATE: 06-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Gerald F. Swiss
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 000324-002
; TELEPHONE: 415-854-7400
; TELEFAX: 415-854-8275
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-241-054-50

Query Match 39.4%; Score 28; DB 1; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 SIWAMQM 13

Db 5 NMLWMMQM 12

RESULT 5

US-08-390-156A-14
; Sequence 14, Application US/08390156A
; Patent No. 5648458
; GENERAL INFORMATION:
; APPLICANT: Cwirla, Steven E.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:26 ; Search time 11.0213 Seconds
(without alignments)
84.242 Million cell updates/sec

Title: US-09-831-253F-6
Perfect score: 71
Sequence: 1 TSLDASIIWAMQN 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 202416

Minimum DB seq length: 0
Maximum DB seq length: 23

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
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2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	40.8	15	4	US-09-255-501-106
2	29	40.8	15	4	US-09-255-501-107
3	28	39.4	12	1	US-08-241-054-34
4	28	39.4	12	1	US-08-241-054-50
5	28	39.4	12	1	US-08-390-156A-14
6	28	39.4	12	1	US-08-390-156A-22
7	28	39.4	12	1	US-08-439-817-14
8	28	39.4	12	1	US-08-439-817-30
9	28	39.4	12	1	US-08-485-508-34
10	28	39.4	12	1	US-08-485-508-50
11	28	39.4	15	4	US-09-255-501-108
12	28	39.4	23	1	US-08-179-632-15
13	28	39.4	23	1	US-08-440-174A-15
14	28	39.4	23	5	PCT-US95-00062-15
15	27	38.0	15	4	US-08-469-141A-32
16	27	38.0	15	4	US-09-073-009-38
17	27	38.0	15	4	US-09-073-010-38
18	27	38.0	15	4	US-09-069-827A-162
19	27	38.0	15	5	PCT-US95-13794-32
20	27	38.0	20	1	US-07-654-839-4
21	27	38.0	20	4	US-09-564-945-39
22	26	36.6	12	1	US-08-241-054-5
23	26	36.6	12	1	US-08-390-156A-76
24	26	36.6	12	1	US-08-439-817-4
25	26	36.6	12	1	US-08-485-508-5
26	26	36.6	12	4	US-09-428-082B-149
27	26	36.6	15	1	US-08-241-054-110

28	26	36.6	15	1	US-08-390-156A-92	Sequence 92, Appl
29	26	36.6	15	1	US-08-439-817-90	Sequence 90, Appl
30	26	36.6	15	1	US-08-485-508-110	Sequence 110, App
31	26	36.6	18	4	US-09-082-358B-16	Sequence 16, Appl
32	26	36.6	20	3	US-08-504-538A-13	Sequence 13, Appl
33	26	36.6	20	3	US-08-464-496-2	Sequence 2, Appli
34	26	36.6	20	3	US-08-630-052-13	Sequence 13, Appl
35	26	36.6	20	5	PCT-US92-07218-2	Sequence 2, Appli
36	26	36.6	20	5	PCT-US95-09307-13	Sequence 13, Appl
37	26	36.6	23	1	US-08-383-753-27	Sequence 27, Appl
38	26	36.6	23	2	US-08-586-772-27	Sequence 27, Appl
39	26	36.6	23	2	US-08-959-512-27	Sequence 27, Appl
40	26	36.6	23	3	US-09-512-983-27	Sequence 27, Appl
41	25	35.2	12	4	US-09-842-164A-10	Sequence 10, Appl
42	25	35.2	14	4	US-09-053-611-29	Sequence 29, Appl
43	25	35.2	15	4	US-09-053-611-19	Sequence 19, Appl
44	25	35.2	15	4	US-09-009-953-244	Sequence 244, App
45	25	35.2	15	4	US-09-073-009-39	Sequence 39, Appl

ALIGNMENTS

RESULT 1
US-09-255-501-106
; Sequence 106, Application US/09255501
; Patent No. 6596525
; GENERAL INFORMATION:
; APPLICANT: Batell, David
; TITLE OF INVENTION: MUTANT PROTEINS HAVING LOWER ALLERGENIC RESPONSE IN HUMANS AND METHODS FOR CONSTRUCTING, IDENTIFYING AND
; TITLE OF INVENTION: PRODUCING SUCH PROTEINS
; FILE REFERENCE: GC527
; CURRENT APPLICATION NUMBER: US/09/255,501
; CURRENT FILING DATE: 1999-02-23
; NUMBER OF SEQ ID NOS: 211
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 106
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-255-501-106

Query Match	40.8%;	Score 29;	DB 4;	Length 15;
Best Local Similarity	40.0%;	Pred. No. 1.1e+02;		
Matches	4;	Conservative	3;	Mismatches 3; Indels 0; Gaps 0;
QY	2	SLDASIIWAM 11		
DB	6	TLQADVLMQM 15		
RESULT 2				
US-09-255-501-107				
; Sequence 107, Application US/09255501				
; Patent No. 6596525				
; GENERAL INFORMATION:				
; APPLICANT: Batell, David				
; TITLE OF INVENTION: MUTANT PROTEINS HAVING LOWER ALLERGENIC RESPONSE IN HUMANS AND METHODS FOR CONSTRUCTING, IDENTIFYING AND				
; TITLE OF INVENTION: PRODUCING SUCH PROTEINS				
; FILE REFERENCE: GC527				
; CURRENT APPLICATION NUMBER: US/09/255,501				
; CURRENT FILING DATE: 1999-02-23				
; NUMBER OF SEQ ID NOS: 211				
; SOFTWARE: Patentin Ver. 2.1				
; SEQ ID NO 107				
; LENGTH: 15				
; TYPE: PRT				

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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 296
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-1308-296

Query Match 39.4%; Score 28; DB 10; Length 20;
Best Local Similarity 50.0%; Pred. No. 6.6e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Caps 0;

Qy 2 SLDASIIWAM 11
||:||||:
Db 5 SLRTVIWAL 14

RESULT 15

US-10-189-123-26
; Sequence 26, Application US/10189123
; Publication No. US20030082586A1
; GENERAL INFORMATION:
; APPLICANT: KIRST, Susan J.
; APPLICANT: HOLTZMAN, Douglas A.
; APPLICANT: FRASER, Christopher C.
; APPLICANT: SHARP, John D.
; APPLICANT: BARNES, Thomas S.
; TITLE OF INVENTION: ANTIBODIES HAVING DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; FILE REFERENCE: 10147-1103
; CURRENT APPLICATION NUMBER: US/10/189,123
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-189-123-26

Query Match 39.4%; Score 28; DB 14; Length 20;
Best Local Similarity 50.0%; Pred. No. 6.6e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Caps 0;

Qy 2 SLDASIIWAM 11
||:||||:
Db 5 SLRTVIWAL 14

Search completed: November 14, 2004, 12:26:59
Job time : 33.0638 secs

RESULT 11
US-10-225-567A-1338
; Sequence 1338, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR FILING DATE: 2001-12-19
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1338
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-1338

Query Match 40.8%; Score 29; DB 14; Length 20;
Best Local Similarity 55.6%; Pred. No. 4.4e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 5 ASIIWAMQ 13
| | | | |
Db 1 ARIIWSLRQ 9

RESULT 12
US-10-280-066-90
; Sequence 90, Application US/10280066
; Publication No. US20030180718A1
; GENERAL INFORMATION:
; APPLICANT: Pillutla, Renuka C.
; APPLICANT: Brissette, Renee
; APPLICANT: Spruyt, Michael
; APPLICANT: Dedova, Olga
; APPLICANT: Blume, Arthur J.
; APPLICANT: Prendergast, John
; APPLICANT: Goldstein, Neil I.
; TITLE OF INVENTION: TARGET SPECIFIC SCREENING AND ITS USE FOR IDENTIFYING TARGET BIND
; FILE REFERENCE: 2598-4009US1
; CURRENT APPLICATION NUMBER: US/10/280,066
; CURRENT FILING DATE: 2002-10-24
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 537
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 90
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Escherichia coli
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: DGI-2-20R-4-E6
US-10-280-066-90

Query Match 40.8%; Score 29; DB 14; Length 20;
Best Local Similarity 62.5%; Pred. No. 4.4e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 4 DASIIWAM 11
| | | | |
Db 5 DAGMIWFM 12

RESULT 13
US-10-296-734-1234
; Sequence 1234, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1234
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: GAGE-1 segment 9
US-10-296-734-1234

Query Match 40.8%; Score 29; DB 14; Length 20;
Best Local Similarity 62.5%; Pred. No. 4.4e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 4 DASIIWAM 11
| | | | |
Db 5 DAGMIWFM 12

RESULT 14
US-09-759-130B-296
; Sequence 296, Application US/09759130B
; Publication No. US20030022279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirt, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; FILE REFERENCE: MPI00-5350MNIM
; CURRENT APPLICATION NUMBER: US/09/759,130B
; CURRENT FILING DATE: 2002-09-16
; PRIOR FILING DATE: 2000-01-07
; PRIOR FILING DATE: 2000-04-27
; PRIOR FILING DATE: 2000-05-24
; PRIOR FILING DATE: 2000-07-14
; PRIOR FILING DATE: 1999-06-14
; PRIOR FILING DATE: 2000-07-14
; PRIOR FILING DATE: 2000-07-14
; PRIOR FILING DATE: 1999-06-29
; PRIOR FILING DATE: 2000-06-30
; PRIOR FILING DATE: 2000-06-30
; PRIOR FILING DATE: 1999-09-10
; PRIOR FILING DATE: 2000-06-23
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460

; SEQ ID NO 294
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homosapiens
US-10-657-022-294

Query Match 40.8%; Score 29; DB 16; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 IHWAMQON 14
|.:|:|
Db 2 ILWLLMNN 9

RESULT 7
US-10-657-022-299
; Sequence 299, Application US/10657022
; Publication No. US20040180354A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Liu, Liping
; APPLICANT: Liu, Zheng
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: MANNK.032A
; CURRENT APPLICATION NUMBER: US/10/657,022
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: 60/409123
; PRIOR FILING DATE: 2002-09-06
; NUMBER OF SEQ ID NOS: 610
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 299
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homosapiens
US-10-657-022-299

Query Match 40.8%; Score 29; DB 16; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 IHWAMQON 14
|.:|:|
Db 1 ILWLLMNN 8

RESULT 8
US-10-657-022-301
; Sequence 301, Application US/10657022
; Publication No. US20040180354A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Liu, Liping
; APPLICANT: Liu, Zheng
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: MANNK.032A
; CURRENT APPLICATION NUMBER: US/10/657,022
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: 60/409123
; PRIOR FILING DATE: 2002-09-06
; NUMBER OF SEQ ID NOS: 610
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 301
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homosapiens
US-10-657-022-301

Query Match 40.8%; Score 29; DB 16; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 IHWAMQON 14
|.:|:|
Db 2 ILWLLMNN 9

RESULT 9
US-10-176-791A-76
; Sequence 76, Application US/10176791A
; Publication No. US20030237101A1
; GENERAL INFORMATION:
; APPLICANT: WEHRLE-HALLER, BERNHARD M.
; APPLICANT: IMHOF, BEAT A.
; TITLE OF INVENTION: Basolateral Sorting Signal and
; TITLE OF INVENTION: Inhibitors Thereof
; FILE REFERENCE: 50275/002001
; CURRENT APPLICATION NUMBER: US/10/176,791A
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: PCT/EP00/13141
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: PCT/CH99/00624
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 76
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Junction of Tac-Tyr Chimera
US-10-176-791A-76

Query Match 40.8%; Score 29; DB 14; Length 17;
Best Local Similarity 66.7%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TSLDASIIW 9
|.:|:|
Db 5 TDLQASRIW 13

RESULT 10
US-10-657-022-606
; Sequence 606, Application US/10657022
; Publication No. US20040180354A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Liu, Liping
; APPLICANT: Liu, Zheng
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: MANNK.032A
; CURRENT APPLICATION NUMBER: US/10/657,022
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: 60/409123
; PRIOR FILING DATE: 2002-09-06
; NUMBER OF SEQ ID NOS: 610
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 606
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homosapiens
US-10-657-022-606

Query Match 40.8%; Score 29; DB 16; Length 18;
Best Local Similarity 50.0%; Pred. No. 4e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 IHWAMQON 14
|.:|:|
Db 6 ILWLLMNN 13

Publication No. US20030144492A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et. al
; TITLE OF INVENTION: 101 Human Secreted Proteins
; FILE REFERENCE: PZ017P1
; CURRENT APPLICATION NUMBER: US/10/195,730
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: US/09/281,976
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: 60/060,837
; PRIOR FILING DATE: 1997-10-02
; PRIOR APPLICATION NUMBER: 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 390
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 319
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-195-730-319

Query Match 47.9%; Score 34; DB 14; Length 22;
Best Local Similarity 50.0%; Pred. No. 65;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 TSLDASIWA 10
:|:|:|:
Db 4 STLDRSVIS 13

RESULT 3

US-10-799-747-319
; Sequence 319, Application US/10799747
; Publication No. US20040157258A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et. al
; TITLE OF INVENTION: 101 Human Secreted Proteins
; FILE REFERENCE: PZ017P1
; CURRENT APPLICATION NUMBER: US/10/799,747
; CURRENT FILING DATE: 2004-03-15
; PRIOR APPLICATION NUMBER: US/10/195,730
; PRIOR FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: US/09/281,976
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: 60/060,837
; PRIOR FILING DATE: 1997-10-02
; PRIOR APPLICATION NUMBER: 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 390
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 319
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-799-747-319

Query Match 47.9%; Score 34; DB 16; Length 22;
Best Local Similarity 50.0%; Pred. No. 65;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 TSLDASIWA 10
:|:|:|:
Db 4 STLDRSVIS 13

RESULT 4

US-10-657-022-295
; Sequence 295, Application US/10657022
; Publication No. US20040180354A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Liu, Liping

APPLICANT: Liu, Zheng
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: MANK.032A
; CURRENT APPLICATION NUMBER: US/10/657,022
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: 60/409123
; PRIOR FILING DATE: 2002-09-06
; NUMBER OF SEQ ID NOS: 610
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 295
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homosapiens
US-10-657-022-295

Query Match 40.8%; Score 29; DB 16; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 IIVAMQON 14
|:|:|:
Db 1 ILWLLMNN 8

RESULT 5

US-10-657-022-300
; Sequence 300, Application US/10657022
; Publication No. US20040180354A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Liu, Liping
; APPLICANT: Liu, Zheng
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: MANK.032A
; CURRENT APPLICATION NUMBER: US/10/657,022
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: 60/409123
; PRIOR FILING DATE: 2002-09-06
; NUMBER OF SEQ ID NOS: 610
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 300
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homosapiens
US-10-657-022-300

Query Match 40.8%; Score 29; DB 16; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 IIVAMQON 14
|:|:|:
Db 1 ILWLLMNN 8

RESULT 6

US-10-657-022-294
; Sequence 294, Application US/10657022
; Publication No. US20040180354A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Liu, Liping
; APPLICANT: Liu, Zheng
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: MANK.032A
; CURRENT APPLICATION NUMBER: US/10/657,022
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: 60/409123
; PRIOR FILING DATE: 2002-09-06
; NUMBER OF SEQ ID NOS: 610
; SOFTWARE: FastSeq for Windows Version 4.0

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OM protein - protein search, using sw model

Run on: November 14, 2004, 12:03:21 ; Search time 33,0638 Seconds
(without alignments)
149.815 Million cell updates/sec

Title: US-09-831-253F-6

Perfect score: 71

Sequence: 1 TSLDASIIWAMQN 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1568699 seqs, 353819137 residues

Total number of hits satisfying chosen parameters: 294451

Minimum DB seq length: 0

Maximum DB seq length: 23

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US07_PUB_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
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12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	50.7	22	16 US-10-742-379-441	Sequence 441, App
2	34	47.9	22	14 US-10-195-730-319	Sequence 319, App
3	34	47.9	22	16 US-10-799-747-319	Sequence 319, App
4	29	40.8	9	16 US-10-657-022-295	Sequence 295, App
5	29	40.8	9	16 US-10-657-022-295	Sequence 300, App
6	29	40.8	10	16 US-10-657-022-294	Sequence 294, App
7	29	40.8	10	16 US-10-657-022-299	Sequence 299, App
8	29	40.8	10	16 US-10-657-022-301	Sequence 301, App
9	29	40.8	17	14 US-10-176-791A-76	Sequence 76, Appl
10	29	40.8	18	16 US-10-657-022-606	Sequence 606, App
11	29	40.8	20	14 US-10-225-567A-1338	Sequence 1338, Ap
12	29	40.8	20	14 US-10-280-066-90	Sequence 90, Appl
13	29	40.8	22	15 US-10-296-734-1234	Sequence 1234, Ap

14	28	39.4	20	10 US-09-759-130B-296	Sequence 296, App
15	28	39.4	20	14 US-10-189-123-26	Sequence 26, Appl
16	28	39.4	20	14 US-10-188-495-26	Sequence 26, Appl
17	28	39.4	20	16 US-10-741-790-296	Sequence 296, Appl
18	27	38.0	7	9 US-09-758-128-41	Sequence 41, Appl
19	27	38.0	7	9 US-09-758-128-44	Sequence 44, Appl
20	27	38.0	7	9 US-09-758-426-41	Sequence 41, Appl
21	27	38.0	7	9 US-09-758-426-44	Sequence 44, Appl
22	27	38.0	7	9 US-09-758-198-41	Sequence 41, Appl
23	27	38.0	7	9 US-09-758-198-44	Sequence 44, Appl
24	27	38.0	7	10 US-09-861-661-41	Sequence 41, Appl
25	27	38.0	7	10 US-09-861-661-44	Sequence 44, Appl
26	27	38.0	11	9 US-09-832-723-35	Sequence 35, Appl
27	27	38.0	11	14 US-10-303-331-35	Sequence 35, Appl
28	27	38.0	15	9 US-09-073-009-38	Sequence 38, Appl
29	27	38.0	15	9 US-09-023-588-38	Sequence 38, Appl
30	27	38.0	15	9 US-09-793-306-38	Sequence 38, Appl
31	27	38.0	15	14 US-10-346-162-42	Sequence 42, Appl
32	27	38.0	15	14 US-10-346-162-123	Sequence 123, App
33	27	38.0	18	14 US-10-125-869A-28	Sequence 28, Appl
34	27	38.0	18	15 US-10-462-262-252	Sequence 252, App
35	27	38.0	20	14 US-10-372-735-39	Sequence 39, Appl
36	27	38.0	20	15 US-10-608-541-39	Sequence 39, Appl
37	26	36.6	9	15 US-10-362-597A-77	Sequence 77, Appl
38	26	36.6	9	16 US-10-407-481-77	Sequence 77, Appl
39	26	36.6	9	17 US-10-816-476-77	Sequence 77, Appl
40	26	36.6	10	15 US-10-362-597A-13	Sequence 13, Appl
41	26	36.6	10	16 US-10-407-481-13	Sequence 13, Appl
42	26	36.6	10	17 US-10-816-476-13	Sequence 13, Appl
43	26	36.6	12	9 US-09-840-277-67	Sequence 67, Appl
44	26	36.6	12	15 US-10-609-217-149	Sequence 149, App
45	26	36.6	12	15 US-10-632-388-149	Sequence 149, App

ALIGNMENTS

RESULT 1
US-10-742-379-441
; Sequence 441, Application US/10742379
; Publication No. US20040181033A1
; GENERAL INFORMATION:
; APPLICANT: Han, HQ
; APPLICANT: Min, Hosung
; APPLICANT: Boone, Thomas Charles
; TITLE OF INVENTION: BINDING AGENTS WHICH INHIBIT MYOSTATIN
; FILE REFERENCE: A-828 (US)
; CURRENT APPLICATION NUMBER: US/10/742,379
; CURRENT FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: US 60/435,923
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 634
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 441
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Myostatin Binding Peptide
US-10-742-379-441

Query Match 50.7%; Score 36; DB 16; Length 22;
Best Local Similarity 38.5%; Pred. No. 29;
Matches 5; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 TSLDASIIWAMQ 13
||| ||| :|| :||
Db 1 TSDRMSILLWELLE 13

RESULT 2
US-10-195-730-319
; Sequence 319, Application US/10195730

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Pending Appl.
Interference
Searches

Query Match 32.4%; Score 23; DB 2; Length 23;
 Best Local Similarity 25.0%; Pred. No. 5.3e+03;
 Matches 3; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TSLDASIIWMM 12
 | : : : : :
 Db 12 TIINRLFWAI 23

RESULT 15

Q9UEK9 PRELIMINARY; PRT; 23 AA.
 AC Q9UEK9;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Keratin (Fragment).
 GN Name=KRT5;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=96121606; PubMed=8595431;
 RA Matsuki M., Hashimoto K., Yoshikawa K., Yasuno H., Yamanishi K.;
 RT "Epidermolysis bullosa simplex (Weber-Cockayne) associated with a
 RT novel missense mutation of Asp328 to Val in Linker 12 domain of
 RT keratin 5.";
 RL Hum. Mol. Genet. 4:1999-2000(1995).
 DR EMBL; D50665; BAA09320.1; -;
 DR GO; GO:0005882; C:intermediate filament; IEA.
 KW Keratin.
 FT NON TER 1 1
 FT NON TER 23 23
 SQ SEQUENCE 23 AA; 2546 MW; 6BA5FPB4FC7E511E CRC64;

Query Match 32.4%; Score 23; DB 2; Length 23;
 Best Local Similarity 36.4%; Pred. No. 5.3e+03;
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 4 DASIIWMMON 14
 | : : : : :
 Db 5 DTSVLSMDNN 15

Search completed: November 14, 2004, 12:07:34
 Job time : 38.383 secs

RESULT 13			
ID	Q80GP4	PRELIMINARY;	PRT; 22 AA.
AC	Q80GP4;		
DT	01-JUN-2003 (TREMBLrel. 24, Created)		
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)		
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)		
DE	Gene 7.		
GN	Name=gene 7;		
OS	Human rotavirus A.		
OC	Viruses; dsRNA viruses; Reoviridae; Rotavirus.		
OX	NCBI_TaxID=10941;		
LN	[1]		
RN	SEQUENCE FROM N.A.		
RC	STRAIN=wa;		
RX	MEDLINE=92352338; PubMed=1339264;		
RY	Mendez E., Arias C.F., Lopez S.;		
RT	"Genomic rearrangements in human rotavirus strain Wa; analysis of		
RT	rearranged RNA segment 7.,";		
RL	Arch. Virol. 125:331-338(1992).		
DR	EMBL; S41238; AAP13880.1; -.		
GO	GO:0003723; F:RNA binding; IEA.		
DR	InterPro; IPR002873; Rota_NSP3.		
SQ	SEQUENCE 22 AA; 2242 MW; 22CC217A1F6BD3AA CRC64;		
Query Match 32.4%; Score 23; DB 2; Length 22;			
Best Local Similarity 40.0%; Pred. No. 5e+03;			
Matches	4; Conservative	4; Mismatches	2; Indels 0; Gaps
QY	1 TSLDASIWA 10		
	:::		
DB	8 TSFEAAVVA 17		
RESULT 14			
ID	Q758F9	PRELIMINARY;	PRT; 23 AA.
AC	Q758F9;		
DT	01-WAR-2004 (TREMBLrel. 26, Created)		
DT	01-WAR-2004 (TREMBLrel. 26, Last sequence update)		
DT	01-WAR-2004 (TREMBLrel. 26, Last annotation update)		
DE	Predicted protein.		
GN	Name=NCU05174.1;		
OS	Neurospora crassa.		
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;		
OX	Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.		
LN	NCBI_TaxID=5141;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=OR74A;		
RA	Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,		
RA	Jaffe D., FitzHugh W., Ma L.-J., Smarnov S., Purcell S., Rahman B.,		
RA	Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,		
RA	Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,		
RA	Selitretnikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,		
RA	Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,		
RA	Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,		
RA	Kamal M., Kamysells M., Maucell C., Rudd S., Frisman D.,		
RA	Kryatova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,		
RA	Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,		
RA	DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,		
RA	Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,		
RA	Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,		
RA	Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.,		
RT	"The Genome Sequence of the Filamentous Fungus Neurospora crassa."		
RL	Nature 0:0-0(2003).		
CC	-!- CAUTION: The sequence shown here is derived from an		
CC	EMBL/GenBank/DBS whole genome shotgun (WGS) entry which is		

Best Local Similarity 50.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 DASIIW 9
| | | | |
Db 10 DESVLW 15

RESULT 7

Q9S818 ID Q9S818 PRELIMINARY; PRT; 18 AA.
AC Q9S818; (Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE 40 kDa PI 8.5 ABCSSSIC acid-induced protein (Fragment).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoidae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE.
RX MEDLINE=95175599; PubMed=7870812;
RA Moons A., Bauw G., Prinsen E., Van Montagu M., Van der Straeten D.;
RT "Molecular and physiological responses to abscisic acid and salts in
roots of salt-sensitive and salt-tolerant indica rice varieties.";
RL Plant Physiol. 107:177-186(1995).
DR Gramine; Q9S818; -.
SQ SEQUENCE 18 AA; 2097 MW; 146450D9A97E6D83 CRC64;

Query Match 35.2%; Score 25; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 DASIIW 9
| | | | |
Db 10 DESVLW 15

RESULT 8

Q9Zy83 ID Q9Zy83 PRELIMINARY; PRT; 18 AA.
AC Q9Zy83; (Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome oxidase II (Fragment).
OS Xylocopa virginica (Carpenter bee).
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Xylocopa.
OX NCBI_TaxID=28638;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95152621; PubMed=10028295;
RA Downton M., Austin A.D.;
RT "Evolutionary dynamics of a mitochondrial rearrangement 'hot spot' in
the hymenoptera.";
RL Mol. Biol. Evol. 16:298-309(1999).
DR ENBL; AF082318; AAD1778.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 1
SQ SEQUENCE 18 AA; 2202 MW; F695A5FD1C36CA16 CRC64;

Query Match 33.8%; Score 24; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 2.6e+03;
Matches 7; Conservative 1; Mismatches 4; Indels 2; Gaps 1;

QY 1 TSLDASIWMQW 14
| | | | |
| | | | |

Db 6 TSYDLFINW--MKN 17

RESULT 9

Q69074 ID Q69074 PRELIMINARY; PRT; 17 AA.
AC Q69074; (Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HSV-1 glycoprotein C (Fragment).
OS Human herpesvirus 1 (HHV-1) (Human herpes simplex virus 1).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10298;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87089706; PubMed=3025606;
RA Homa F.L., Otal T.M., Glorioso J.C., Levine M.;
RT "Transcriptional control signals of a herpes simplex virus type 1 late
(gamma-2) gene lie within bases -34 to +124 relative to the 5'
terminus of the mRNA.";
RL Mol. Cell. Biol. 6:3652-3666(1986).
DR ENBL; M14128; AAA45784.1; -.
FT NON TER 17
SQ SEQUENCE 17 AA; 1868 MW; B4ED3CEC6ABAEC92 CRC64;

Query Match 32.4%; Score 23; DB 2; Length 17;
Best Local Similarity 25.0%; Pred. No. 3.8e+03;
Matches 2; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 5 ASIIVAMM 12
| | | | |
Db 9 AVVLMSLL 16

RESULT 10

Q7MOC6 ID Q7MOC6 PRELIMINARY; PRT; 19 AA.
AC Q7MOC6; (Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cytochrome P450-C-M/F, hepatic (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RX MEDLINE=88163652; PubMed=3349056;
RA Sugita O., Sassa S., Miyairi S., Fishman J., Kubota I., Noguchi T.,
RA Kappas A.;
RT "Cytochrome P-450-C-M/F, a new constitutive form of microsomal
cytochrome P-450 in male and female rat liver with estrogen 2- and 16-
alpha-hydroxylase activity.";
RL Biochemistry 27:678-686(1988).
DR PIR; A28702; A28702.
FT NON TER 19
SQ SEQUENCE 19 AA; 2242 MW; FF1DD2C9CDF9C8FA CRC64;

Query Match 32.4%; Score 23; DB 2; Length 19;
Best Local Similarity 60.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 IWAMM 12
| | | | |
Db 8 LWAVM 12

RESULT 11

Q9S8L0 ID Q9S8L0 PRELIMINARY; PRT; 21 AA.

DR GO; GO:0005739; C-mitochondrion; IEA.
KW Mitochondrion.
FT NON TER
SQ SEQUENCE 19 AA; 2291 MW; B964CCC7FDAC36C3 CRC64;

Query Match 38.0%; Score 27; DB 2; Length 19;
Best Local Similarity 42.9%; Pred. No. 7.4e+02;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 TSLDASIIWAMQON 14
|||:|:|:|:
DB 6 TSLNSFFNKLKMFN 19

RESULT 3
Q9TWP7 PRELIMINARY; PRT; 20 AA.
AC Q9TWP7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Cathepsin B-like cysteine protease (Fragment).
OS Leishmania mexicana.
OC Eukaryota; Euzoenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5665;
RN [1]
RP SEQUENCE.
RX MEDLINE=94187801; PubMed=8139620;
RA Robertson C.D., Coombs G.H.;
RT "Cathepsin B-like cysteine proteases of Leishmania mexicana."
RL Mol. Biochem. Parasitol. 62:271-279(1993).
SQ SEQUENCE 20 AA; 2203 MW; FE1A260FA1DBE41F CRC64;

Query Match 38.0%; Score 27; DB 2; Length 20;
Best Local Similarity 60.0%; Pred. No. 7.8e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 SLDASIIWAM 11
|||:|:|:|:
DB 5 SFDASEKQPM 14

RESULT 4
Q8ZS29 PRELIMINARY; PRT; 18 AA.
AC Q8ZS29
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein PAE3501a.
GN Name=PAE3501a;
OS Pyrobaculum aerophilum.
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
OC Thermoproteaceae; Pyrobaculum.
OX NCBI_TaxID=13773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IM2 / DSM 7523;
RX MEDLINE=21664397; PubMed=11792869;
RA Fitz-Gibbon S.T., Ladher H., Kim U.-J., Stetter K.O., Simon M.I.,
RA Miller J.H.;
RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
aerophilum";
RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
RL EMBL; AE009934; AL64964.1; --
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 18 AA; 2262 MW; BCF4D6923A98943 CRC64;

Query Match 36.6%; Score 26; DB 2; Length 18;
Best Local Similarity 40.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 LDASIIWAM 12

DB 1 MDESIVWPIV 10
|||:|:|:|:

RESULT 5
Q25012 PRELIMINARY; PRT; 22 AA.
AC Q25012
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein HP0225.
GN OrderedLocusNames=HP0225;
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=26695 / ATCC 700392;
RX MEDLINE=97394467; PubMed=9252185; DOI=10.1038/41483;
RA Tomb J.-P., White O., Kervatage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S.R.,
RA Dougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness E.F.,
RA Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.J., Khalak H.G.,
RA Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams M.D.,
RA Hickey E.K., Berg D.E., Gocayne J.D., Uterback T.R., Peterson J.D.,
RA Kelley J.M., Cotton M.D., Weidman J.F., Fujii C., Bowman C.,
RA Watthey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D.,
RA Smith H.O., Fraser C.M., Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
pylori";
RL Nature 388:539-547(1997).
DR EMBL; AE000542; RAD07297.1; --
DR FIR; A64548; A64548.
DR TIGR; HP0225; --
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 22 AA; 2624 MW; 9B98024022F049BE CRC64;

Query Match 36.6%; Score 26; DB 2; Length 22;
Best Local Similarity 25.0%; Pred. No. 1.3e+03;
Matches 2; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 7 IIVAMQON 14
|||:|:|:|:
DB 9 VLVWILKN 16

RESULT 6
Q9S817 PRELIMINARY; PRT; 18 AA.
AC Q9S817
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE 40 kDa PI 8.5 ABSCISSIC acid-induced histidine rich protein
DE (Fragment).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartioideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE.
RX MEDLINE=95175599; PubMed=7870812;
RA Moons A., Bauw G., Prinsen E., Van Montagu M., Van der Straeten D.;
RT "Molecular and physiological responses to abscisic acid and salts in
RT roots of salt-sensitive and salt-tolerant Indica rice varieties.";
RL Plant Physiol. 107:177-186(1995).
DR Gramene; Q9S817; --
SQ SEQUENCE 18 AA; 2094 MW; OCD245DB237E7520 CRC64;

Query Match 35.2%; Score 25; DB 2; Length 18;

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OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:26 ; Search time 37.383 Seconds
(without alignments)
215.479 Million cell updates/sec

Title: US-09-831-253F-6
Perfect score: 71
Sequence: 1 TSLDASIIWAMQN 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 17482

Minimum DB seq length: 0
Maximum DB seq length: 23

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 02:.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	39.4	23	Q9UR71	Q9ur71 lentinula e
2	27	38.0	19	Q9ZYW5	Q9zyw5 jarra phoro
3	27	38.0	20	Q9TWP7	Q9twp7 leishmania
4	26	36.6	18	Q8ZS29	Q8zsz9 pyrobaculum
5	26	36.6	22	O25012	O25012 helicobacte
6	25	35.2	18	Q9S817	Q9s817 oryza sativ
7	25	35.2	18	Q9S818	Q9s818 oryza sativ
8	24	33.8	18	Q9ZY83	Q9zy83 xylocopa vi
9	23	32.4	17	Q69074	Q69074 human herpe
10	23	32.4	19	Q7M0C6	Q7m0c6 rattus norv
11	23	32.4	21	Q9S8L0	Q9s8l0 cucumis sat
12	23	32.4	22	Q38287	Q38287 lactococcus
13	23	32.4	22	Q80GP4	Q80gp4 human rotav
14	23	32.4	23	Q7S8F9	Q7s8f9 neurospora
15	23	32.4	23	Q9UEK9	Q9uek9 homo sapien
16	23	32.4	23	Q8HA22	Q8ha22 bacterioph
17	23	32.4	23	Q07939	Q07939 nicotiana t
18	22	31.0	10	Q9ESU5	Q9eus5 mus musculu
19	22	31.0	11	Q77894	Q77894 oreochromis
20	22	31.0	11	Q77898	Q77898 oreochromis
21	22	31.0	11	Q7MIU2	Q7miu2 oryza sativ
22	22	31.0	14	Q99902	Q99902 homo sapien
23	22	31.0	15	Q8HIF6	Q8hif6 trichophyto
24	22	31.0	15	Q8HIF8	Q8hif8 arthroderma
25	22	31.0	17	LPW_AZOB	P50871 azospirillum
26	22	31.0	17	Q6LAP9	Q6lap9 homo sapien
27	22	31.0	17	CAA65527	CAA65527 homo sapi
28	22	31.0	19	Q7S645	Q7s645 neurospora
29	22	31.0	19	Q8W128	Q8w128 scaevola pr
30	22	31.0	19	Q9QV70	Q9qv70 rattus sp.
31	22	31.0	20	Q49132	Q49132 methylobact

32 22 31.0 21 2 Q6LERS
33 22 31.0 21 2 Q9PRQ1
34 22 31.0 21 2 BAA0902
35 22 31.0 22 2 Q6YID4
36 22 31.0 22 2 AAN52159
37 22 31.0 23 2 Q8NPF7
38 21 29.6 8 2 Q86SL0
39 21 29.6 10 1 APE CAPGI
40 21 29.6 10 2 Q7MIJ3
41 21 29.6 11 2 Q77895
42 21 29.6 14 2 Q9RSQ6
43 21 29.6 15 2 Q8SL36
44 21 29.6 16 2 Q9TWC0
45 21 29.6 16 2 Q9AXW2

Q6ler5 homo sapien
Q9prq1 oncorhynchu
Baa0902 homo sapi
Q6yid4 theromyzo
Aan52159 theromyzo
Q8nfp7 homo sapien
Q86sl0 homo sapien
P80474 capnocytoph
Q7mlj3 spinacia ol
Q77895 oreochromis
Q9rsq6 burkholderi
Q8sl36 monanthesi
Q9twc0 acanthamoeb
Q9axw2 brassica na

ALIGNMENTS

RESULT 1
Q9UR71 PRELIMINARY; PRT; 23 AA.
ID Q9UR71 AC Q9UR71;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE 5'-nucleotide-forming nuclease (Fragment).
OS Lentinula edodes (Shiitake mushroom) (Lentinus edodes).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Agaricales; Tricholomataceae; Lentinula.
OX NCBI_TaxID=5353;
RN [1]
RP SEQUENCE.
RA MEDLINE=95337563; PubMed=7613009;
RX Kobayashi H., Inokuchi N., Koyama T., Tomita M., Irie M.;
RT "Purification and characterization of the 2nd 5'-nucleotide-forming
RT nuclease from Lentinus edodes";
RL Biosci. Biotechnol. Biochem. 59:1169-1171(1995).
DR PIR; PC4030; PC4030.
DR InterPro; IPR008947; PLC Nuclease.
SQ SEQUENCE 23 AA; 2535 MW; 978082B3B161FCC6 CRC64;

Query Match 39.4%; Score 28; DB 2; Length 23;
Best Local Similarity 50.0%; Pred. No. 5.9e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 SLDASIIW 9
DB 16 ALDPSFVW 23

RESULT 2
Q9ZYW5 PRELIMINARY; PRT; 19 AA.
ID Q9ZYW5 AC Q9ZYW5;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome oxidase II (Fragment).
OS Jarra phorocantha.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonidea;
OC Braconidae; Doryctinae; Jarra.
OX NCBI_TaxID=64830;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=99152621; PubMed=10028295;
RA Downton M., Austin A.D.;
RT "Evolutionary dynamics of a mitochondrial rearrangement 'hot spot' in
RT the hymenoptera";
RL Mol. Biol. Evol. 16:298-309(1999).
DR EMBL; AF034596; AAC79744.1; -.

TELEPHONE: 415-496-2300
TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-485-508-50

Query Match 39.4%; Score 28; DB 1; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 SIWAMMQ 13
: : : : :
Db 5 NMLWNMQ 12

RESULT 9
US-08-241-054-5
; Sequence 5, Application US/08241054
; Patent No. 5643873
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Cwirla, Steven E.
; APPLICANT: Dower, William J.
; APPLICANT: Koller, Kerry J.
; APPLICANT: Lee, Jung
; APPLICANT: Martens, Christine L.
; APPLICANT: Ruhland-Fritsch, Beatrice
; TITLE OF INVENTION: Peptides and Compounds That Bind
; TITLE OF INVENTION: Peptides and Compounds That Bind
; TITLE OF INVENTION: Selectins Including Endothelium Leukocyte Adhesion
; TITLE OF INVENTION: Molecule 1
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/241,054
; FILING DATE: 11-MAY-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,295
; FILING DATE: 05-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/881,395
; FILING DATE: 06-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Gerald F. Swiss
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 000324-002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-7400
; TELEFAX: 415-854-8275
; INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-241-054-5

Query Match 36.6%; Score 26; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 IWAMMQ 13
: : : : :
Db 7 LWDMMQ 12

RESULT 10
US-08-390-156A-76
; Sequence 76, Application US/08390156A
; Patent No. 5648458
; GENERAL INFORMATION:
; APPLICANT: Cwirla, Steven E.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Dower, William J.
; APPLICANT: Martens, Christine L.
; TITLE OF INVENTION: Peptides and Compounds That Bind to
; TITLE OF INVENTION: ELAM-1
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies, N.V.
; STREET: 4001 Miranda Ave.
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,156A
; FILING DATE: 16-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,295
; FILING DATE: 05-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/881,395
; FILING DATE: 06-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Swiss, Gerald F.
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 1023.1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-390-156A-76

Query Match 36.6%; Score 26; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 IWAMMQ 13
: : : : :
Db 7 LWDMMQ 12

RESULT 11
US-08-439-817-4
; Sequence 4, Application US/08439817
; Patent No. 5728802
; GENERAL INFORMATION:

/ APPLICANT: Barrett, Ronald W.
/ APPLICANT: Cwirla, Steven E.
/ APPLICANT: Dower, William J.
/ APPLICANT: Koller, Kerry J.
/ APPLICANT: Lee, Jung
/ APPLICANT: Martens, Christine L.
/ APPLICANT: Ruhland-Fritsch, Beatrice
/ TITLE OF INVENTION: Peptides and Compounds That Bind
/ TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion
/ TITLE OF INVENTION: Molecule I (ELAM-1)
/ NUMBER OF SEQUENCES: 209
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Affymax Technologies, NV
/ STREET: 4001 Miranda Ave.
/ CITY: Palo Alto
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC Compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION NUMBER: US/08/439,817
/ FILING DATE: 12-MAY-1995
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/241,054
/ FILING DATE: 11-MAY-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/057,295
/ FILING DATE: 05-MAY-1993
/ APPLICATION NUMBER: US 07/881,395
/ FILING DATE: 06-MAY-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Stevens, Lauren L.
/ REGISTRATION NUMBER: 36,691
/ REFERENCE/DOCKET NUMBER: 000324-046/1056.1
/ TELEPHONE: 415-496-2300
/ TELEFAX: 415-424-0832
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 12 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-439-817-4

Query Match 36.6%; Score 26; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 IWAMQ 13
DB 7 LWDMMQ 12

RESULT 12
US-08-485-508-5
/ Sequence 5, Application US/08485508
/ Patent No. 5786322
/ GENERAL INFORMATION:
/ APPLICANT: Barrett, Ronald W.
/ APPLICANT: Cwirla, Steven E.
/ APPLICANT: Dower, William J.
/ APPLICANT: Koller, Kerry J.
/ APPLICANT: Lee, Jung
/ APPLICANT: Martens, Christine L.
/ APPLICANT: Ruhland-Fritsch, Beatrice

/ TITLE OF INVENTION: Peptides and Compounds That Bind
/ TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion
/ TITLE OF INVENTION: Molecule I
/ NUMBER OF SEQUENCES: 162
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Affymax Technologies, NV
/ STREET: 4001 Miranda Ave.
/ CITY: Palo Alto
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC Compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION NUMBER: US/08/485,508
/ FILING DATE: Herewith
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/241,054
/ FILING DATE: 11-MAY-1994
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/057,295
/ FILING DATE: 05-MAY-1993
/ APPLICATION NUMBER: US 07/881,395
/ FILING DATE: 06-MAY-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Stevens, Lauren L.
/ REGISTRATION NUMBER: 36,691
/ REFERENCE/DOCKET NUMBER: 000324-002/1056
/ TELEPHONE: 415-496-2300
/ TELEFAX: 415-424-0832
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 12 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-485-508-5

Query Match 36.6%; Score 26; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 IWAMQ 13
DB 7 LWDMMQ 12

RESULT 13
US-09-428-082B-149
/ Sequence 149, Application US/09428082B
/ Patent No. 6660843
/ GENERAL INFORMATION:
/ APPLICANT: FEIGE, ULRICH
/ APPLICANT: LIU, CHUAN-FA
/ APPLICANT: CHEETHAM, JANET C.
/ APPLICANT: BOONE, THOMAS CHARLES
/ TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
/ FILE REFERENCE: A-527
/ CURRENT APPLICATION NUMBER: US/09/428,082B
/ CURRENT FILING DATE: 1999-10-22
/ PRIOR APPLICATION NUMBER: 60/105,371
/ PRIOR FILING DATE: 1998-10-23
/ NUMBER OF SEQ ID NOS: 1133
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 149

; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SELECTIN ANTAGONIST PEPTIDE
US-09-428-082B-149

Query Match 36.6%; Score 26; DB 4; Length 12;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 IWAMMQ 13
Db 7 LWDMMQ 12

RESULT 14

US-09-842-164A-10
; Sequence 10, Application US/09842164A
; Patent No. 6544754
; GENERAL INFORMATION:
; APPLICANT: INOUE, SATOSHI
; TITLE OF INVENTION: LUCIFERASE AND PHOTOPROTEIN
; FILE REFERENCE: 206497US0
; CURRENT APPLICATION NUMBER: US/09/842,164A
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: JP 2000-125053
; PRIOR FILING DATE: 2000-04-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Oplophorus gracilorostris
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (11)..(11)
; OTHER INFORMATION: Xaa = any amino acid
US-09-842-164A-10

Query Match 35.2%; Score 25; DB 4; Length 12;
Best Local Similarity 41.7%; Pred. No. 4e+02;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 SLDASIIWAMMQ 13
Db 1 NLDPAVFHAMXQ 12

RESULT 15

US-09-053-611-29
; Sequence 29, Application US/09053611
; Patent No. 6410245
; GENERAL INFORMATION:
; APPLICANT: No. 6410245throp, Jeffrey P.
; APPLICANT: Hart, Charles P.
; APPLICANT: Schatz, Peter J.
; APPLICANT: Glaxo Group Limited
; TITLE OF INVENTION: Compositions and Methods for Detecting Ligand Dependent
; FILE REFERENCE: 2064
; CURRENT APPLICATION NUMBER: US/09/053,611
; CURRENT FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Selected clone
US-09-053-611-29

Query Match 35.2%; Score 25; DB 4; Length 14;
Best Local Similarity 42.9%; Pred. No. 4.7e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 SIIWAMM 12
Db 5 SLLWKML 11

Search completed: November 14, 2004, 13:46:47
Job time : 27.5 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: November 14, 2004, 11:57:25 ; Search time 8.6383 Seconds
(without alignments)
155.938 Million cell updates/sec

Title: US-09-831-253F-6
Perfect score: 71
Sequence: 1 TSLDASIIWAMQON 14
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 4495

Minimum DB seq length: 0
Maximum DB seq length: 23

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	39.4	23	2 PC4030	rRNA endonuclease
2	26	36.6	14	2 A35105	hypothetical prote
3	26	36.6	22	2 A64548	hypothetical prote
4	24	33.8	22	2 S07966	T-cell receptor be
5	23	32.4	19	2 A28702	cytochrome P450-C
6	23	32.4	20	2 PH1326	Ig heavy chain DJ
7	23	32.4	23	2 T03261	glutamate-ammonia
8	22	31.0	11	2 PQ0731	unidentified 5.7/3
9	22	31.0	12	2 S69123	proton-translocati
10	22	31.0	19	2 B46592	lactase-phlorizin
11	22	31.0	20	2 A44921	hydroxypruvate re
12	22	31.0	21	2 S62893	cold-inducible pro
13	22	31.0	22	2 PQ0007	killer toxin - yea
14	21	29.6	7	2 PT0586	T-cell receptor be
15	21	29.6	10	2 S69159	cystathionine gamm
16	21	29.6	12	2 I64829	gene HEXA protein
17	21	29.6	14	2 PH1327	Ig heavy chain DJ
18	21	29.6	14	2 A44920	2-halobenzoate 1,2
19	21	29.6	19	2 T49422	L-lactate dehydrog
20	21	29.6	20	2 DIRT	dental fluid tra
21	20	28.2	15	2 PH1769	T cell receptor al
22	20	28.2	14	2 A45103	7 alpha-hydroxy-4-
23	20	28.2	19	2 S61279	nikkomycin synthe
24	20	28.2	19	2 S29212	protein C - oat (f
25	20	28.2	20	2 S50175	kallikrein (PK-120
26	20	28.2	21	2 B59325	probable bacteriop
27	20	28.2	22	2 I58038	MHC class I transp
28	20	28.2	23	2 S34739	trans-cinnamate 4-
29	19.5	27.5	21	2 S01816	hemoglobin BIV - t

30	19	26.8	6	2 PT0519	T-cell receptor be
31	19	26.8	7	2 S09652	hypothetical prote
32	19	26.8	7	2 PH1602	Ig H chain V-D-J r
33	19	26.8	10	2 S62248	processing enzyme,
34	19	26.8	14	2 PH1768	T cell receptor al
35	19	26.8	15	2 PH0782	T-cell receptor al
36	19	26.8	15	2 PL0109	complement factor
37	19	26.8	16	2 A46236	transforming prote
38	19	26.8	20	2 AC0269	probable trp opero
39	19	26.8	21	2 S23361	protein-tyrosine k
40	19	26.8	21	2 A44139	RNA-polymerase- α
41	18	25.4	6	2 S66195	alcohol dehydrogen
42	18	25.4	9	2 S13889	phosphoenolpyruvat
43	18	25.4	10	2 D61440	polylactatase
44	18	25.4	11	2 S66196	alcohol dehydrogen
45	18	25.4	12	2 PN0581	tyrosine 3-monoxy

ALIGNMENTS

RESULT 1
PC4030
rRNA endonuclease (EC 3.1.27.10) - shiitake mushroom (fragment)
N;Alternate names: nuclease Le3
C;Species: Lentinula edodes (shiitake mushroom)
C;Date: 21-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: PC4030
R;Kobayashi, H.; Inokuchi, N.; Koyama, T.; Tomita, M.; Irie, M.
Bioeci. Biotechnol. Biochem. 59, 1169-1171, 1995
A;Title: Purification and characterization of the 2nd 5'-nucleotide-forming nuclease fr.
A;Reference number: PC4030; MUID:95337563; PMID:7613009
A;Accession: PC4030
A;Molecule type: DNA
A;Residues: 1-23 <KOB>
A;Cross-references: UNIPROT:Q9UR71
C;Comment: This enzyme has 3'-nucleotidase activity.
C;Keywords: endonuclease; hydrolase

Query Match 39.4%; Score 28; DB 2; Length 23;
Best Local Similarity 50.0%; Pred. No. 81;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 SLDASIIW 9
:|:|:|:
Db 16 ALDPSFW 23

RESULT 2
A35105
hypothetical protein - Neurospora crassa mitochondrion (fragment)
C;Species: mitochondrion Neurospora crassa
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 07-Dec-1999
C;Accession: A35105
R;Saville, B.J.; Collins, R.A.
Cell 61, 685-696, 1990
A;Title: A site-specific self-cleavage reaction performed by a novel RNA in neurospora
A;Reference number: A35105; MUID:90263093; PMID:2160856
A;Accession: A35105
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-14 <SAV>
C;Genetics:
C;Genome: mitochondrion
A;Genetic code: SGC3
C;Keywords: mitochondrion

Query Match 36.6%; Score 26; DB 2; Length 14;
Best Local Similarity 37.5%; Pred. No. 11e+02;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 6 SIIWAMQ 13
|:|:|:
|:|:|:

```

Db      2 SFLWTLQ 9

RESULT 3
A64548
hypothetical protein HP0225 - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C>Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C:Accession: A64548
R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A>Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467; PMID:9252185
A:Accession: A64548
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-22 <TOM>
A:Cross-references: UNIPROT:O25012; GB:AE000542; GB:AE000511; NID:g2313310; PIDN:AAD0729

Query Match      36.6%; Score 26; DB 2; Length 22;
Best Local Similarity 25.0%; Pred. No. 1.8e+02;
Matches 2; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY      7 IIVMMQN 14
      :|:|:|
Db      9 VLWVILKN 16

RESULT 4
S07966
T-cell receptor beta chain V-D-J region (clone 15 BEM 21) - mouse (fragment)
C:Species: Mus musculus (house mouse)
A:Variety: strain C57BL/10
C>Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 23-Jul-1999
C:Accession: S07966; S08057
R:Bill, J.; Yaguee, J.; Appel, V.B.; White, J.; Horn, G.; Erlich, H.A.; Palmer, E.
J. Exp. Med. 169, 115-133, 1989
A>Title: Molecular genetic analysis of 178 I-A(bm12)-reactive T cells.
A:Reference number: S05590; MUID:89080476; PMID:2783331
A:Accession: S07966
A:Molecule type: mRNA
A:Residues: 1-22 <BIL>
A:Cross-references: EMBL:X14936
A>Note: this sequence was determined from the differentiated gene
R:Bill, J.
submitted to the EMBL Data Library, April 1989
A:Reference number: S08057
A:Accession: S08057
A:Molecule type: mRNA
A:Residues: 1-19, 21-22 <BIW>
A:Cross-references: EMBL:X14936; PIDN:CAA33062.1; PID:g773251
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor
F;1-4/Domain: V region (V-beta 14) (fragment) #status predicted <VRE>
F;6-7/Domain: D region #status predicted <DRE>
F;8-21/Domain: J region (J-beta 1.1) #status predicted <JRE>

Query Match      33.8%; Score 24; DB 2; Length 22;
Best Local Similarity 50.0%; Pred. No. 4.4e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      9 WAMQON 14
      :|:|
Db      3 WSLRQN 8

RESULT 5
A28702
cytochrome P450-C-M/F, hepatic - rat (fragment)
N:Contains: oxidoreductase (EC 1.-.-.-)

C:Species: Rattus norvegicus (Norway rat)
C>Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
C:Accession: A28702
R:Sugita, O.; Sassa, S.; Miyairi, S.; Fishman, J.; Kubota, I.; Noguchi, T.; Kappas, A.
Biochemistry 27, 678-686, 1988
A>Title: Cytochrome P-450-C-M/F, a new constitutive form of microsomal cytochrome P-450
A:Reference number: A28702; MUID:88163652; PMID:3349056
A:Accession: A28702
A:Molecule type: protein
A:Residues: 1-19 <SUG>
A:Cross-references: UNIPROT:Q7MOC6
C:Genetics:
A:Gene: CYP2D
C:Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C:Keywords: electron transfer; heme; liver; monoxygenase; oxidoreductase; transmembrane

Query Match      32.4%; Score 23; DB 2; Length 19;
Best Local Similarity 60.0%; Pred. No. 5.7e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      8 IWAMM 12
      :|:|
Db      8 LWAVM 12

RESULT 6
PH1326
Ig heavy chain DJ region (clone C515-116) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PH1326
R:Wasserman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A>Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A:Reference number: PH1302; MUID:93094761; PMID:1460419
A:Accession: PH1326
A:Molecule type: DNA
A:Residues: 1-20 <WAS>
C:Keywords: heterotetramer; immunoglobulin

Query Match      32.4%; Score 23; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 6e+02;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      2 SLDASIIWMMQ 13
      :|:|:|
Db      9 SNDAPDIWQQGQ 20

RESULT 7
T03261
glutamate-ammonia ligase (EC 6.3.1.2), cytosolic - common tobacco (fragment)
N:Alternate names: glutamine synthetase
C:Species: Nicotiana tabacum (common tobacco)
C>Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C:Accession: T03261
R:Hirel, B.; Marsollier, M.C.; Hoarau, A.; Hoarau, J.; Brangeon, J.; Schafer, R.; Verma,
Plant Mol. Biol. 20, 207-218, 1992
A>Title: Forcing expression of a soybean root glutamine synthetase gene in tobacco leave
A:Reference number: Z14867; MUID:93004474; PMID:1356501
A:Accession: T03261
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-23 <HIR>
A:Cross-references: UNIPROT:Q07939; EMBL:X68604; NID:g312275; PIDN:CAA48594.1; PID:g3122
C:Superfamily: glutamate-ammonia ligase
C:Keywords: cytosol; ligase

Query Match      32.4%; Score 23; DB 2; Length 23;
Best Local Similarity 50.0%; Pred. No. 7.1e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      4 DASIIW 9

```

Db 16 DPTILW 21

RESULT 8

PQ0731

unidentified 5.7/35K protein [imported] - rice (fragment)
C;Species: Oryza sativa (rice)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: PQ0731
R;Komatsu, S.; Kajiura, H.; Hirano, H.
Theor. Appl. Genet. 86, 935-942, 1993
A;Title: A rice protein library; a data-file of rice proteins separated by two-dimensional

A;Reference number: PQ0696

A;Accession: PQ0731

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <KOW>

A;Cross-references: UNIPROT:Q7M1U2

Query Match 31.0%; Score 22; DB 2; Length 11;
Best Local Similarity 40.0%; Pred. No. 4.7e+02;

Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 5 ASIIW 9

| : | : |

Db 1 ATVVW 5

RESULT 9

S69123

proton-translocating transhydrogenase - Rhodospirillum rubrum (fragment)
C;Species: Rhodospirillum rubrum
C;Date: 10-Mar-1998 #sequence_revision 24-Apr-1998 #text_change 24-Apr-1998
C;Accession: S69123
R;Diggle, C.; Hutton, M.; Jones, G.R.; Thomas, C.M.; Jackson, J.B.
Eur. J. Biochem. 228, 719-726, 1995

A;Title: Properties of the soluble polypeptide of the proton-translocating transhydrogenase
A;Reference number: S69123; MUID:95255277; PMID:7737169

A;Accession: S69123

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-12 <DIG>

Query Match 31.0%; Score 22; DB 2; Length 12;
Best Local Similarity 22.2%; Pred. No. 5.2e+02;

Matches 2; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 5 ASIIWMMQ 13

| : | : |

Db 2 ADVVVKVQR 10

RESULT 10

B46592

lactase-phlorizin hydrolase 140K isoform - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)

C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 01-Nov-1996

C;Accession: B46592

R;Dudley, M.A.; Hachey, D.L.; Quaroni, A.; Hutchens, T.W.; Nichols, B.L.; Rosenberger, J.

J. Biol. Chem. 268, 13609-13616, 1993

A;Title: In vivo sucrose-isomaltase and lactase-phlorizin hydrolase turnover in the fed

A;Reference number: A46592; MUID:93293888; PMID:8514793

A;Accession: B46592

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-19 <DUD>

A;Note: sequence extracted from NCBI backbone (NCBIP:134560)

C;Keywords: carbohydrate digestion; intestine

Query Match 31.0%; Score 22; DB 2; Length 19;
Best Local Similarity 60.0%; Pred. No. 8.8e+02;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 ASIIW 9

| : | : |

Db 12 AKIVW 16

RESULT 11

A44921

hydroxypyruvate reductase (EC 1.1.1.81) - Methylobacterium extorquens (fragment)
C;Species: Methylobacterium extorquens
C;Date: 01-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C;Accession: A44921
R;Chistoserdova, L.V.; Lidstrom, M.E.
J. Bacteriol. 174, 71-77, 1992

A;Title: Cloning, mutagenesis, and physiological effect of a hydroxypyruvate reductase

A;Reference number: A44921; MUID:92104992; PMID:1729225

A;Contents: AM1

A;Accession: A44921

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-20 <CHI>

A;Cross-references: GB:M81443; NID:G150010; PIDN:AAA25378.1; PID:G150011

A;Note: sequence extracted from NCBI backbone (NCBIN:75202, NCBIP:75203)

C;Keywords: oxidoreductase

Query Match 31.0%; Score 22; DB 2; Length 20;
Best Local Similarity 66.7%; Pred. No. 9.3e+02;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SLDASI 7

| : | : |

Db 12 SLDATV 17

RESULT 12

S62893

cold-inducible protein, 70K - rainbow trout (fragment)
C;Species: Oncorhynchus mykiss (rainbow trout)

C;Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 09-Jul-2004

C;Accession: S62893

R;Yamashita, M.; Ojima, N.; Sakamoto, T.

FEBS Lett. 382, 261-264, 1996

A;Title: Induction of proteins in response to cold acclimation of rainbow trout cells.

A;Reference number: S62893; MUID:96184500; PMID:8605981

A;Accession: S62893

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-21 <YAM>

A;Cross-references: UNIPROT:Q9PRQ1

Query Match 31.0%; Score 22; DB 2; Length 21;
Best Local Similarity 37.5%; Pred. No. 9.8e+02;

Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 7 IIVAMQON 14

| : | : |

Db 14 LIWGAHAN 21

RESULT 13

PQ0007

killer toxin - yeast (Pichia farinosa) (fragment)

C;Species: Pichia farinosa

C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004

C;Accession: PQ0007

R;Suzuki, C.; Nikkuni, S.

Agric. Biol. Chem. 53, 2599-2604, 1989

A;Title: Purification and properties of the killer toxin produced by a halotolerant yeast

A;Reference number: PQ0007

A;Accession: PQ0007

A;Molecule type: protein

A;Residues: 1-22 <SUZ>

A;Cross-references: UNIPROT:P19972

A;Experimental source: strain KK1

A;Note: the full activity of this toxin depends on NaCl or KCl

Query Match 31.0%; Score 22; DB 2; Length 22;
Best Local Similarity 37.5%; Pred. No. 1e+03;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 DASIIWAM 11
:|:|:|:
Db 2 EATIIWGV 9

RESULT 14

PT0586

T-cell receptor beta chain V-D-J region (141-1CN) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C;Accession: PT0586; PT0592

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0586

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-7 <FE>

A;Experimental source: day 19 fetal thymus, strain BALB/c (clones 141-1CN and 141-1CD)

C;Keywords: T-cell receptor

Query Match 29.6%; Score 21; DB 2; Length 7;
Best Local Similarity 80.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ASIIW 9
|||
Db 1 ASSIW 5

RESULT 15

S69159

cystathionine gamma-synthase - spinach (fragment)

C;Species: Spinacia oleracea (spinach)

C;Date: 12-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004

C;Accession: S69159

R;Ravanel, S.; Droux, M.; Douce, R.

Arch. Biochem. Biophys. 316, 572-584, 1995

A;Title: Methionine biosynthesis in higher plants. I. Purification and characterization

A;Reference number: S69159; MUID:95142682; PMID:7840669

A;Accession: S69159

A;Molecule type: protein

A;Residues: 1-10 <RAV>

A;Cross-references: UNIPROT:Q7MLJ3

C;Keywords: chloroplast

Query Match 29.6%; Score 21; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 TSLDASII 8
|:|:|:
Db 2 TAVDAAAI 9

Search completed: November 14, 2004, 12:03:13
Job time : 9.6383 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:25 ; Search time 40.5106 Seconds
(without alignments)
123.973 Million cell updates/sec

Title: US-09-831-253F-6

Perfect score: 71

Sequence: 1 TSLDASIIWMMQN 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 718658

Minimum DB seq length: 0

Maximum DB seq length: 23

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: A_Geneseq_23Sep04.*
- 2: Geneseqp1980s.*
- 3: Geneseqp1990s.*
- 4: Geneseqp2000s.*
- 5: Geneseqp2001s.*
- 6: Geneseqp2002s.*
- 7: Geneseqp2003as.*
- 8: Geneseqp2003bs.*
- 9: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	71	100.0	14	3 AAY93098	Aay93098 Transform
2	71	100.0	14	3 AAY92950	Aay92950 Transform
3	50	70.4	12	3 AAY93009	Aay93009 Transform
4	50	70.4	12	3 AAY92947	Aay92947 Transform
5	50	70.4	12	3 AAY93008	Aay93008 Transform
6	40	56.3	12	3 AAY93093	Aay93093 Transform
7	37	52.1	11	3 AAY93094	Aay93094 Transform
8	37	52.1	12	3 AAY93010	Aay93010 Transform
9	33	46.5	14	4 AAB88161	Aab88161 CD66 pept
10	31	43.7	21	4 AAB88161	Aab88161 CD66 pept
11	30	42.3	15	2 AAB88161	Aab88161 CD66 pept
12	30	42.3	15	2 AAB88161	Aab88161 CD66 pept
13	29	40.8	9	8 ADM73036	Adm73036 Human GAG
14	29	40.8	9	8 ADM73041	Adm73041 Human GAG
15	29	40.8	10	8 ADM73042	Adm73042 Human GAG
16	29	40.8	10	8 ADM73040	Adm73040 Human GAG
17	29	40.8	10	8 ADM73035	Adm73035 Human GAG
18	29	40.8	12	3 AAY93007	Aay93007 Transform
19	29	40.8	15	3 AAY54720	Aay54720 Human sub
20	29	40.8	15	3 AAY54721	Aay54721 Human sub
21	29	40.8	15	3 AAY67084	Aay67084 Human pro
22	29	40.8	15	3 AAY67083	Aay67083 Human pro
23	29	40.8	15	4 AAU38622	Aau38622 Human sub
24	29	40.8	15	4 AAU38623	Aau38623 Human sub
25	29	40.8	15	5 AABG91198	Abg91198 Peptide a

ALIGNMENTS

RESULT 1

AA93098

ID AAY93098 standard; peptide; 14 AA.

AC AAY93098;

XX XX

DT 08-NOV-2000 (first entry)

XX XX

DE Transforming growth factor inhibitory peptide P144.

XX XX

KW Hepatotrophic; antagonist; transforming growth factor betaf; TGF-bi;
KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW extracellular matrix degradation inhibitor; mimotope; cirrhosis.

OS Homo sapiens.

XX XX

PN WO200031135-A1.

XX XX

PD 02-JUN-2000.

XX XX

PF 23-NOV-1999; 99WO-ES000375.

XX XX

PR 24-NOV-1998; 98ES-00002465.

XX XX

(CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.

XX XX

PI Ezquerro Saenz JJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;

XX XX

PI Borras Cuesta F;

XX XX

WPI; 2000-411935/35.

XX XX

PT Peptides that antagonize binding of transforming growth factor betaf.

XX XX

PT useful for treatment of liver disease, especially cirrhosis, are partial

XX XX

PT sequences of the factor or its receptors.

XX XX

PS Disclosure; Page 31; 86pp; Spanish.

XX XX

CC The invention relates to synthetic peptides that antagonise the binding

XX XX

CC of transforming growth (TGF) factor betaf (TGF-b1) to its receptor in

XX XX

CC vivo which have partial amino acid sequences identical, or similar, with

XX XX

CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent

XX XX

CC examples of the peptides of the invention. The peptides act by

XX XX

CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.

XX XX

CC they are inhibitors of stimulation of collagen synthesis in liver cells

XX XX

CC and inhibitors of synthesis of proteolytic enzymes able to degrade the

XX XX

CC extracellular matrix. The peptides, their mimetopes and/or DNA (or

XX XX

CC expression systems) encoding the peptides are used for treatment of liver

XX XX

CC disease, specifically cirrhosis

```

XX
SQ Sequence 14 AA;
Query Match 100.0%; Score 71; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLDASIIWAMQON 14
Db 1 TSLDASIIWAMQON 14

RESULT 2
AAY92950
ID AAY92950 standard; peptide; 14 AA.
XX
AC AAY92950;
XX
XX
DT 08-NOV-2000 (first entry)
XX
DE Transforming growth factor inhibitory peptide #6.
XX
KW Hepatotropic; antagonist; transforming growth factor beta1; TGF-beta1;
KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX
XX Homo sapiens.
XX
XX WO200031135-A1.
XX
XX 02-JUN-2000.
XX
XX 23-NOV-1999; 99WO-ES000375.
XX
XX 24-NOV-1998; 98ES-00002465.
XX
XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
XX
XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
XX Borrás Cuesta F;
XX
XX WPI; 2000-411935/35.
XX
XX Peptides that antagonize binding of transforming growth factor beta1,
XX useful for treatment of liver disease, especially cirrhosis, are partial
XX sequences of the factor or its receptors.
XX
XX Claim 7; Page 81; 86pp; Spanish.
XX
XX The invention relates to synthetic peptides that antagonise the binding
XX of transforming growth (TGF) factor beta1 (TGF-beta1) to its receptor in
XX vivo which have partial amino acid sequences identical, or similar, with
XX those of TGF-beta1 and/or its receptors. Peptides AAY92945-Y93133 represent
XX examples of the peptides of the invention. The peptides act by
XX competitive inhibition of the binding of TGF-beta1 to its receptors, e.g.
XX they are inhibitors of stimulation of collagen synthesis in liver cells
XX and inhibitors of synthesis of proteolytic enzymes able to degrade the
XX extracellular matrix. The peptides, their mimetopes and/or DNA (or
XX expression systems) encoding the peptides are used for treatment of liver
XX disease, specifically cirrhosis
XX
XX Sequence 14 AA;
Query Match 100.0%; Score 71; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLDASIIWAMQON 14
Db 1 TSLDASIIWAMQON 14

RESULT 3
AAY92947
ID AAY92947 standard; peptide; 12 AA.
XX
AC AAY92947;
XX
XX
DT 08-NOV-2000 (first entry)
XX
DE Transforming growth factor inhibitory peptide #3.
XX
KW Hepatotropic; antagonist; transforming growth factor beta1; TGF-beta1;
KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX
XX

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```

AAY93009
ID AAY93009 standard; peptide; 12 AA.
XX
AC AAY93009;
XX
XX
DT 08-NOV-2000 (first entry)
XX
DE Transforming growth factor inhibitory peptide P55.
XX
KW Hepatotropic; antagonist; transforming growth factor beta1; TGF-beta1;
KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX
XX Rattus sp.
XX
XX WO200031135-A1.
XX
XX 02-JUN-2000.
XX
XX 23-NOV-1999; 99WO-ES000375.
XX
XX 24-NOV-1998; 98ES-00002465.
XX
XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
XX
XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
XX Borrás Cuesta F;
XX
XX WPI; 2000-411935/35.
XX
XX Peptides that antagonize binding of transforming growth factor beta1,
XX useful for treatment of liver disease, especially cirrhosis, are partial
XX sequences of the factor or its receptors.
XX
XX Disclosure; Page 27; 86pp; Spanish.
XX
XX The invention relates to synthetic peptides that antagonise the binding
XX of transforming growth (TGF) factor beta1 (TGF-beta1) to its receptor in
XX vivo which have partial amino acid sequences identical, or similar, with
XX those of TGF-beta1 and/or its receptors. Peptides AAY92945-Y93133 represent
XX examples of the peptides of the invention. The peptides act by
XX competitive inhibition of the binding of TGF-beta1 to its receptors, e.g.
XX they are inhibitors of stimulation of collagen synthesis in liver cells
XX and inhibitors of synthesis of proteolytic enzymes able to degrade the
XX extracellular matrix. The peptides, their mimetopes and/or DNA (or
XX expression systems) encoding the peptides are used for treatment of liver
XX disease, specifically cirrhosis
XX
XX Sequence 12 AA;
Query Match 70.4%; Score 50; DB 3; Length 12;
Best Local Similarity 75.0%; Pred. No. 0.046;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 SLDASIIWAMQO 13
Db 1 SLDATWIIWMMQ 12

RESULT 4
AAY92947
ID AAY92947 standard; peptide; 12 AA.
XX
AC AAY92947;
XX
XX
DT 08-NOV-2000 (first entry)
XX
DE Transforming growth factor inhibitory peptide #3.
XX
KW Hepatotropic; antagonist; transforming growth factor beta1; TGF-beta1;
KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX
XX

```

OS Homo sapiens.
 XX WO200031135-A1.
 XX
 PD 02-JUN-2000.
 XX
 XX 23-NOV-1999; 99WO-ES000375.
 PF
 XX 24-NOV-1998; 98ES-00002465.
 PR
 XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
 PA
 XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
 PI Borrás Cuesta F;
 XX WPI; 2000-411935/35.
 DR
 XX Peptides that antagonize binding of transforming growth factor betal,
 XX useful for treatment of liver disease, especially cirrhosis, are partial
 PT sequences of the factor or its receptors.
 PT
 XX Claim 4; Page 80; 86pp; Spanish.
 PS
 XX The invention relates to synthetic peptides that antagonise the binding
 CC of transforming growth (TGF) factor betal (TGF-b1) to its receptor in
 CC vivo which have partial amino acid sequences identical, or similar, with
 CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
 CC examples of the peptides of the invention. The peptides act by
 CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
 CC they are inhibitors of stimulation of collagen synthesis in liver cells
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
 CC expression systems) encoding the peptides are used for treatment of liver
 CC disease, specifically cirrhosis
 XX
 SQ Sequence 12 AA;
 Query Match 70.4%; Score 50; DB 3; Length 12;
 Best Local Similarity 75.0%; Pred. No. 0.046;
 Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TSLDASIIWMM 12
 Db 1 TSLDATMIWTMM 12
 |||||:|
 |||||:|
 RESULT 5
 AAY93008
 ID AAY93008 standard; peptide; 12 AA.
 XX
 AC AAY93008;
 XX
 DT 08-NOV-2000 (first entry)
 XX
 DE Transforming growth factor inhibitory peptide P54.
 XX
 KW Hepatotropic; antagonist; transforming growth factor betal; TGF-b1;
 KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
 KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
 XX
 OS Rattus sp.
 XX
 XX WO200031135-A1.
 PN
 XX 02-JUN-2000.
 PD
 XX 23-NOV-1999; 99WO-ES000375.
 PF
 XX 24-NOV-1998; 98ES-00002465.
 PR
 XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
 PA
 XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
 PI Borrás Cuesta F;
 XX WPI; 2000-411935/35.
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 XX Peptides that antagonize binding of transforming growth factor betal,
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 PT sequences of the factor or its receptors.
 PT
 XX Claim 4; Page 80; 86pp; Spanish.
 PS
 XX The invention relates to synthetic peptides that antagonise the binding
 CC of transforming growth (TGF) factor betal (TGF-b1) to its receptor in
 CC vivo which have partial amino acid sequences identical, or similar, with
 CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
 CC examples of the peptides of the invention. The peptides act by
 CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
 CC they are inhibitors of stimulation of collagen synthesis in liver cells
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
 CC expression systems) encoding the peptides are used for treatment of liver
 CC disease, specifically cirrhosis
 XX
 SQ Sequence 12 AA;
 Query Match 70.4%; Score 50; DB 3; Length 12;
 Best Local Similarity 75.0%; Pred. No. 0.046;
 Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TSLDASIIWMM 12
 Db 1 TSLDATMIWTMM 12
 |||||:|
 |||||:|
 RESULT 6
 AAY93093
 ID AAY93093 standard; peptide; 12 AA.
 XX
 AC AAY93093;
 XX
 DT 08-NOV-2000 (first entry)
 XX
 DE Transforming growth factor inhibitory peptide P139.
 XX
 KW Hepatotropic; antagonist; transforming growth factor betal; TGF-b1;
 KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
 KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
 XX
 OS Homo sapiens.
 XX
 XX WO200031135-A1.
 PN
 XX 02-JUN-2000.
 PD
 XX 23-NOV-1999; 99WO-ES000375.
 PF
 XX 24-NOV-1998; 98ES-00002465.
 PR
 XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
 PA
 XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
 PI Borrás Cuesta F;
 XX WPI; 2000-411935/35.
 DR
 XX Peptides that antagonize binding of transforming growth factor betal,
 XX useful for treatment of liver disease, especially cirrhosis, are partial
 PT sequences of the factor or its receptors.
 PT
 XX Claim 4; Page 31; 86pp; Spanish.
 PS
 XX The invention relates to synthetic peptides that antagonise the binding
 CC of transforming growth (TGF) factor betal (TGF-b1) to its receptor in
 CC vivo which have partial amino acid sequences identical, or similar, with
 CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
 CC examples of the peptides of the invention. The peptides act by
 CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
 CC they are inhibitors of stimulation of collagen synthesis in liver cells
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
 CC expression systems) encoding the peptides are used for treatment of liver
 CC disease, specifically cirrhosis
 XX
 SQ Sequence 12 AA;
 Query Match 70.4%; Score 50; DB 3; Length 12;
 Best Local Similarity 75.0%; Pred. No. 0.046;
 Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TSLDASIIWMM 12
 Db 1 TSLDATMIWTMM 12
 |||||:|
 |||||:|

CC those of TGF- β 1 and/or its receptors. Peptides AAY92945-Y93133 represent
 CC examples of the peptides of the invention. The peptides act by
 CC competitive inhibition of the binding of TGF- β 1 to its receptors, e.g.
 CC they are inhibitors of stimulation of collagen synthesis in liver cells
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
 CC expression systems) encoding the peptides are used for treatment of liver
 CC disease, specifically cirrhosis
 XX Sequence 12 AA;

Query Match 56.3%; Score 40; DB 3; Length 12;
 Best Local Similarity 77.8%; Pred. No. 2.7;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLDASIIW 9
 Db 1 TSLDATMIW 9
 |||:|||

RESULT 7
 AAY93094
 ID AAY93094 standard; peptide; 11 AA.
 XX
 AC AAY93094;
 XX
 DT 08-NOV-2000 (first entry)
 XX
 DE Transforming growth factor inhibitory peptide P140.
 XX
 KW Hepatotropic; antagonist; transforming growth factor beta1; TGF- β 1;
 KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
 KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.

XX Homo sapiens.
 XX WO200031135-A1.
 XX
 PD 02-JUN-2000.
 XX
 PF 23-NOV-1999; 99WO-ES000375.
 XX
 PR 24-NOV-1998; 98ES-00002465.
 XX
 PA (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.

XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
 PI Borrás Cuesta F;
 XX
 DR WPI; 2000-411935/35.
 XX
 PT Peptides that antagonize binding of transforming growth factor beta1,
 PT useful for treatment of liver disease, especially cirrhosis, are partial
 PT sequences of the factor or its receptors.
 XX
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 CC of transforming growth (TGF) factor beta1 (TGF- β 1) to its receptor in
 CC vivo which have partial amino acid sequences identical, or similar, with
 CC those of TGF- β 1 and/or its receptors. Peptides AAY92945-Y93133 represent
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 CC competitive inhibition of the binding of TGF- β 1 to its receptors, e.g.
 CC they are inhibitors of stimulation of collagen synthesis in liver cells
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
 CC expression systems) encoding the peptides are used for treatment of liver
 CC disease, specifically cirrhosis

XX Sequence 11 AA;
 Query Match 52.1%; Score 37; DB 3; Length 11;
 Best Local Similarity 66.7%; Pred. No. 8.4;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 4 DASIIWAMQ 12
 Db 3 DATMIWTWM 11
 ||:|||||

RESULT 8
 AAY93010
 ID AAY93010 standard; peptide; 12 AA.

XX
 AC AAY93010;
 XX
 DT 08-NOV-2000 (first entry)
 XX
 DE Transforming growth factor inhibitory peptide P56.
 XX
 KW Hepatotropic; antagonist; transforming growth factor beta1; TGF- β 1;
 KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
 KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.

XX Rattus sp.
 XX WO200031135-A1.
 XX
 PD 02-JUN-2000.
 XX
 PF 23-NOV-1999; 99WO-ES000375.
 XX
 PR 24-NOV-1998; 98ES-00002465.
 XX
 PA (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.

XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
 PI Borrás Cuesta F;
 XX
 DR WPI; 2000-411935/35.
 XX
 PT Peptides that antagonize binding of transforming growth factor beta1,
 PT useful for treatment of liver disease, especially cirrhosis, are partial
 PT sequences of the factor or its receptors.
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 PS Disclosure; Page 27; 86pp; Spanish.

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 CC of transforming growth (TGF) factor beta1 (TGF- β 1) to its receptor in
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 CC those of TGF- β 1 and/or its receptors. Peptides AAY92945-Y93133 represent
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 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
 CC expression systems) encoding the peptides are used for treatment of liver
 CC disease, specifically cirrhosis

XX Sequence 12 AA;

Query Match 52.1%; Score 37; DB 3; Length 12;
 Best Local Similarity 75.0%; Pred. No. 9.2;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 IIWAMQON 14
 Db 1 MIWTMWN 8
 :|||

RESULT 9
 AAB88161
 ID AAB88161 standard; peptide; 14 AA.
 XX
 AC AAB88161;
 XX

DT 17-MAY-2001 (first entry)
 XX CD66 peptide CD66f(11)-10.
 XX
 XX CD66; CEACAM; adhesion molecule; antiviral; antibacterial;
 KW antiinflammatory; cytostatic; neutrophil activation; proliferation;
 KW differentiation; cancer; angiogenesis.
 XX
 XX Unidentified.
 OS
 XX WO200113937-A1.
 PN
 XX 01-MAR-2001.
 PD
 XX
 XX 25-AUG-2000; 2000WO-US023482.
 XX
 XX 26-AUG-1999; 99US-0150791P.
 PR
 XX 02-SEP-1999; 99US-0152501P.
 PR
 XX (SKUB/) SKUBITZ K M.
 PA (SKUB/) SKUBITZ A P N.
 PA
 XX Skubitz KM, Skubitz APN;
 PI
 XX WPI; 2001-234981/24.
 DR
 XX Novel peptides useful for activating neutrophils or blocking activation
 PT of neutrophils, modulating homotypic or heterotypic adhesion of CD66
 PT polypeptides, and modulating immune cell activation.
 XX
 PS Claim 1; Page 54; 102pp; English.
 XX
 CC The present sequence is an isolated peptide that was tested for its
 CC ability to modulate the function of CD66 family polypeptides and CD66
 CC ligands. 106 sequences of 13 or 14 amino acids in length, and their
 CC analogues, were identified that modulate the function of at least one
 CC CD66 family polypeptide and/or at least one ligand of the polypeptide.
 CC The peptides are capable of modulating activation of neutrophils,
 CC activation or inhibition, proliferation and/or differentiation of T-
 CC cells, B-cells, NK cells, LAK cells, dendritic cells, or other immune
 CC system cells, proliferation and/or differentiation of epithelial cells,
 CC homotypic and/or heterotypic adhesion among CD66 family polypeptides and
 CC adhesion of CD66 family polypeptides to other ligands. The peptides are
 CC useful for delivering a therapeutically active agent to a patient, for
 CC modifying the metastasis of malignant cells, for altering bacterial or
 CC viral binding to cells or a biomaterial, for altering cell adhesion to a
 CC biomaterial, for detecting tumours, for detecting inflammation, for
 CC detecting a CD66 protein or its ligand, for altering angiogenesis by
 CC contacting endothelial cells, tumour cells or immune cells, for altering
 CC an immune response, and for altering keratinocyte proliferation
 XX
 SQ Sequence 14 AA;
 Query Match 46.5%; Score 33; DB 4; Length 14;
 Best Local Similarity 60.0%; Pred. No. 55;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 2 SLDASIIWAM 11
 :|||:|
 Db 3 TLDASYLWWM 12
 RESULT 10
 ABG25633
 ID ABG25633 standard; protein; 21 AA.
 XX
 AC ABG25633;
 XX
 XX 18-FEB-2002 (first entry)
 DT
 XX Novel human diagnostic protein #25624.
 DE
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW

KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX Homo sapiens.
 XX WO200175067-A2.
 PN
 XX 11-OCT-2001.
 PD
 XX 30-MAR-2001; 2001WO-US008631.
 XX
 XX 31-MAR-2000; 2000US-00540217.
 PR
 XX 23-AUG-2000; 2000US-00649167.
 PR
 XX (HYSE-) HYSEQ INC.
 PA
 XX Drmanac RT, Liu C, Tang YT;
 PI
 XX WPI; 2001-639362/73.
 DR
 XX N-PSDB; AAS89820.
 DR
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 PT
 XX Claim 20; SEQ ID NO 55992; 103pp; English.
 PS
 XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 21 AA;
 Query Match 43.7%; Score 31; DB 4; Length 21;
 Best Local Similarity 42.1%; Pred. No. 1.9e+02;
 Matches 8; Conservative 2; Mismatches 3; Indels 6; Gaps 1;
 QY 1 TSLD-----ASIIWAMQ 13
 :|||:|
 Db 1 TSLDEVOTGKPSLIWISQ 19
 :|||:|
 RESULT 11
 AAR13972
 ID AAR13972 standard; protein; 15 AA.
 XX
 AC AAR13972;
 XX
 XX 25-MAR-2003 (revised)
 DT
 XX 27-NOV-1991 (first entry)
 DT
 XX [Asp14]Melittin-(7-21) (5).
 DE
 XX Bioassay; immunoassay; polystyrene; polyethylene; sheet; carrier;
 KW support; solid-phase.
 KW

11/27/99

XX OS Synthetic.
 XX PN WO9113098-A.
 XX PD 05-SEP-1991.
 XX PF 02-MAR-1990; 90DK-00000559.
 XX PR 02-MAR-1990; 90DK-00000559.
 XX (RISO-) RISO FORSKNINGSCENTER.
 XX PA (RISO-) RISO FORSKNINGSCENTER.
 XX PI Berg RH, Almdal K, Pedersen W, Holm A;
 XX WPI; 1991-281427/38.
 XX PT Polymer substrate with grafted polystyrene chains - functionalised to
 PT attach aminoacid(s), peptide(s) or proteins, for peptide synthesis, bio-
 PT or immunoassays.
 XX PS Disclosure; Fig 3; 92pp; English.
 XX CC Protected melittin-(7-21) and twelve analogs (AAR13969-79) derived by
 CC substitutions in position 12 and 14 were each assembled stepwise on a
 CC labelled sheet. The sheet was an aminomethylated 285% polystyrene-
 CC grafted polyethylene sheet labelled by graphite-based ink. The common
 CC steps of deprotection, neutralisation, washing and coupling of identical
 CC amino acids were performed simultaneously in a single reaction vessel,
 CC while the coupling of different amino acids was carried out in separate
 CC vessels. The polymer substrate serves as an efficient solid-phase carrier
 CC on which the peptide may be synthesised or attached and remain covalently
 CC bound in a stable, permanent manner. The resulting support can be used in
 CC solid-phase bioassays, esp. immunoassays. See also AAR13968-79. (Updated
 CC on 25-MAR-2003 to correct PA field.)
 XX SQ Sequence 15 AA;
 Query Match 42.3%; Score 30; DB 2; Length 15;
 Best Local Similarity 66.7%; Pred. No. 2e+02;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 TSLDASIIW 9
 Db 5 TGLDALISW 13
 RESULT 12
 AAR61463
 ID AAR61463 standard; peptide; 15 AA.
 AC AAR61463;
 XX 16-SEP-1995 (first entry)
 DT [Asp-14] melittin-(7-21) analogue.
 DE Peptide solid phase synthesis; polystyrene-grafted substrate; melittin.
 XX Synthetic.
 XX OS US5373053-A.
 XX PN 13-DEC-1994.
 XX PD 14-DEC-1992; 92US-00990584.
 XX PR 01-SEP-1988; 88US-00239525.
 XX PR 25-AUG-1989; 89US-00398846.
 XX PR 12-MAY-1992; 92US-00882059.
 XX (RISO-) RISO NAT LAB.

XX PI Berg RH, Holm A, Tam JP, Pedersen WB, Merrifield RB, Almdal K;
 XX WPI; 1995-030351/04.
 XX PT substrate grafted with polystyrene - used in peptide synthesis giving
 PT high yields.
 XX PS Example 9; Fig 3; 20pp; English.
 XX CC The invention relates to a solid phase peptide synthesis method using a
 CC support consisting of a functionalised polystyrene-grafted polymer
 CC substrate. The peptides are prepared in high yield and purity. The
 CC process may be used for compartmentalised synthesis of a number of
 CC different peptides in parallel. The present sequence is one of 13
 CC melittin-(7-21) analogues prepared in parallel by the process (AAR61460-
 CC R61470)
 XX SQ Sequence 15 AA;
 Query Match 42.3%; Score 30; DB 2; Length 15;
 Best Local Similarity 66.7%; Pred. No. 2e+02;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 TSLDASIIW 9
 Db 5 TGLDALISW 13
 RESULT 13
 ADM73036
 ID ADM73036 standard; peptide; 9 AA.
 AC ADM73036;
 XX 03-JUN-2004 (first entry)
 DT Human GAGE-1 epitope SEQ ID NO:295.
 XX epitope; epitope cluster; virucide; cytostatic; vaccine; viral infection;
 KW cancer; tumour; human; GAGE-1.
 XX Homo sapiens.
 OS Synthetic.
 XX WO2004022709-A2.
 PN 18-MAR-2004.
 PD 05-SEP-2003; 2003WO-US027706.
 PF 06-SEP-2002; 2002US-0409123P.
 PR (MANN-) MANNKIND CORP.
 PA Simard JLL, Diamond DC, Liu L, Liu Z;
 PI WPI; 2004-315564/29.
 XX New polypeptides and encoding nucleic acids that are useful epitopes of
 PT target-associated antigens, useful for diagnosing and/or treating viral
 PT infections, cancers and tumors.
 XX Claim 1; SEQ ID NO 295; 357pp; English.
 CC The present invention describes a polypeptide (I) comprising a component
 CC selected from: (a) a polypeptide epitope having any of the 503 fully
 CC defined sequences of 8-33 amino acids (SEQ ID NO:108-610); (b) an epitope
 CC cluster comprising the polypeptide of (a); (c) a polypeptide having
 CC substantial similarity to (a) or (b); (d) a polypeptide having functional
 CC similarity to any of (a)-(c); or (e) a nucleic acid encoding the
 CC polypeptide of (a)-(d). (I) has virucide and cytostatic activities, and
 CC can be used in vaccines. The methods and compositions of the present

CC invention are useful for the diagnosis and/or treatment of viral
 CC infections, cancers and tumours. The present sequence is used in the
 CC exemplification of the present invention.

XX SQ Sequence 9 AA;

Query Match 40.8%; Score 29; DB 8; Length 9;
 Best Local Similarity 50.0%; Pred. No. 1.7e+06;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 IIWAMMON 14

Db 1 ILWLLMNN 8

RESULT 14

ADM73041

ID ADM73041 standard; peptide; 9 AA.

XX ADM73041;

XX 03-JUN-2004 (first entry)

XX Human GAGE-1 epitope SEQ ID NO:300.

XX epitope; epitope cluster; virucide; cytostatic; vaccine; viral infection;
 KW cancer; tumour; human; GAGE-1.

XX Homo sapiens.

OS Synthetic.

XX WO2004022709-A2.

PN 18-MAR-2004.

XX 05-SEP-2003; 2003WO-US027706.

XX 06-SEP-2002; 2002US-0409123P.

XX (MANN-) MANNKIND CORP.

PI Simard JYL, Diamond DC, Liu L, Liu Z;

XX WPI; 2004-315564/29.

XX New polypeptides and encoding nucleic acids that are useful epitopes of
 PT target-associated antigens, useful for diagnosing and/or treating viral
 PT infections, cancers and tumors.

PS Claim 1; SEQ ID NO 300; 357pp; English.

XX The present invention describes a polypeptide (I) comprising a component
 CC selected from: (a) a polypeptide epitope having any of the 503 fully
 CC defined sequences of 8-33 amino acids (SEQ ID NO:108-610); (b) an epitope
 CC cluster comprising the polypeptide of (a); (c) a polypeptide having
 CC substantial similarity to (a) or (b); (d) a polypeptide having functional
 CC similarity to any of (a)-(c); or (e) a nucleic acid encoding the
 CC polypeptide of (a)-(d). (I) has virucide and cytostatic activities, and
 CC can be used in vaccines. The methods and compositions of the present
 CC invention are useful for the diagnosis and/or treatment of viral
 CC infections, cancers and tumors. The present sequence is used in the
 CC exemplification of the present invention.

XX SQ Sequence 9 AA;

Query Match 40.8%; Score 29; DB 8; Length 9;

Best Local Similarity 50.0%; Pred. No. 1.7e+06;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 IIWAMMON 14

Db 1 ILWLLMNN 8

RESULT 15

ADM73042

ID ADM73042 standard; peptide; 10 AA.

XX ADM73042;

XX 03-JUN-2004 (first entry)

XX Human GAGE-1 epitope SEQ ID NO:301.

XX epitope; epitope cluster; virucide; cytostatic; vaccine; viral infection;
 KW cancer; tumour; human; GAGE-1.

XX Homo sapiens.

OS Synthetic.

XX WO2004022709-A2.

PN 18-MAR-2004.

XX 05-SEP-2003; 2003WO-US027706.

XX 06-SEP-2002; 2002US-0409123P.

XX (MANN-) MANNKIND CORP.

PI Simard JYL, Diamond DC, Liu L, Liu Z;

XX WPI; 2004-315564/29.

XX New polypeptides and encoding nucleic acids that are useful epitopes of
 PT target-associated antigens, useful for diagnosing and/or treating viral
 PT infections, cancers and tumors.

PS Claim 1; SEQ ID NO 301; 357pp; English.

XX The present invention describes a polypeptide (I) comprising a component
 CC selected from: (a) a polypeptide epitope having any of the 503 fully
 CC defined sequences of 8-33 amino acids (SEQ ID NO:108-610); (b) an epitope
 CC cluster comprising the polypeptide of (a); (c) a polypeptide having
 CC substantial similarity to (a) or (b); (d) a polypeptide having functional
 CC similarity to any of (a)-(c); or (e) a nucleic acid encoding the
 CC polypeptide of (a)-(d). (I) has virucide and cytostatic activities, and
 CC can be used in vaccines. The methods and compositions of the present
 CC invention are useful for the diagnosis and/or treatment of viral
 CC infections, cancers and tumors. The present sequence is used in the
 CC exemplification of the present invention.

XX SQ Sequence 10 AA;

Query Match 40.8%; Score 29; DB 8; Length 10;

Best Local Similarity 50.0%; Pred. No. 2e+02;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 IIWAMMON 14

Db 2 ILWLLMNN 9

Search completed: November 14, 2004, 12:02:12

Job time : 41.5106 secs

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OM protein - protein search, using sw model

Run on: November 14, 2004, 13:04:13 ; Search time 23.3333 Seconds
(without alignments)
42.633 Million cell updates/sec

Title: US-09-831-253F-9
Perfect score: 77
Sequence: 1 LBSLSFQLGLYLSPH 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 157298

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
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3: /cgn2_6/prodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PTUS COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	39.0	15	4	US-09-514-245-55
2	30	39.0	15	4	US-09-514-245-98
3	29	37.7	13	4	US-08-753-750B-64
4	28	36.4	15	4	US-09-514-245-99
5	27	35.1	7	4	US-09-463-239-29
6	27	35.1	9	4	US-09-239-043D-1855
7	27	35.1	10	3	US-08-159-339A-458
8	27	35.1	10	4	US-09-239-043D-620
9	27	35.1	11	4	US-09-239-043D-1944
10	27	35.1	10	4	US-09-239-043D-467
11	27	35.1	11	4	US-09-239-043D-580
12	27	35.1	11	4	US-09-239-043D-1867
13	27	35.1	15	1	US-08-102-738-20
14	27	35.1	15	4	US-09-009-953-264
15	27	35.1	15	4	US-09-239-043D-2188
16	26.5	34.4	12	3	US-09-298-924-19
17	26	33.8	8	3	US-08-913-842-28
18	26	33.8	9	4	US-09-311-784A-271
19	26	33.8	9	4	US-09-601-729-70
20	26	33.8	10	3	US-08-159-339A-472
21	26	33.8	10	3	US-08-159-339A-503
22	26	33.8	12	4	US-09-407-687-34
23	26	33.8	14	1	US-07-914-280-14
24	26	33.8	14	5	PCT-US93-06625-14
25	26	33.8	15	4	US-09-148-712-7
26	25	32.5	8	3	US-08-444-818-557
27	25	32.5	9	1	US-08-336-618-2

28	25	32.5	12	4	US-09-389-956-52	Sequence 52, Appl
29	25	32.5	15	1	US-08-049-783-11	Sequence 11, Appl
30	25	32.5	15	1	US-08-158-232-22	Sequence 22, Appl
31	25	32.5	15	1	US-08-304-626-22	Sequence 22, Appl
32	25	32.5	15	1	US-08-316-301A-23	Sequence 23, Appl
33	25	32.5	15	2	US-08-611-928-22	Sequence 22, Appl
34	25	32.5	15	3	US-09-224-024-5	Sequence 5, Appl
35	25	32.5	15	3	US-09-173-891-22	Sequence 23, Appl
36	25	32.5	15	3	US-09-076-137-23	Sequence 23, Appl
37	25	32.5	15	4	US-09-738-363-23	Sequence 23, Appl
38	25	32.5	15	4	US-09-514-245-151	Sequence 151, App
39	25	32.5	15	4	US-09-514-245-152	Sequence 152, App
40	25	32.5	15	5	PCT-US92-03624-23	Sequence 23, Appl
41	25	32.5	15	5	PCT-US94-07902-5	Sequence 5, Appl
42	24	31.2	8	3	US-08-444-818-558	Sequence 558, App
43	24	31.2	13	1	US-08-290-919-15	Sequence 15, Appl
44	24	31.2	14	1	US-08-798-897-14	Sequence 14, Appl
45	24	31.2	14	2	US-08-978-523-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1

US-09-514-245-55
; Sequence 55, Application US/09514245
; Patent No. 6703023
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Philippe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADSEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS DISEASES
; FILE REFERENCE: 065691/0176
; CURRENT APPLICATION NUMBER: US/09/514,245
; CURRENT FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 55
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Type B PWD circovirus
US-09-514-245-55

Query Match 39.0%; Score 30; DB 4; Length 15;
Best Local Similarity 35.7%; Pred. No. 23;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LBSLSFQLGLYLSP 14

Db 2 VNELRFNIGQLPFP 15

RESULT 2

US-09-514-245-98
; Sequence 98, Application US/09514245
; Patent No. 6703023
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Philippe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine

```
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS DISEASE
; FILE REFERENCE: 065691/0176
; CURRENT APPLICATION NUMBER: US/09/514,245
; CURRENT FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 98
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Type A PWD circovirus
US-09-514-245-98

Query Match 39.0%; Score 30; DB 4; Length 15;
Best Local Similarity 35.7%; Pred. No. 23;
Matches 5; Conservative 4; Mismatches 5; Indels 5; Gaps 0;

QY 1 LBSLSFQLGLYLSP 14
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Db 2 VNELRFNIGQFLPP 15

RESULT 3
US-08-753-750B-64
; Sequence 64, Application US/08753750B
; Patent No. 6610506
; GENERAL INFORMATION:
; APPLICANT: LO, Reggie Y.C.
; APPLICANT: Schryvers, Anthony B.
; TITLE OF INVENTION: TRANSFERRIN BINDING PROTEINS OF
; FILE REFERENCE: A34762 021645.0105
; CURRENT APPLICATION NUMBER: US/08/753,750B
; CURRENT FILING DATE: 1996-11-29
; PRIOR APPLICATION NUMBER: CA 2,164,274
; PRIOR FILING DATE: 1995-12-01
; PRIOR APPLICATION NUMBER: 60/008,569
; PRIOR FILING DATE: 1995-12-01
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Escherichia coli
US-08-753-750B-64

Query Match 37.7%; Score 29; DB 4; Length 13;
Best Local Similarity 66.7%; Pred. No. 31;
Matches 6; Conservative 2; Mismatches 1; Indels 1; Gaps 0;

QY 3 SLSFQLGLY 11
   |||::|||
Db 4 SESWELGLY 12

RESULT 4
US-09-514-245-99
; Sequence 99, Application US/09514245
; Patent No. 6703023
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Philippe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
```

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; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS DISEASE
; FILE REFERENCE: 065691/0176
; CURRENT APPLICATION NUMBER: US/09/514,245
; CURRENT FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 99
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Type A PWD circovirus
US-09-514-245-99

Query Match 36.4%; Score 28; DB 4; Length 15;
Best Local Similarity 45.5%; Pred. No. 58;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 LSFQLGLYLSP 14
   |||::|||
Db 1 LRFNIGQFLPP 11

RESULT 5
US-09-463-239-29
; Sequence 29, Application US/09463239
; Patent No. 6700039
; GENERAL INFORMATION:
; APPLICANT: Jepson, Ian
; APPLICANT: Ebneeth, Marcus
; APPLICANT: Sonnewald, Uwe
; TITLE OF INVENTION: Genetic Method for Controlling Sprouting
; FILE REFERENCE: 109846.178
; CURRENT APPLICATION NUMBER: US/09/463,239
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: PCT/GB98/02023
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: EP 97113118.0
; PRIOR FILING DATE: 1997-07-30
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 29
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence encoding MOT isolated from potato.
US-09-463-239-29

Query Match 35.1%; Score 27; DB 4; Length 7;
Best Local Similarity 85.7%; Pred. No. 3.8e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 FQLGLYL 12
   |||||
Db 1 FQLGLNL 7

RESULT 6
US-09-239-043D-1855
; Sequence 1855, Application US/09239043D
; Patent No. 6689363
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Vitiello, Maria A.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
```

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; APPLICANT: Chesnut, Robert
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; FILE REFERENCE: 2060.0060007
; CURRENT APPLICATION NUMBER: US/09/239,043D
; CURRENT FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/978,291
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: US 08/820,360
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,363
; PRIOR FILING DATE: 1996-03-13
; PRIOR APPLICATION NUMBER: US 08/461,603
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23
; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/197,484
; PRIOR FILING DATE: 1994-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2579
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1855
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Orthohepadnaviridae hepatitis B virus
US-09-239-043D-1855

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Query Match 35.1%; Score 27; DB 4; Length 9;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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QY 8 LGLYLSPH 15
DB 1 LGIHLNPN 8

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RESULT 7
US-08-159-339A-458
; Sequence 458, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-0050300S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 458:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-458

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Query Match 35.1%; Score 27; DB 3; Length 10;
Best Local Similarity 50.0%; Pred. No. 55;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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QY 8 LGLYLSPH 15
DB 2 LGIHLNPN 9

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RESULT 8
US-09-239-043D-620
; Sequence 620, Application US/09239043D
; Patent No. 6689363
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Vitiello, Maria A.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Chesnut, Robert
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; FILE REFERENCE: 2060.0060007
; CURRENT APPLICATION NUMBER: US/09/239,043D
; CURRENT FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/978,291
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: US 08/820,360
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,363
; PRIOR FILING DATE: 1996-03-13
; PRIOR APPLICATION NUMBER: US 08/461,603
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23
; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/197,484
; PRIOR FILING DATE: 1994-02-16

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; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2579
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 620
;   LENGTH: 10
;   TYPE: PRT
; ORGANISM: Orthohepadnaviridae hepatitis B virus
US-09-239-043D-620

Query Match      35.1%; Score 27; DB 4; Length 10;
Best Local Similarity 50.0%; Pred. No. 55;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      8 LGLYLSPH 15
DB      2 LGIHLNPN 9

RESULT 9
US-09-239-043D-1944
; Sequence 1944, Application US/09239043D
; Patent No. 6689363
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Vitello, Maria A.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Chesnut, Robert
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; FILE REFERENCE: 2060.0060007
; CURRENT FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/978,291
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: US 08/820,360
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,363
; PRIOR FILING DATE: 1996-03-13
; PRIOR APPLICATION NUMBER: US 08/461,603
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23
; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/197,484
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2579
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1944
;   LENGTH: 10
;   TYPE: PRT
; ORGANISM: Orthohepadnaviridae hepatitis B virus
US-09-239-043D-1944

Query Match      35.1%; Score 27; DB 4; Length 10;
Best Local Similarity 50.0%; Pred. No. 55;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      8 LGLYLSPH 15
DB      2 LGIHLNPN 9

US-09-239-043D-1944

Query Match      35.1%; Score 27; DB 4; Length 10;
Best Local Similarity 50.0%; Pred. No. 55;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      8 LGLYLSPH 15
DB      2 LGIHLNPN 9
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Db      2 LGIHLNPN 9

RESULT 10
US-09-239-043D-467
; Sequence 467, Application US/09239043D
; Patent No. 6689363
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Vitello, Maria A.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Chesnut, Robert
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; FILE REFERENCE: 2060.0060007
; CURRENT FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/978,291
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: US 08/820,360
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,363
; PRIOR FILING DATE: 1996-03-13
; PRIOR APPLICATION NUMBER: US 08/461,603
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23
; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/197,484
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2579
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 467
;   LENGTH: 11
;   TYPE: PRT
; ORGANISM: Orthohepadnaviridae hepatitis B virus
US-09-239-043D-467

Query Match      35.1%; Score 27; DB 4; Length 11;
Best Local Similarity 50.0%; Pred. No. 62;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      8 LGLYLSPH 15
DB      2 LGIHLNPN 9

RESULT 11
US-09-239-043D-580
; Sequence 580, Application US/09239043D
; Patent No. 6689363
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Vitello, Maria A.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph T.
```

```

; APPLICANT: Grey, Howard M.
; APPLICANT: Chesnut, Robert
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; FILE REFERENCE: Using Peptide and Nucleic Acid Compositions
; CURRENT APPLICATION NUMBER: US 09/239,043D
; PRIORITY FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/978,291
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: US 08/820,360
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,363
; PRIOR FILING DATE: 1996-03-13
; PRIOR APPLICATION NUMBER: US 08/461,603
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23
; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/197,484
; PRIOR FILING DATE: 1994-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2579
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 580
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Orthohepadnaviridae hepatitis B virus
US-09-239-043D-580

Query Match      35.1%; Score 27; DB 4; Length 11;
Best Local Similarity 50.0%; Pred. No. 62;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0

Qy      8 LGLYLSPH 15
Db      3 LGTHLPN 10
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|||::|:|

RESULT 12
US-09-239-043D-1867
; Sequence 1867, Application US/09239043D
; Patent No. 6689363
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Vitello, Maria A.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Chesnut, Robert
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; FILE REFERENCE: 2060.0060007
; CURRENT APPLICATION NUMBER: US/09/239,043D
; PRIORITY FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/978,291
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: US 08/820,360
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,363

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OM protein - protein search, using sw model

Run on: November 14, 2004, 13:16:33 ; Search time 79.6667 Seconds
(without alignments)
66.619 Million cell updates/sec

Title: US-09-831-253F-9

Perfect score: 77

Sequence: 1 LPSLSFQLGLYLSPH 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1568699 seqs, 353819137 residues

Total number of hits satisfying chosen parameters: 238011

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications, AA.*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	40.3	10	10	US-09-572-270A-102
2	30	39.0	15	15	US-10-682-420-55
3	30	39.0	15	15	US-10-682-420-98
4	30	39.0	15	15	US-10-409-613-55
5	30	39.0	15	15	US-10-409-613-55
6	30	39.0	15	15	US-10-442-180-55
7	30	39.0	15	15	US-10-442-180-98
8	29	37.7	11	14	US-10-197-954-26
9	28	36.4	9	14	US-10-119-536A-101
10	28	36.4	10	15	US-10-462-452-757
11	28	36.4	10	15	US-10-601-953-60
12	28	36.4	10	16	US-10-322-266-758
13	28	36.4	14	10	US-09-820-649-319

14	28	36.4	14	14	US-10-160-162-319	Sequence 319, Appl
15	28	36.4	15	15	US-10-682-420-99	Sequence 99, Appl
16	28	36.4	15	15	US-10-409-613-99	Sequence 99, Appl
17	28	36.4	15	15	US-10-442-180-99	Sequence 99, Appl
18	27	35.1	9	14	US-10-163-499-12	Sequence 12, Appl
19	27	35.1	10	10	US-09-572-404B-1179	Sequence 1179, Ap
20	27	35.1	10	10	US-09-572-270A-100	Sequence 100, Appl
21	27	35.1	15	13	US-10-103-395-264	Sequence 264, Appl
22	27	35.1	15	14	US-10-163-499-31	Sequence 31, Appl
23	27	35.1	15	15	US-10-296-734-808	Sequence 808, Appl
24	26.5	34.4	12	16	US-10-688-276-19	Sequence 19, Appl
25	26	33.8	9	14	US-10-371-525-271	Sequence 271, Appl
26	26	33.8	9	14	US-10-371-069-271	Sequence 271, Appl
27	26	33.8	9	14	US-10-371-645-271	Sequence 271, Appl
28	26	33.8	9	14	US-10-371-260-271	Sequence 271, Appl
29	26	33.8	9	16	US-10-415-014-19	Sequence 19, Appl
30	26	33.8	9	16	US-10-415-014-49	Sequence 49, Appl
31	26	33.8	9	16	US-10-415-014-202	Sequence 202, Appl
32	26	33.8	9	16	US-10-415-014-301	Sequence 301, Appl
33	26	33.8	10	16	US-10-415-014-64	Sequence 64, Appl
34	26	33.8	10	16	US-10-415-014-89	Sequence 89, Appl
35	26	33.8	10	16	US-10-415-014-165	Sequence 165, Appl
36	26	33.8	10	16	US-10-415-014-253	Sequence 253, Appl
37	26	33.8	10	16	US-10-415-014-364	Sequence 364, Appl
38	26	33.8	11	14	US-10-369-736-26	Sequence 26, Appl
39	26	33.8	11	14	US-10-369-738-26	Sequence 26, Appl
40	26	33.8	12	14	US-10-075-869-40	Sequence 40, Appl
41	26	33.8	12	14	US-10-366-493-40	Sequence 40, Appl
42	26	33.8	12	14	US-10-191-540-154	Sequence 154, Appl
43	26	33.8	12	15	US-10-302-100B-34	Sequence 34, Appl
44	26	33.8	13	14	US-10-199-820-274	Sequence 274, Appl
45	26	33.8	14	14	US-10-081-119-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1

US-09-572-270A-102
; Sequence 102, Application US/09572270A
; Publication No. US20030148368A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Inter- complementary peptide listing
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/572,270A
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 1144
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 102
; LENGTH: 10
; TYPE: PPT
; ORGANISM: Arabidopsis Thaliana
; OTHER INFORMATION: Sequence located in ILI2. at 8-17 and may interact with
US-09-572-270A-102

Query Match 40.3%; Score 31; DB 10; Length 10;
Best Local Similarity 70.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 SLSFQLGLYL 12

Db 1 SLTFQLLLFL 10
|||:|:|
||:|:|:|

RESULT 2

US-10-682-420-55
; Sequence 55, Application US/10682420
; Publication No. US20040062775A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre


```
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Type A PWD circovirus
US-10-409-613-98

Query Match      39.0%; Score 30; DB 15; Length 15;
Best Local Similarity 35.7%; Pred. No. 2.8e+02;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 LDSLSFQLGLYLSP 14
   :|:|:|:|:|:|
Db 2 VNELRFNIGQFLPP 15

RESULT 6
US-10-442-180-55
; Sequence 55, Application US/10442180
; Publication No. US20040091502A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Phillipe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS
; TITLE OF INVENTION: DISEASE (PWD)
; FILE REFERENCE: 065691/0176
; CURRENT APPLICATION NUMBER: US/10/442,180
; CURRENT FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: US/09/514,245
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 55
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Type B PWD circovirus
US-10-442-180-55

Query Match      39.0%; Score 30; DB 15; Length 15;
Best Local Similarity 35.7%; Pred. No. 2.8e+02;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 LDSLSFQLGLYLSP 14
   :|:|:|:|:|:|
Db 2 VNELRFNIGQFLPP 15

RESULT 7
US-10-442-180-98
; Sequence 98, Application US/10442180
; Publication No. US20040091502A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Phillipe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS
; TITLE OF INVENTION: DISEASE (PWD)
; FILE REFERENCE: 065691/0176
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; CURRENT APPLICATION NUMBER: US/10/442,180
; CURRENT FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: US/09/514,245
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 98
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Type A PWD circovirus
US-10-442-180-98

Query Match      39.0%; Score 30; DB 15; Length 15;
Best Local Similarity 35.7%; Pred. No. 2.8e+02;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 LDSLSFQLGLYLSP 14
   :|:|:|:|:|:|
Db 2 VNELRFNIGQFLPP 15

RESULT 8
US-10-197-954-26
; Sequence 26, Application US/10197954
; Publication No. US20030119021A1
; GENERAL INFORMATION:
; APPLICANT: K'ster, Hubert
; APPLICANT: Siddiqi, Suhaib
; APPLICANT: Little, Daniel
; TITLE OF INVENTION: Capture Compounds, Collections Thereof
; TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: 24743-2305
; CURRENT APPLICATION NUMBER: US/10/197,954
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 60/306,019
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/314,123
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/363,433
; PRIOR FILING DATE: 2002-03-11
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo Sapien
; NAME/KEY: AMIDATION
; FEATURE:
; LOCATION: 11
US-10-197-954-26

Query Match      37.7%; Score 29; DB 14; Length 11;
Best Local Similarity 60.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LDSLSFQLGL 10
   :|:|:|:|:|
Db 2 MDLAFSGGL 11

RESULT 9
US-10-119-536A-101
; Sequence 101, Application US/10119536A
; Publication No. US20030199438A1
; GENERAL INFORMATION:
; APPLICANT: Shaw, Allan Christian
; APPLICANT: Vandahl, Brian Berg
; TITLE OF INVENTION: Method for Identification of Proteins from Intracellular Bacteri
; FILE REFERENCE: 4305/IJ091US1
; CURRENT APPLICATION NUMBER: US/10/119,536A
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; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: DK PA 200100581
; PRIOR FILING DATE: 2001-04-09
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 101
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (1)..(9)
; OTHER INFORMATION: CPN0998 immunogenic peptide
US-10-119-536A-101

Query Match 36.4%; Score 28; DB 14; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.4e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 LGLYLSP 14
|||
Db 2 IGLYLSP 8

RESULT 10
US-10-462-452-757
; Sequence 757, Application US/10462452
; Publication No. US20040037809A1
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven
; APPLICANT: Gupta, Mohammed Abd
; APPLICANT: de Meireles, Jorge
; TITLE OF INVENTION: Compositions and Methods for Enhanced
; TITLE OF INVENTION: Mucosal-Delivery of Interferon Beta
; FILE REFERENCE: 02-02US
; CURRENT APPLICATION NUMBER: US/10/462,452
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/393,066
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 790
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 757
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-462-452-757

Query Match 36.4%; Score 28; DB 15; Length 10;
Best Local Similarity 50.0%; Pred. No. 4e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 DSLSPQLG 9
|||
Db 3 DSMKFEIG 10

RESULT 11
US-10-601-953-60
; Sequence 60, Application US/10601953
; Publication No. US2004007540A1
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven C.
; TITLE OF INVENTION: Compositions and Methods For Modulating Physiology of Epithelial
; TITLE OF INVENTION: Junctional Adhesion Molecules For Enhanced Mucosal Delivery Of
; TITLE OF INVENTION: Therapeutic Compounds
; FILE REFERENCE: 02-03US
; CURRENT APPLICATION NUMBER: US/10/601,953
; CURRENT FILING DATE: 2003-06-24
; PRIOR APPLICATION NUMBER: 60/392,512
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 900
; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 60
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-601-953-60

Query Match 36.4%; Score 28; DB 15; Length 10;
Best Local Similarity 50.0%; Pred. No. 4e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 DSLSPQLG 9
|||
Db 3 DSMKFEIG 10

RESULT 12
US-10-322-266-758
; Sequence 758, Application US/10322266
; Publication No. US20040115135A1
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven C.
; TITLE OF INVENTION: Compositions and Methods For Enhanced Mucosal Delivery Of Peptide
; TITLE OF INVENTION: YY And Methods For Treating And Preventing Obesity
; FILE REFERENCE: NPCI0567
; CURRENT APPLICATION NUMBER: US/10/322,266
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 797
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 758
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-322-266-758

Query Match 36.4%; Score 28; DB 16; Length 10;
Best Local Similarity 50.0%; Pred. No. 4e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 DSLSPQLG 9
|||
Db 3 DSMKFEIG 10

RESULT 13
US-09-820-649-319
; Sequence 319, Application US/09820649
; Publication No. US20030199683A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 83 Human Secreted Proteins
; FILE REFERENCE: P2012P1
; CURRENT APPLICATION NUMBER: US/09/820,649
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US/09/236,557
; PRIOR FILING DATE: 1999-01-26
; PRIOR APPLICATION NUMBER: PCT/US98/15949
; PRIOR FILING DATE: 1998-07-29
; PRIOR APPLICATION NUMBER: 60/054,212
; PRIOR FILING DATE: 1997-07-30
; PRIOR APPLICATION NUMBER: 60/054,209
; PRIOR FILING DATE: 1997-07-30
; PRIOR APPLICATION NUMBER: 60/054,234
; PRIOR FILING DATE: 1997-07-30
; PRIOR APPLICATION NUMBER: 60/054,218
; PRIOR FILING DATE: 1997-07-30
; PRIOR APPLICATION NUMBER: 60/054,214
; PRIOR FILING DATE: 1997-07-30
; PRIOR APPLICATION NUMBER: 60/054,236
; PRIOR FILING DATE: 1997-07-30

; PRIOR APPLICATION NUMBER: 60/054,215
; PRIOR FILING DATE: 1997-07-30
; PRIOR APPLICATION NUMBER: 60/054,211
; PRIOR FILING DATE: 1997-07-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 353
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 319
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-820-649-319

Query Match 36.4%; Score 28; DB 10; Length 14;
Best Local Similarity 50.0%; Pred. No. 5.7e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 SLSFQLGLYL 12
|:|:|:|
Db 5 SISYSIGLVL 14

RESULT 14
US-10-160-162-319
; Sequence 319, Application US/10160162
; Publication No. US20030166541A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 83 Human Secreted Proteins
; FILE REFERENCE: P2012P2
; CURRENT APPLICATION NUMBER: US/10/160,162
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/295,558
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 09/236,557
; PRIOR FILING DATE: 1999-01-26
; PRIOR APPLICATION NUMBER: PCT/US98/15949
; PRIOR FILING DATE: 1998-07-29
; PRIOR APPLICATION NUMBER: 60/054,212
; PRIOR FILING DATE: 1997-07-30
; PRIOR APPLICATION NUMBER: 60/054,209
; PRIOR FILING DATE: 1997-07-30
; PRIOR APPLICATION NUMBER: 60/054,234
; PRIOR FILING DATE: 1997-07-30
; PRIOR APPLICATION NUMBER: 60/054,218
; PRIOR FILING DATE: 1997-07-30
; PRIOR APPLICATION NUMBER: 60/054,214
; PRIOR FILING DATE: 1997-07-30
; PRIOR APPLICATION NUMBER: 60/054,236
; PRIOR FILING DATE: 1997-07-30
; PRIOR APPLICATION NUMBER: 60/054,215
; PRIOR FILING DATE: 1997-07-30
; PRIOR APPLICATION NUMBER: 60/054,211
; PRIOR FILING DATE: 1997-07-30
; PRIOR APPLICATION NUMBER: 60/054,217
; PRIOR FILING DATE: 1997-07-30
; PRIOR APPLICATION NUMBER: 60/054,213
; PRIOR FILING DATE: 1997-07-30
; PRIOR APPLICATION NUMBER: 60/055,968
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,969
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,972
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/056,561
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,534
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,729
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,543
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,727

; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,554
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,730
; PRIOR FILING DATE: 1997-08-19
; NUMBER OF SEQ ID NOS: 353
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 319
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-160-162-319

Query Match 36.4%; Score 28; DB 14; Length 14;
Best Local Similarity 50.0%; Pred. No. 5.7e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 SLSFQLGLYL 12
|:|:|:|
Db 5 SISYSIGLVL 14

RESULT 15
US-10-682-420-99
; Sequence 99, Application US/10682420
; Publication No. US20040062775A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Philippe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS
; FILE REFERENCE: 065691/0176
; CURRENT APPLICATION NUMBER: US/10/682,420
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US/10/637,011
; PRIOR FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: US/09/514,245B
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 99
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Type A PWD circovirus
US-10-682-420-99

Query Match 36.4%; Score 28; DB 15; Length 15;
Best Local Similarity 45.5%; Pred. No. 6.2e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 LSFQLGLYLS 14
|:|:|:|
Db 1 LRFNIGQLPP 11

Search completed: November 14, 2004, 13:37:00
Job time : 80.6667 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2004, 12:55:26 ; Search time 93.3333 Seconds
(without alignments)
57.653 Million cell updates/sec

Title: US-09-831-253F-9

Perfect score: 77

Sequence: 1 LBSLSFQLGLYLSPH 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 605831

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2002s:*

6: Geneseq2003as:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	77	100.0	15	3 AAY93106	Aay93106 Transform
2	77	100.0	15	3 AAY92953	Aay92953 Transform
3	31	40.3	10	4 AAG83462	Aag83462 Arabidops
4	31	40.3	15	5 ABP58975	Abp58975 Human I k
5	30	39.0	15	5 AAM47809	Aam47809 Miniature
6	29	37.7	11	8 ADN03302	Adn03302 Exemplary
7	29	37.7	12	3 AAB07274	Aab07274 Human pep
8	29	37.7	12	6 ABR00682	Abr00682 HCV nonst
9	29	37.7	13	6 ABR00699	Abr00699 HCV nonst
10	29	37.7	13	6 ABR00693	Abr00693 HCV nonst
11	29	37.7	14	4 AAM37619	Aam37619 Human pep
12	29	37.7	14	6 ABR00703	Abr00703 HCV nonst
13	29	37.7	14	6 ABR00706	Abr00706 HCV nonst
14	29	37.7	15	6 ABR00715	Abr00715 HCV nonst
15	29	37.7	15	6 ABR00714	Abr00714 HCV nonst
16	28	36.4	9	6 ABP75290	Abp75290 Chlamydia
17	28	36.4	10	8 ADI46351	Adi46351 Permeabil
18	28	36.4	10	8 ADP87353	Adp87353 Human cla
19	28	36.4	11	1 AAP50351	Aap50351 Antigenic
20	28	36.4	11	1 AAP50388	Aap50388 Adult T-c
21	28	36.4	13	3 AAB34406	Aab34406 Gene 33 h
22	28	36.4	14	7 ADD90504	Add90504 Novel hum
23	28	36.4	14	7 ADG90323	Adg90323 Human sec
24	27	35.1	9	4 AAE03688	Aae03688 Python re
25	27	35.1	9	5 ABJ08453	Abj08453 Hepatitis

ALIGNMENTS

RESULT 1
AAY93106
ID AAY93106 standard; peptide; 15 AA.
XX
AC AAY93106;
XX
DT 08-NOV-2000 (first entry)
XX
DE Transforming growth factor inhibitory peptide P152.
XX
KW Hepatotrophic; antagonist; transforming growth factor beta1; TGF-beta1;
KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX
OS Homo sapiens.
XX
PN WO200031135-A1.
XX
PD 02-JUN-2000.
XX
PF 23-NOV-1999; 99WO-ES000375.
XX
PR 24-NOV-1998; 98ES-00002465.
(CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
Borras Cuesta F;
WPI; 2000-411935/35.
Peptides that antagonize binding of transforming growth factor beta1,
useful for treatment of liver disease, especially cirrhosis, are partial
sequences of the factor or its receptors.
Disclosure; Page 33; 86pp; Spanish.
The invention relates to synthetic peptides that antagonise the binding
of transforming growth (TGF) factor beta1 (TGF-beta1) to its receptor in
vivo which have partial amino acid sequences identical, or similar, with
those of TGF-beta1 and/or its receptors. Peptides AAY92945-Y93133 represent
examples of the peptides of the invention. The peptides act by
competitive inhibition of the binding of TGF-beta1 to its receptors, e.g.
they are inhibitors of stimulation of collagen synthesis in liver cells
and inhibitors of synthesis of proteolytic enzymes able to degrade the
extracellular matrix. The peptides, their mimetopes and/or DNA (or
expression systems) encoding the peptides are used for treatment of liver
disease, specifically cirrhosis

```

XX
SQ Sequence 15 AA;
Query Match 100.0%; Score 77; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 5e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDSLSPQLGLYLSPPH 15
Db 1 LDSLSPQLGLYLSPPH 15

RESULT 2
AAY2953
ID AAY2953 standard; peptide; 15 AA.
XX
AC AAY2953;
XX
DT 08-NOV-2000 (first entry)
XX
DE Transforming growth factor inhibitory peptide #9.
XX
KW Hepatotropic; antagonist; transforming growth factor beta1; TGF-b1;
KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW extracellular matrix degradation inhibitor; mimotope; cirrhosis.
XX
OS Homo sapiens.
XX
PN WO200031135-A1.
XX
PD 02-JUN-2000.
XX
PF 23-NOV-1999; 99WO-ES000375.
XX
PR 24-NOV-1998; 98ES-00002465.
XX
PA (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
XX
PI Ezquerro Saenz IJ, Lasarte Segastibelza JJ, Prieto Valtuena J;
PI Borrás Cuesta F;
XX
DR WPI; 2000-411935/35.
XX
PT Peptides that antagonize binding of transforming growth factor beta1,
PT useful for treatment of liver disease, especially cirrhosis, are partial
PT sequences of the factor or its receptors.
XX
PS Claim 10; Page 82; 86pp; Spanish.
XX
CC The invention relates to synthetic peptides that antagonise the binding
CC of transforming growth (TGF) factor beta1 (TGF-b1) to its receptor in
CC vivo which have partial amino acid sequences identical, or similar, with
CC those of TGF-b1 and/or its receptors. Peptides AAY2945-Y93133 represent
CC examples of the peptides of the invention. The peptides act by
CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
CC they are inhibitors of stimulation of collagen synthesis in liver cells
CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
CC expression systems) encoding the peptides are used for treatment of liver
CC disease, specifically cirrhosis
XX
SQ Sequence 15 AA;
Query Match 100.0%; Score 77; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 5e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDSLSPQLGLYLSPPH 15
Db 1 LDSLSPQLGLYLSPPH 15

RESULT 3
AAG83462
ID AAG83462 standard; peptide; 10 AA.
XX
AC AAG83462;
XX
DT 11-SEP-2001 (first entry)
XX
DE Arabidopsis thaliana peptide ligand #102.
XX
KW Plant; peptide pesticide; peptide herbicide; agricultural research.
XX
OS Arabidopsis thaliana.
XX
PN WO200142279-A2.
XX
PD 14-JUN-2001.
XX
PF 13-DEC-2000; 2000WO-GB004781.
XX
PR 13-DEC-1999; 99GB-00029469.
XX
PA (PROT-) PROTEOM LTD.
XX
PI Roberts GW, Heal JR;
XX
DR WPI; 2001-381629/40.
XX
PT A set of peptide ligands for agricultural research and development of
PT therapeutic agents comprise specific complementary peptides to proteins
PT encoded by genes of plant genomes.
XX
PS Example 4; Page 45; 201pp; English.
XX
CC The present invention relates to a set of peptide ligands consisting of
CC specific complementary peptides to proteins encoded by genes of plant
CC genomes. The present sequence is one such peptide from Arabidopsis
CC thaliana. The peptides of the present invention are useful in an assay to
CC identify a peptide, especially a peptide pesticide or herbicide. The
CC peptides are also useful for tools for agricultural research and
CC development
XX
SQ Sequence 10 AA;
Query Match 40.3%; Score 31; DB 4; Length 10;
Best Local Similarity 70.0%; Pred. No. 98;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 SLSFQLGLYL 12
Db 1 SLTFQLLLFL 10

RESULT 4
ABP58975
ID ABP58975 standard; peptide; 15 AA.
XX
AC ABP58975;
XX
DT 14-APR-2003 (first entry)
XX
DE Human I kappa B kinase inhibitor 37.40 N-terminal peptide.
XX
KW Human; I kappa B kinase inhibitor 37.40; recombinant production;
KW gene therapy; cancer; tumour; angiodysplasia; cardiovascular disorder;
KW neurological disorder; immune disorder; inflammatory condition;
KW cytostatic; antiinflammatory; immunomodulator; N-terminal peptide;
KW enzyme linked immunosorbent assay; ELISA.
XX
OS Homo sapiens.
XX
PN CN1361264-A.
XX
PD 31-JUL-2002.

```

XX 26-DEC-2000; 2000CN-00136306.
XX
XX
XX
XX
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
XX Mao Y, Xie Y;
XX WPI; 2002-751595/82.
XX
XX Human inhibitor molecule I kappa B kinase 37.40 polypeptides and
PT polynucleotides encoding this polypeptide.
XX
XX Example 5; Page 18 (Disclosure); 33pp; Chinese.
XX
XX The invention relates to human I kappa B kinase inhibitor 37.40
CC (ABP8974) and nucleic acids encoding it (ABZ70827). The protein has a
CC molecular weight of 37.4 kD. The invention also relates to a method for
CC the recombinant production of the protein, an antagonist of the protein,
CC and the use of the protein, gene and antagonist in therapeutic
CC applications. I kappa B kinase inhibitor 37.40 can be used in the
CC treatment of a variety of diseases such as cancer, angiocardiopathy,
CC neurological disorders, immune disorders and inflammatory conditions. The
CC present sequence represents the 15 N-terminal amino acids of human I
CC kappa B kinase inhibitor 37.40 used in ELISA (enzyme linked immunosorbent
CC assay) in an exemplification of the invention
XX
XX Sequence 15 AA;
SQ

Query Match 40.3%; Score 31; DB 5; Length 15;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 6 FQLGLYLS 13
DB 5 FLLGLYIS 12
| | | | | |
| | | | | |

RESULT 5
AA047809
ID AA047809 standard; peptide; 15 AA.
XX
XX AA047809;
XX
XX 15-FEB-2002 (first entry)
XX
XX Miniature protein 9.
XX
XX Avian pancreatic polypeptide; alpha helix domain; modulate transcription;
KW miniature protein.
XX
XX Synthetic.
XX
XX WO200181375-A2.
XX
XX 01-NOV-2001.
XX
XX 24-APR-2001; 2001WO-US013023.
XX
XX 24-APR-2000; 2000US-0199408P.
XX 16-OCT-2000; 2000US-0240566P.
XX 30-JAN-2001; 2001US-0265059P.
XX 23-FEB-2001; 2001US-0271368P.
XX
XX (UYUA) UNIV YALE.
XX
XX Schepartz Shrader A, Chin JWK, Zutshi R, Rutledge SE;
PI Kehlbeck Martin JD, Zondlo NJ;
XX
XX WPI; 2002-041395/05.
XX
XX Polypeptide scaffold e.g. an avian pancreatic polypeptide that comprises

PT modification by substitution of an amino acid residue, that is exposed on
PT the alpha helix domain of the polypeptide is useful for screening for
XX drugs.
XX
XX Example 17; Fig 5; 81pp; English.
XX
XX The invention relates to an avian pancreatic polypeptide, modified by
CC substitution of at least one amino acid residue, where the residue is
CC being exposed on the alpha helix domain of the polypeptide when the
CC polypeptide is in a tertiary form. The polypeptide is useful for
CC screening drugs to identify agents capable of binding to the same binding
CC site as the avian pancreatic polypeptide. It is also useful for
CC diagnostic purposes to identify the presence and/or detect the levels of
CC DNA or protein that binds to the polypeptide, in treatment of diseases
CC associated with the presence of a particular DNA or protein, where the
CC polypeptide can be used to bind to DNA to promote or inhibit
CC transcription and for identifying binding partners. The present sequence
CC is that of a miniature protein of the invention used to modulate the
CC interaction between a known protein and another molecule
XX
XX Sequence 15 AA;
SQ

Query Match 39.0%; Score 30; DB 5; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 FQLGLYLS 12
DB 6 FQLGWYL 12
| | | | | |
| | | | | |

RESULT 6
ADN03302
ID ADN03302 standard; peptide; 11 AA.
XX
XX ADN03302;
XX
XX 17-JUN-2004 (first entry)
XX
XX Exemplary peptide ligand for proteome analysis #26.
XX
XX Peptide ligand; proteome; capture compound; mass spectrometry;
KW protein separation;
KW matrix assisted laser desorption ionisation-time of flight; MALDI-TOF.
XX
XX Unidentified.
XX
XX US2003119021-A1.
XX
XX 26-JUN-2003.
XX
XX 16-JUL-2002; 2002US-00197954.
XX
XX 16-JUL-2001; 2001US-0306019P.
XX 21-AUG-2001; 2001US-0314123P.
XX 11-MAR-2002; 2002US-0363433P.
XX
XX (KOST/) KOSTER H.
XX (SIDD/) SIDIQI S.
XX (LITT/) LITTLE D P.
XX
XX Koster H, Siddiqi S, Little DP;
XX
XX WPI; 2004-059185/06.
XX
XX Collection of capture compounds capable of binding to biomolecules to
PT form complexes that are stable under mass spectrometry conditions, useful
PT for analysis of biomolecules, especially proteins.
XX
XX Disclosure; SEQ ID NO 26; 165pp; English.
XX
XX The invention relates to a collection of capture compounds capable of
CC binding to biomolecules to form complexes that are stable under mass

CC spectrometry conditions. The formulae for the capture compounds comprises
 CC sets of compounds of formula (I)-(III) given in the specification. Also
 CC included are analysis of biomolecules (by contacting a composition
 CC comprising a biomolecule with the above collection and identifying or
 CC detecting bound biomolecules), separating protein conformers (by
 CC contacting a composition comprising a biomolecule with the above
 CC collection, separating the members of the collection and identifying
 CC bound proteins), reducing diversity of a complex mixture of biomolecules
 CC (by contacting the mixture with the above collection and separating each
 CC set of complexes of capture compounds with biomolecules from the other
 CC sets) and identifying phenotype-specific biomolecules (by sorting cells
 CC from a single subject into sets according to a phenotype, contacting
 CC mixtures of biomolecules from each set with the above collection and
 CC comparing the patterns of biomolecule binding from each set). The
 CC collection of capture compounds is useful for the analysis of
 CC biomolecules, especially proteins (e.g. analysis of a proteome), using
 CC mass spectrometry, especially matrix assisted laser desorption ionisation
 CC -time of flight (MALDI-TOF) mass spectrometry. The present sequence is an
 CC exemplary peptide ligand which may be incorporated into a capture
 CC compound of the invention.

XX Sequence 11 AA;

Query Match 37.7%; Score 29; DB 8; Length 11;
 Best Local Similarity 60.0%; Pred. No. 2.5e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LDSLFSQGL 10
 :||:| ||
 Db 2 MDLAFSGGL 11

RESULT 7

AB07274
 ID AAB07274 standard; peptide; 12 AA.

XX AC

XX AAB07274;

XX 17-OCT-2000 (first entry)

XX Human peptido-mimetic # 108.

XX Human; peptido-mimetic; tumour metastasis; E-selectin; adhesion molecule;
 KW Lewis antigen; anti-adhesion therapy.

XX Homo sapiens.

XX WO200027420-A1.

XX 18-MAY-2000.

XX 05-NOV-1999; 99WO-US026277.

XX 06-NOV-1998; 98US-0107478P.

XX (WIST-) WISTAR INST ANATOMY & BIOLOGY.

XX (UYPE-) UNIV PENNSYLVANIA.

XX Blaszczyk-Thurin M, Kieber-Emmons T;

XX WPI; 2000-376309/32.

XX Peptidomimetics of carbohydrate Lewis ligands useful for modulating
 PT inflammation, metastasis and angiogenesis.

XX Claim 8; Page 58; 107pp; English.

XX Tumour metastasis requires detachment of malignant cells from the primary
 CC tumour, penetration of blood or lymph vessels and attachment to the
 CC endothelium of distant organs, ultimately resulting in the formation of
 CC new tumours. The selectin family of adhesion molecules is implicated in
 CC this process. E-selectin is a calcium-dependent molecule expressed by
 CC activated vascular endothelium. E-selectins bind to glycoconjugates

CC carrying a terminal tetrasaccharide Lewis antigen, which are found on
 CC tumour cell surfaces. One such Lewis antigen is sialyl (SA)-Lea. The
 CC binding of selectin molecules to their ligands is thought to be an
 CC important step in metastasis. Therefore, inhibition of E-selectin-
 CC dependent carbohydrate-mediated interactions is thought to be a target
 CC for anti-cancer therapy. The present sequence is a Human Family II
 CC peptido-mimetic of E-selectin-SA-Lea binding. This sequence blocks E-
 CC selectin-SA-Lea binding and therefore blocks adhesion of tumour cells and
 CC leukocytes to endothelial cells and hence metastasis. This sequence is
 CC therefore an E-selectin antagonist

XX Sequence 12 AA;

Query Match 37.7%; Score 29; DB 3; Length 12;
 Best Local Similarity 50.0%; Pred. No. 2.8e+02;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 DSLFSQGL 11
 :||:| ||
 Db 1 DKETFEGLF 10

RESULT 8

ABR00682

ID ABR00682 standard; peptide; 12 AA.

XX AC ABR00682;

XX 01-APR-2003 (first entry)

XX HCV nonstructural protein NS5A complementary peptide 88.

XX HCV; hepatitis C virus; amphipathic helix; N-terminal; hepatotropic;
 KW non-structural protein; virucide; gene therapy; immunological; NS5A;
 KW complementary peptide.

XX Hepatitis C virus.

XX WO200289731-A2.

XX 14-NOV-2002.

XX 03-MAY-2002; 2002WO-US013951.

XX 03-MAY-2001; 2001US-0288687P.

XX 31-AUG-2001; 2001US-0316805P.

XX (STRD) UNIV STANFORD.

XX (ELIL) LILLY & CO ELI.

XX Glenn JS, Myers TM, Glass JI;

XX WPI; 2003-201229/19.

XX Identifying a compound for treating Hepatitis C virus (HCV) infection by
 PT assessing the ability of a compound to interfere the binding of an
 PT amphipathic helix of an HCV nonstructural protein with cytoplasmic
 PT membranes of eukaryotic cell.

XX Claim 44; Page 13; 43pp; English.

XX The invention relates to a novel method for identifying a compound useful
 CC for treating Hepatitis C virus (HCV) infection. The method comprises
 CC assessing the ability of a candidate compound to interfere with the
 CC binding of an amphipathic helix present in the N-terminal region of an
 CC HCV non-structural protein with cytoplasmic membranes of a eukaryotic
 CC cell, where a compound that interferes with the binding is useful for
 CC treating the infection. The compounds of the invention have virucide, and
 CC hepatotropic activity. The peptides may have a use in gene therapy. The
 CC methods and compounds are useful for treating Hepatitis C virus (HCV)
 CC infection. The composition is useful for eliciting an immunological
 CC response against HCV. The peptides are useful for the preparation of a
 CC medicament for the prevention or treatment of HCV infection in a human.

CC The sequences shown in ABR00595-ABR00746 represent complementary peptides
CC of varying lengths to the amphipathic helix of the HCV nonstructural
CC protein NS5A

XX SQ Sequence 12 AA;

Query Match 37.7%; Score 29; DB 6; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 LSFQLGLYLSPH 15
DB 1 LGFQPLKVAQH 12

RESULT 9

ABR00699
ID ABR00699 standard; peptide; 13 AA.

XX AC ABR00699;

XX DT 01-APR-2003 (first entry)

XX DE HCV nonstructural protein NS5A complementary peptide 105.

XX HCV; hepatitis C virus; amphipathic helix; N-terminal; hepatotropic;
KW non-structural protein; virucide; gene therapy; immunological; NS5A;
KW complementary peptide.

XX OS Hepatitis C virus.

XX PN WO200289731-A2.

XX PD 14-NOV-2002.

XX PF 03-MAY-2002; 2002WO-US013951.

XX PR 03-MAY-2001; 2001US-0288687P.

XX PR 31-AUG-2001; 2001US-0316805P.

XX PA (STRD) UNIV STANFORD.

XX PA (ELIL) LILLY & CO ELI.

XX PI Glenn JS, Myers TM, Glass JI;

XX PS WPI; 2003-201229/19.

XX PT Identifying a compound for treating Hepatitis C virus (HCV) infection by
PT assessing the ability of a compound to interfere the binding of an
PT amphipathic helix of an HCV nonstructural protein with cytoplasmic
PT membranes of eukaryotic cell.

XX PS Claim 44; Page 14; 43pp; English.

XX CC The invention relates to a novel method for identifying a compound useful
CC for treating Hepatitis C virus (HCV) infection. The method comprises
CC assessing the ability of a candidate compound to interfere with the
CC binding of an amphipathic helix present in the N-terminal region of an
CC HCV non-structural protein with cytoplasmic membranes of a eukaryotic
CC cell, where a compound that interferes with the binding is useful for
CC treating the infection. The compounds of the invention have virucide, and
CC hepatotropic activity. The peptides may have a use in gene therapy. The
CC methods and compounds are useful for treating Hepatitis C virus (HCV)
CC infection. The composition is useful for eliciting an immunological
CC response against HCV. The peptides are useful for the preparation of a
CC medicament for the prevention or treatment of HCV infection in a human.
CC The sequences shown in ABR00595-ABR00746 represent complementary peptides
CC of varying lengths to the amphipathic helix of the HCV nonstructural
CC protein NS5A

XX SQ Sequence 13 AA;

Query Match 37.7%; Score 29; DB 6; Length 13;

Best Local Similarity 50.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 LSFQLGLYLSPH 15
DB 2 LGFQPLKVAQH 13

RESULT 10

ABR00693
ID ABR00693 standard; peptide; 13 AA.

XX AC ABR00693;

XX DT 01-APR-2003 (first entry)

XX DE HCV nonstructural protein NS5A complementary peptide 99.

XX HCV; hepatitis C virus; amphipathic helix; N-terminal; hepatotropic;
KW non-structural protein; virucide; gene therapy; immunological; NS5A;
KW complementary peptide.

XX OS Hepatitis C virus.

XX PN WO200289731-A2.

XX PD 14-NOV-2002.

XX PF 03-MAY-2002; 2002WO-US013951.

XX PR 03-MAY-2001; 2001US-0288687P.

XX PR 31-AUG-2001; 2001US-0316805P.

XX PA (STRD) UNIV STANFORD.

XX PA (ELIL) LILLY & CO ELI.

XX PI Glenn JS, Myers TM, Glass JI;

XX PS WPI; 2003-201229/19.

XX PT Identifying a compound for treating Hepatitis C virus (HCV) infection by
PT assessing the ability of a compound to interfere the binding of an
PT amphipathic helix of an HCV nonstructural protein with cytoplasmic
PT membranes of eukaryotic cell.

XX PS Claim 44; Page 14; 43pp; English.

XX CC The invention relates to a novel method for identifying a compound useful
CC for treating Hepatitis C virus (HCV) infection. The method comprises
CC assessing the ability of a candidate compound to interfere with the
CC binding of an amphipathic helix present in the N-terminal region of an
CC HCV non-structural protein with cytoplasmic membranes of a eukaryotic
CC cell, where a compound that interferes with the binding is useful for
CC treating the infection. The compounds of the invention have virucide, and
CC hepatotropic activity. The peptides may have a use in gene therapy. The
CC methods and compounds are useful for treating Hepatitis C virus (HCV)
CC infection. The composition is useful for eliciting an immunological
CC response against HCV. The peptides are useful for the preparation of a
CC medicament for the prevention or treatment of HCV infection in a human.
CC The sequences shown in ABR00595-ABR00746 represent complementary peptides
CC of varying lengths to the amphipathic helix of the HCV nonstructural
CC protein NS5A

XX SQ Sequence 13 AA;

Query Match 37.7%; Score 29; DB 6; Length 13;

Best Local Similarity 50.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 LSFQLGLYLSPH 15
DB 1 LGFQPLKVAQH 12

```
RESULT 11
AAM97619
ID AAM97619 standard; peptide; 14 AA.
XX
XX
AC AAM97619;
XX
XX
DT 24-JAN-2002 (first entry)
XX
XX
DE Human peptide #894 encoded by a SNP oligonucleotide.
XX
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease.
XX
XX
OS Homo sapiens.
XX
XX
PN WO200147944-A2.
XX
XX
PD 05-JUL-2001.
XX
XX
PF 28-DEC-2000; 2000WO-US035498.
XX
XX
PR 28-DEC-1999; 99US-0173419F.
XX
XX
PR 27-DEC-2000; 2000US-00173419.
XX
XX
PA (CURA-) CUPAGEN CORP.
XX
XX
PI Shinkets RA, Leach M;
XX
XX
DR WPI; 2001-465210/50.
XX
XX
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
PT autoimmune diseases and infections.
XX
XX
PS Disclosure; Page 3863; 4143pp; English.
XX
XX
CC The present invention relates to oligonucleotides (see AAL26793-AAL34659)
CC encoding polymorphic variants of proteins related to amylases, amyloid
CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,
CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
CC complement related proteins, cytochromes, kinesins, cytokines,
CC interferons, interleukins, G-protein coupled receptors and thioesterases.
CC The present sequence is a peptide encoded by one such oligonucleotide.
CC The oligonucleotides and the peptides encoded by them may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate expression of the proteins listed above. Disorders that may
CC be prevented, diagnosed and/or treated include multifactorial diseases
CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
CC brain, breast, colon and kidney, leukaemia), diseases of the nervous
CC system and an infection of pathogenic organisms
XX
XX
SQ Sequence 14 AA;
Query Match 37.7%; Score 29; DB 4; Length 14;
Best Local Similarity 46.2%; Pred. No. 3.3e+02;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 3 SLSFQGLGLVSPH 15
| | | | | :
Db 2 SLSFRTGCKVKKH 14
| | | | | :
RESULT 12
ABR00703
ID ABR00703 standard; peptide; 14 AA.
XX
XX
AC ABR00703;
XX
XX
DT 01-APR-2003 (first entry)
XX
XX
DE HCV nonstructural protein NS5A complementary peptide 109.
XX
XX
KW HCV; hepatitis C virus; amphipathic helix; N-terminal; hepatotropic;
KW non-structural protein; virucide; gene therapy; immunological; NS5A;
KW complementary peptide.
XX
XX
OS Hepatitis C virus.
XX
XX
PN WO200289731-A2.
XX
XX
PD 14-NOV-2002.
XX
XX
PF 03-MAY-2002; 2002WO-US013951.
XX
XX
PR 03-MAY-2001; 2001US-0288687P.
XX
XX
PR 31-AUG-2001; 2001US-0316805P.
XX
XX
PA (STRD ) UNIV STANFORD.
XX
XX
PA (ELIL ) LILLY & CO ELI.
XX
XX
PI Glenn JS, Myers TM, Glass JI;
XX
XX
DR WPI; 2003-201229/19.
XX
XX
PT Identifying a compound for treating Hepatitis C virus (HCV) infection by
PT assessing the ability of a compound to interfere the binding of an
PT amphipathic helix of an HCV nonstructural protein with cytoplasmic
PT membranes of eukaryotic cell.
XX
XX
PS Claim 44; Page 14; 43pp; English.
XX
XX
CC The invention relates to a novel method for identifying a compound useful
CC for treating Hepatitis C virus (HCV) infection. The method comprises
CC assessing the ability of a candidate compound to interfere with the
CC binding of an amphipathic helix present in the N-terminal region of an
CC HCV non-structural protein with cytoplasmic membranes of a eukaryotic
CC cell, where a compound that interferes with the binding is useful for
CC treating the infection. The compounds of the invention have virucide, and
CC hepatotropic activity. The peptides may have a use in gene therapy. The
CC methods and compounds are useful for treating Hepatitis C virus (HCV)
CC infection. The composition is useful for eliciting an immunological
CC response against HCV. The peptides are useful for the preparation of a
CC medicament for the prevention or treatment of HCV infection in a human.
CC The sequences shown in ABR00595-ABR00746 represent complementary peptides
CC of varying lengths to the amphipathic helix of the HCV nonstructural
XX
XX
SQ Sequence 14 AA;
Query Match 37.7%; Score 29; DB 6; Length 14;
Best Local Similarity 50.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 4 LSFQGLGLVSPH 15
| | | | | :
Db 2 LGFQGLKVAQH 13
| | | | | :
RESULT 13
ABR00706
ID ABR00706 standard; peptide; 14 AA.
XX
XX
AC ABR00706;
XX
XX
DT 01-APR-2003 (first entry)
XX
XX
DE HCV nonstructural protein NS5A complementary peptide 112.
```

XX HCV; hepatitis C virus; amphipathic helix; N-terminal; hepatotropic;
KW non-structural protein; virucide; gene therapy; immunological; NS5A;
KW complementary peptide.
XX Hepatitis C virus.
OS
XX WO200289731-A2.
PN
XX 14-NOV-2002.
PD
XX
XX 03-MAY-2002; 2002WO-US013951.
PF
XX 03-MAY-2001; 2001US-0288687P.
PR
XX 31-AUG-2001; 2001US-0316805P.
PR
XX (STRD) UNIV STANFORD.
PA (ELIL) LILLY & CO ELI.
PA
XX Glenn JS, Myers TM, Glass JI;
PI WPI; 2003-201229/19.
PI
XX
XX Identifying a compound for treating Hepatitis C virus (HCV) infection by
PT assessing the ability of a compound to interfere the binding of an
PT amphipathic helix of an HCV nonstructural protein with cytoplasmic
PT membranes of eukaryotic cell.
PT
XX Claim 44; Page 14; 43pp; English.
PS
XX The invention relates to a novel method for identifying a compound useful
CC for treating Hepatitis C virus (HCV) infection. The method comprises
CC assessing the ability of a candidate compound to interfere with the
CC binding of an amphipathic helix present in the N-terminal region of an
CC HCV non-structural protein with cytoplasmic membranes of a eukaryotic
CC cell, where a compound that interferes with the binding is useful for
CC treating the infection. The compounds of the invention have virucide, and
CC hepatotropic activity. The peptides may have a use in gene therapy. The
CC methods and compounds are useful for treating Hepatitis C virus (HCV)
CC infection. The composition is useful for eliciting an immunological
CC response against HCV. The peptides are useful for the preparation of a
CC medicament for the prevention or treatment of HCV infection in a human.
CC The sequences shown in ABR00595-ABR00746 represent complementary peptides
CC of varying lengths to the amphipathic helix of the HCV nonstructural
CC protein NS5A
XX
SQ Sequence 14 AA;
Query Match 37.7%; Score 29; DB 6; Length 14;
Best Local Similarity 50.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 4 LSFQLGLYLSPH 15
DB 1 LGFQPLKVAQH 12
RESULT 14
ABR00715
ID ABR00715 standard; peptide; 15 AA.
XX
AC ABR00715;
XX
DT 01-APR-2003 (first entry)
XX
DE HCV nonstructural protein NS5A complementary peptide 121.
XX
KW HCV; hepatitis C virus; amphipathic helix; N-terminal; hepatotropic;
KW non-structural protein; virucide; gene therapy; immunological; NS5A;
KW complementary peptide.
XX
OS Hepatitis C virus.
XX

PN WO200289731-A2.
XX
XX 14-NOV-2002.
XX
XX 03-MAY-2002; 2002WO-US013951.
PF
XX 03-MAY-2001; 2001US-0288687P.
PR
XX 31-AUG-2001; 2001US-0316805P.
PR
XX (STRD) UNIV STANFORD.
PA (ELIL) LILLY & CO ELI.
PA
XX Glenn JS, Myers TM, Glass JI;
PI WPI; 2003-201229/19.
PI
XX
XX Identifying a compound for treating Hepatitis C virus (HCV) infection by
PT assessing the ability of a compound to interfere the binding of an
PT amphipathic helix of an HCV nonstructural protein with cytoplasmic
PT membranes of eukaryotic cell.
PT
XX Claim 44; Page 14; 43pp; English.
PS
XX The invention relates to a novel method for identifying a compound useful
CC for treating Hepatitis C virus (HCV) infection. The method comprises
CC assessing the ability of a candidate compound to interfere with the
CC binding of an amphipathic helix present in the N-terminal region of an
CC HCV non-structural protein with cytoplasmic membranes of a eukaryotic
CC cell, where a compound that interferes with the binding is useful for
CC treating the infection. The compounds of the invention have virucide, and
CC hepatotropic activity. The peptides may have a use in gene therapy. The
CC methods and compounds are useful for treating Hepatitis C virus (HCV)
CC infection. The composition is useful for eliciting an immunological
CC response against HCV. The peptides are useful for the preparation of a
CC medicament for the prevention or treatment of HCV infection in a human.
CC The sequences shown in ABR00595-ABR00746 represent complementary peptides
CC of varying lengths to the amphipathic helix of the HCV nonstructural
CC protein NS5A
XX
SQ Sequence 15 AA;
Query Match 37.7%; Score 29; DB 6; Length 15;
Best Local Similarity 50.0%; Pred. No. 3.6e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 4 LSFQLGLYLSPH 15
DB 1 LGFQPLKVAQH 12
RESULT 15
ABR00714
ID ABR00714 standard; peptide; 15 AA.
XX
AC ABR00714;
XX
DT 01-APR-2003 (first entry)
XX
DE HCV nonstructural protein NS5A complementary peptide 120.
XX
KW HCV; hepatitis C virus; amphipathic helix; N-terminal; hepatotropic;
KW non-structural protein; virucide; gene therapy; immunological; NS5A;
KW complementary peptide.
XX
OS Hepatitis C virus.
XX
PN WO200289731-A2.
XX
PD 14-NOV-2002.
XX
PF 03-MAY-2002; 2002WO-US013951.
XX
PR 03-MAY-2001; 2001US-0288687P.

PR 31-AUG-2001; 2001US-031680SP.
XX (STED) UNIV STANFORD.
PA (ELIL) LILLY & CO ELI.
XX
XX Glenn JS, Myers TM, Glass JI;
PI WPI; 2003-201229/19.
XX
XX
XX Identifying a compound for treating Hepatitis C virus (HCV) infection by
PT assessing the ability of a compound to interfere the binding of an
PT amphipathic helix of an HCV nonstructural protein with cytoplasmic
PT membranes of eukaryotic cell.
XX
XX
PS Claim 44; Page 14; 43pp; English.
XX
CC The invention relates to a novel method for identifying a compound useful
CC for treating Hepatitis C virus (HCV) infection. The method comprises
CC assessing the ability of a candidate compound to interfere with the
CC binding of an amphipathic helix present in the N-terminal region of an
CC HCV non-structural protein with cytoplasmic membranes of a eukaryotic
CC cell, where a compound that interferes with the binding is useful for
CC treating the infection. The compounds of the invention have virucide, and
CC hepatotropic activity. The peptides may have a use in gene therapy. The
CC methods and compounds are useful for treating Hepatitis C virus (HCV)
CC infection. The composition is useful for eliciting an immunological
CC response against HCV. The peptides are useful for the preparation of a
CC medicament for the prevention or treatment of HCV infection in a human.
CC The sequences shown in ABR00595-ABR00746 represent complementary peptides
CC of varying lengths to the amphipathic helix of the HCV nonstructural
CC protein NSSA
XX
XX
SQ Sequence 15 AA;

Query Match 37.7%; Score 29; DB 6; Length 15;
Best Local Similarity 50.0%; Pred. No. 3.6e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 LSFQLGLYLSPH 15
| | | | | : |
Db 2 LGFQFGLKVAQH 13

Search completed: November 14, 2004, 13:11:18
Job time : 94.3333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2004, 12:56:07 ; Search time 100 Seconds
(without alignments)
86.306 Million cell updates/sec

Title: US-09-831-253F-9
Perfect score: 77
Sequence: 1 LDSLSFQLGLYLSPH 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 7754

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	35.1	12	1 FREI_LITIN	P82021 litoria inf
2	26	33.8	15	1 ASPI_LACSN	P82648 lactobacill
3	25	32.5	15	2 Q9R470	Q9r4t0 rhodobacter
4	24	31.2	15	2 Q7M3G3	Q7m3g3 bos taurus
5	23	29.9	9	2 P92072	P92072 euhadra her
6	23	29.9	15	2 Q9TR52	Q9tr52 bos taurus
7	22	28.6	12	1 CD11_LITCH	P62567 litoria chl
8	22	28.6	12	1 CD11_LITGI	P62566 litoria gil
9	22	28.6	12	1 CD11_LITSP	P62565 litoria spl
10	22	28.6	12	1 CD11_LITXA	P62564 litoria xan
11	22	28.6	15	1 TRPA_LEUMA	P81753 leucophaea
12	22	28.6	15	2 Q9MYT7	Q9myt7 sus scrofa
13	21	27.3	8	2 Q6LDP8	Q6ldp8 pseudomonas
14	21	27.3	8	2 AAA26011	Aaa26011 pseudomon
15	21	27.3	8	2 AAA26012	Aaa26012 pseudomon
16	21	27.3	12	1 CD14_LITCH	P62581 litoria chl
17	21	27.3	13	1 CD14_LITXA	P62582 litoria xan
18	21	27.3	13	1 RAN7_RANCA	P82822 rana catesb
19	20	26.0	8	2 P92211	P92211 agropyron c
20	20	26.0	8	2 P92215	P92215 amblyopyrum
21	20	26.0	8	2 P92219	P92219 australopyr
22	20	26.0	8	2 P92222	P92222 bromus iner
23	20	26.0	8	2 P92227	P92227 crithopsis
24	20	26.0	8	2 P92373	P92373 haynaldia v
25	20	26.0	8	2 P92382	P92382 hordeum bra
26	20	26.0	8	2 P92384	P92384 hordeum mur
27	20	26.0	8	2 P92388	P92388 henrardia p
28	20	26.0	8	2 P92391	P92391 heteranthe
29	20	26.0	8	2 P92394	P92394 hordeum vul
30	20	26.0	8	2 P92404	P92404 lophopyrum
31	20	26.0	8	2 P92422	P92422 psathyrosta

32	20	26.0	8	2	P92426	P92426 pseudoroegn
33	20	26.0	8	2	P92428	P92428 peridictyon
34	20	26.0	8	2	P92431	P92431 aegilops ta
35	20	26.0	8	2	P92441	P92441 thimopyrum
36	20	26.0	8	2	P92443	P92443 taeniatheru
37	20	26.0	8	2	P93955	P93955 festucopsis
38	20	26.0	8	2	P93957	P93957 festucopsis
39	20	26.0	8	2	P93959	P93959 hordeum ere
40	20	26.0	8	2	P93961	P93961 psathyrosta
41	20	26.0	8	2	P93963	P93963 psathyrosta
42	20	26.0	8	2	P93965	P93965 secale stri
43	20	26.0	8	2	P93966	P93966 aegilops ep
44	20	26.0	8	2	P93970	P93970 eremopyrum
45	20	26.0	8	2	P93973	P93973 eremopyrum

ALIGNMENTS

RESULT 1
FREI_LITIN STANDARD; PRT; 12 AA.
AC P82021;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Frenatin 1.
OS Litoria infrenata (Giant tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
OC Pelodyadinae; Litoria.
OC NCBI_TaxID=61195;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX MEDLINE=97368637; PubMed=9225251;
RA Raftery M.J., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "The structures of the frenatin peptides from the skin secretion of
the giant tree frog Litoria infrenata.";
RL J. Pept. Sci. 2:117-124(1996).
CC -!- FUNCTION: Wide spectrum antimicrobial peptide.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin parotoid and/or rostral
glands.
CC -!- MASS SPECTROMETRY: MW=1140; METHOD=PAB; RANGE=1-12; NOTE=Ref.1.
KW Amidation; Amphibian defense peptide; Antibiotic;
KW Direct protein sequencing.
FT MOD_RES 12 12 Leucine amide.
SQ SEQUENCE 12 AA; 1141 MW; C622550BC365B72D CRC64;

Query Match 35.1%; Score 27; DB 1; Length 12;
Best Local Similarity 70.0%; Pred. No. 8.9e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY	1	LDSLSFQLGL 10
		:
Db	3	LDALSGILGL 12

RESULT 2
ASPI_LACSN STANDARD; PRT; 15 AA.
AC P82648;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Acid shock protein 1 (Fragment).
OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OC NCBI_TaxID=16295;
RN [1]
RP SEQUENCE.

```
RC STRAIN=CB1;
RX MEDLINE=21322712; PubMed=11429463;
RA De Angelis M., Bini L., Pallini V., Coccconcelli P.S., Gobbetti M.;
RT "The acid-stress response in Lactobacillus sanfranciscensis CB1.";
RL Microbiology 147:1863-1873(2001).
CC -I- INDUCTION: Overexpressed in acid environments.
KW Direct protein sequencing.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1509 MW; 575853B4DFB030A8 CRC64;

Query Match 33.8%; Score 26; DB 1; Length 15;
Best Local Similarity 62.5%; Pred. No. 1.7e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 SFQLGLYL 12
Db 1 SPKGLFL 8

RESULT 3
Q9R4T0 PRELIMINARY; PRT; 15 AA.
AC Q9R4T0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Periplasmic protein 5 (Fragment).
OS Rhodobacter sphaeroides (Rhodospirillum rubrum) sphaeroides.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Rhodobacter.
OX NCBI_TaxID=1063;
RN [1]
RP SEQUENCE.
RX MEDLINE=95160605; PubMed=78571198;
RA Sabaty M., Gagnon J., Vermeglio A.;
RT "Induction by nitrate of cytoplasmic and periplasmic proteins in the
RT photodinitrifier Rhodobacter sphaeroides forma sp. denitrificans under
RT anaerobic or aerobic condition.";
RL Arch. Microbiol. 162:335-343(1994).
SQ SEQUENCE 15 AA; 1718 MW; DA5BF4BD9AEBE157 CRC64;

Query Match 32.5%; Score 25; DB 2; Length 15;
Best Local Similarity 55.6%; Pred. No. 2.6e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 DSLSFQLGL 10
Db 4 DSFTFQSGM 12

RESULT 4
Q7M3G3 PRELIMINARY; PRT; 15 AA.
AC Q7M3G3;
DT 01-WAR-2004 (TrEMBLrel. 26, Created)
DT 01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE 28K serine proteinase homolog (fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=90343797; PubMed=2200404;
RA Ho P.L., Carpenter M.R., Smillie L.B., Gambarini A.G.;
RT "Co-purification of proteases with basic fibroblast growth factor
RT (FGF).";
RL Biochem. Biophys. Res. Commun. 170:769-774(1990).
DR FIR; A35417; A35417.
FT NON_TER 1 1
FT NON_TER 15 15
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```
SQ SEQUENCE 15 AA; 1710 MW; 6358BCB0D3627321 CRC64;

Query Match 31.2%; Score 24; DB 2; Length 15;
Best Local Similarity 30.8%; Pred. No. 4e+03;
Matches 4; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 DSLSFQLGLYLSP 14
Db 3 DSIDYRKGYVTP 15

RESULT 5
P92072 PRELIMINARY; PRT; 9 AA.
AC P92072;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE ATPase subunit 8 (Fragment).
OS Euhadra herklotsi.
OG Mitochondrion.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Helicoidea; Bradybaenidae; Euhadra.
OX NCBI_TaxID=58912;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hepatopancreas;
RA Yamazaki N., Ueshima R., Terrett J.A., Yokobori S., Kaifu M.,
RA Segawa R., Kobayashi T., Numachi K., Ueda T., Nishikawa K.,
RA Watanabe K., Thomas R.H.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; 271697; CAA96373.1; -
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1009 MW; 380CB1F775B736C7 CRC64;

Query Match 29.9%; Score 23; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LSPH 15
Db 4 LSPH 7

RESULT 6
Q9TR52 PRELIMINARY; PRT; 15 AA.
AC Q9TR52;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE LMP7 multicatalytic proteinase complex subunit (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=95403474; PubMed=7673255;
RA Cardozo C., Eleuteri A.M., Orłowski M.;
RT "Differences in catalytic activities and subunit pattern of
RT multicatalytic proteinase complexes (proteasomes) isolated from bovine
RT pituitary, lung, and liver. Changes in LMP7 and the component
RT necessary for expression of the chymotrypsin-like activity.";
RL J. Biol. Chem. 270:22645-22651(1995).
SQ SEQUENCE 15 AA; 1640 MW; DB334789F42EB2DD CRC64;

Query Match 29.9%; Score 23; DB 2; Length 15;
Best Local Similarity 27.3%; Pred. No. 6.1e+03;
Matches 3; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
```

QY 3 SLSFQLGLYL 13
: ||| :
Db 5 AFKFXGVFA 15

RESULT 7

CD11_LITX
ID -CD11_LITX STANDARD; PRT; 12 AA.
AC P62567; P56245; P81253;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Caeridin 1.1/1.2/1.3.
OS Litoria chloris (Blue-thighed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=86064;
RN [1]
RP SEQUENCE.

RC TISSUE=SKIN secretion;
RX MEDLINE=98175802; PubMed=9516047;
RA Steinborner S.T., Currie G.J., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "New antibiotic caerin 1 peptides from the skin secretion of the
RT Australian tree frog Litoria chloris. Comparison of the activities of
RT the caerin 1 peptides from the genus Litoria.";
RL J. Pept. Res. 51:121-126(1998).
RC -!- FUNCTION: Caeridins show neither neuropeptide activity nor
CC antibiotic activity.
CC -!- TISSUE SPECIFICITY: Secreted by the skin.
CC -!- PTM: Isomerization alpha-beta of the Asp-4 residue in caeridin
CC 1.2; a cyclic succinimide may be formed between Asp-4 and Gly-5
CC residues in caeridin 1.3 (By similarity).
KW Amidation; Amphibian defense peptide; Direct protein sequencing.
MOD RES 12 12
FT MOD RES 12 12 Leucine amide.
SQ SEQUENCE 12 AA; 1141 MW; 2822551A33772728 CRC64;

Query Match 28.6%; Score 22; DB 1; Length 12;
Best Local Similarity 60.0%; Pred. No. 7.3e+03;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 LDSLSFQLGL 10
: ||| :
Db 3 LDGLLGLGL 12

RESULT 8

CD11_LITX
ID -CD11_LITX STANDARD; PRT; 12 AA.
AC P62566; P56245; P81253;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Caeridin 1.1/1.2/1.3.
OS Litoria gilleni (Centralian tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=39405;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.

RC TISSUE=Parotoid gland;
RA Waugh R.J., Stone D.J.M., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "Peptides from Australian frogs. The structures of the caerins and
RT caeridins from Litoria gilleni.";
RL J. Chem. Res. 139:937-961(1993).
RN [2]
RP SEQUENCE, AND MASS SPECTROMETRY.
RA Waugh R.J., Steinborner S.T., Bowie J.H., Wallace J.C., Tyler M.J.,
RA Hu P., Gross M.L.;
RT "Two isomeric alpha and beta aspartyl dodecapeptides and their cyclic
RT amino succinyl analogue from the Australian tree frog Litoria

RT gilleni.";
RL Aust. J. Chem. 48:1981-1987(1995).
CC -!- FUNCTION: Caeridins show neither neuropeptide activity nor
CC antibiotic activity.
CC -!- TISSUE SPECIFICITY: Specifically secreted by the skin parotoid
CC and/or rostral glands.
CC -!- PTM: Isomerization alpha-beta of the Asp-4 residue in caeridin
CC 1.2; a cyclic succinimide may be formed between Asp-4 and Gly-5
CC residues in caeridin 1.3.
CC -!- MASS SPECTROMETRY: MW=1140; METHOD=FAB; RANGE=1-12; NOTE=Ref.1.
KW Amidation; Amphibian defense peptide; Direct protein sequencing.
MOD RES 12 12 Leucine amide.
SQ SEQUENCE 12 AA; 1141 MW; 2822551A33772728 CRC64;

Query Match 28.6%; Score 22; DB 1; Length 12;

Best Local Similarity 60.0%; Pred. No. 7.3e+03;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 LDSLSFQLGL 10
: ||| :
Db 3 LDGLLGLGL 12

RESULT 9

CD11_LITSP
ID -CD11_LITSP STANDARD; PRT; 12 AA.
AC P62565; P56245; P81253;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Caeridin 1.1/1.2/1.3.
OS Litoria splendida (Magnificent tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=30345;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.

RC TISSUE=Parotoid gland;
RA Stone D.J.M., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "Peptides from Australian frogs. Structures of the caerins and
RT caeridin 1 from Litoria splendida.";
RL J. Chem. Soc. Perkin Trans. I 1:3173-3178(1992).
CC -!- FUNCTION: Caeridins show neither neuropeptide activity nor
CC antibiotic activity.
CC -!- TISSUE SPECIFICITY: Specifically secreted by the skin parotoid
CC and/or rostral glands.
CC -!- PTM: Isomerization alpha-beta of the Asp-4 residue in caeridin
CC 1.2; a cyclic succinimide may be formed between Asp-4 and Gly-5
CC residues in caeridin 1.3 (By similarity).
CC -!- MASS SPECTROMETRY: MW=1139; METHOD=FAB; RANGE=1-12; NOTE=Ref.1.
KW Amidation; Amphibian defense peptide; Direct protein sequencing.
MOD RES 12 12 Leucine amide.
SQ SEQUENCE 12 AA; 1141 MW; 2822551A33772728 CRC64;

Query Match 28.6%; Score 22; DB 1; Length 12;

Best Local Similarity 60.0%; Pred. No. 7.3e+03;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 LDSLSFQLGL 10
: ||| :
Db 3 LDGLLGLGL 12

RESULT 10

CD11_LITXA
ID -CD11_LITXA STANDARD; PRT; 12 AA.
AC P62564; P56245; P81253;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Caeridin 1.1/1.2/1.3.
OS Litoria xanthomera (Orange-thighed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=79697;
 RN [1]
 RN SEQUENCE, AND MASS SPECTROMETRY.
 RX MEDLINE=97374000; PubMed=9230483;
 RA Steinbörner S.T., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.,
 RA Ramsey S.L., antibacterial peptides from the skin glands of the
 RT Australian tree frog *Litoria xanthomera*.
 RL J. Pept. Sci. 3:181-185(1997).
 CC -!- FUNCTION: Caeridins show neither neuropeptide activity nor
 CC antibiotic activity.
 CC -!- TISSUE SPECIFICITY: Secreted by the skin dorsal glands.
 CC -!- PTM: isomerization alpha-beta of the Asp-4 residue in caeridin
 CC 1,2; a cyclic succinimide may be formed between Asp-4 and Gly-5
 CC residues in caeridin 1.3 (By similarity).
 CC -!- MASS SPECTROMETRY: MW=1140; METHOD=FAB; RANGE=1-12; NOTE=Ref.1.
 CC Amidation; Amphibian defense peptide; Direct protein sequencing.
 KW MOD_RES 12 12 Leucine amide.
 FT MOD_RES 12 12
 SQ SEQUENCE 12 AA; 1141 MW; 2822551A33772728 CRC64;
 Query Match 28.6%; Score 22; DB 1; Length 12;
 Best Local Similarity 60.0%; Pred. No. 7.3e+03;
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 LDSLFSQGL 10
 DB 3 LDGLLGLGL 12
 RESULT 11
 TRPA_LEUMA STANDARD; PRT; 15 AA.
 AC P81753;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Tachykinin-related peptide 10 (leuTRP 10).
 OS Leucophaea madagascariensis (Madagascar cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
 OC Blaberidae; Leucophaea.
 OX NCBI_TaxID=6988;
 RN [1]
 RN SEQUENCE, AND MASS SPECTROMETRY.
 RX TISSUE=Brain;
 RX MEDLINE=97269266; PubMed=9114447;
 RA Muren J.E., Naessel D.R.,
 RT "Seven tachykinin-related peptides isolated from the brain of the
 RT madagascar cockroach; evidence for tissue-specific expression of
 RT isoforms".
 RL Peptides 18:7-15(1997).
 CC -!- FUNCTION: Myoactive peptide. Increases the amplitude and frequency
 CC of spontaneous contractions and tonus of hindgut muscle.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Brain.
 CC -!- MASS SPECTROMETRY: MW=1436.0; METHOD=MALDI; RANGE=1-15;
 CC NOTE=Ref.1.
 KW Direct protein sequencing; Neuropeptide; Tachykinin.
 SQ SEQUENCE 15 AA; 1438 MW; 298572F373FA7007 CRC64;
 Query Match 28.6%; Score 22; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 9.2e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LDSL 5
 DB 3 LDSL 7

RESULT 12

Q9MYT7 PRELIMINARY; PRT; 15 AA.
 AC Q9MYT7;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Type I collagen alpha 1 chain (Fragment).
 GN Name=collal;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Intestine;
 RX MEDLINE=21560060; PubMed=11704606;
 RA Alho H.S., Inkinen K.A., Salminen U.S., Maasilta P.K., Taskinen E.I.,
 RA Glumoff V., Vuorio E.I., Ikonen T.S., Harjula A.L.J.,
 RT "Collagens I and III in a porcine bronchial model of obliterative
 RT bronchiolitis".
 RL Am. J. Respir. Crit. Care Med. 164:1519-1525(2001).
 DR EMBL; AJ289757; CAB94729.1; -.
 KW Collagen.
 FT NON_TER 1 1
 SQ SEQUENCE 15 AA; 1680 MW; 895303298274A63A CRC64;
 Query Match 28.6%; Score 22; DB 2; Length 15;
 Best Local Similarity 50.0%; Pred. No. 9.2e+03;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 7 OLGLYLSP 14
 DB 4 EFGDLSP 11
 RESULT 13
 Q6LDP8 PRELIMINARY; PRT; 8 AA.
 AC Q6LDP8;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE (strain Pa388) toxA gene encoding exotoxin A, 5' end ((strain PA103)
 DE toxA gene encoding exotoxin A, 5' end (Fragment).
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RN SEQUENCE FROM N.A.
 RA Pritchard A.E., Vasil M.L.;
 RL Submitted (NOV-1989) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=90202723; PubMed=2156808;
 RA Pritchard A.E., Vasil M.L.;
 RT "Possible insertion sequences in a mosaic genome organization upstream
 RT of the exotoxin A gene in *Pseudomonas aeruginosa*".
 RL J. Bacteriol. 172:2020-2028(1990).
 DR EMBL; M27186; AAA26012.1; -.
 DR EMBL; M27175; AAA26011.1; -.
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA; 1046 MW; F94371F7605721B6 CRC64;
 Query Match 27.3%; Score 21; DB 2; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 10 LYLSPH 15
 DB 1 MHLIPH 6


```
RESULT 14
AAA26011 PRELIMINARY; PRT; 8 AA.
AC AAA26011;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE (STRAIN PA103) TOXA GENE ENCODING EXOTOXIN A, 5' END
DE (Fragment).
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90202723; PubMed=2156808;
RA Pritchard A.E., Vasil M.L.;
RT "Possible insertion sequences in a mosaic genome organization upstream
RT of the exotoxin A gene in Pseudomonas aeruginosa.";
RL J. Bacteriol. 172:2020-2028(1990).
DR EMBL; M27175; AAA26011.1; -
FT NON TER 8
SQ SEQUENCE 8 AA; 1046 MW; F94371F7605721E6 CRC64;

Query Match 27.3%; Score 21; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 LYLSPH 15
DB 1 MHLIPH 6

RESULT 15
AAA26012 PRELIMINARY; PRT; 8 AA.
AC AAA26012;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE (STRAIN PS388) TOXA GENE ENCODING EXOTOXIN A, 5' END
DE (Fragment).
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RA Pritchard A.E., Vasil M.L.;
RT "A mosaic genome organization upstream of the exotoxin A gene in
RT Pseudomonas aeruginosa: Possible insertion sequences.";
RL Submitted (NOV-1989) to the EMBL/GenBank/DBJ databases.
DR EMBL; M27186; AAA26012.1; -
FT NON TER 8
SQ SEQUENCE 8 AA; 1046 MW; F94371F7605721E6 CRC64;

Query Match 27.3%; Score 21; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 LYLSPH 15
DB 1 MHLIPH 6
```

Search completed: November 14, 2004, 13:16:24
Job time : 101 secs

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OM protein - protein search, using sw model

Run on: November 14, 2004, 13:03:52 ; Search time 18.3333 Seconds
(without alignments)
78.723 Million cell updates/sec

Title: US-09-831-253F-9

Perfect score: 77

Sequence: 1 LDSLSPQLGLYLSPH 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	37.7	11	2 A35594	buccalin - Califor
2	24	31.2	15	2 A35417	28K serine protein
3	24	31.2	15	4 I38335	hypothetical TEL/M
4	23	29.9	11	2 PH0914	T-cell receptor be
5	23	29.9	12	2 C36201	1-aminocyclopropan
6	21	27.3	15	2 A47628	FC gamma receptor
7	20	26.0	11	4 PC2124	aminotransferase c
8	20	26.0	12	2 B61497	seed protein ws-17
9	20	26.0	14	2 B61597	cytochrome P450 AL
10	19	24.7	7	2 A11483	aspartate transami
11	19	24.7	10	2 A30823	bothropatoxin - ja
12	19	24.7	10	2 D60787	sperm-activating p
13	19	24.7	14	2 A28018	very late antigen-
14	19	24.7	15	2 T46625	hypothetical prote
15	19	24.7	15	2 PC1317	large granule L4 c
16	19	24.7	15	2 B45115	peptidylprolyl iso
17	19	24.7	15	2 C32521	hexokinase (EC 2.7
18	18.5	24.0	11	2 PT0301	Ig heavy chain CRD
19	18	23.4	6	2 JN0861	peptidyl-di-peptida
20	18	23.4	8	2 PC4131	hypothetical prote
21	18	23.4	10	2 PC2044	beta-Kirilowin - M
22	18	23.4	12	2 S01749	collagen alpha 1(I
23	18	23.4	12	2 S01122	photosystem II 3.7
24	18	23.4	12	2 H41946	T-cell receptor ga
25	18	23.4	13	2 B61620	locustamyotropin I
26	17	22.1	8	2 A37521	R-phycocerythrin ga
27	17	22.1	8	2 T13618	cytochrome oxidase
28	17	22.1	9	2 PS0253	glycine cleavage s
29	17	22.1	10	1 ECLQ3M	tachykinin III - m

30	17	22.1	10	2 A47364	placental lactogen
31	17	22.1	11	2 S19775	wound-induced prot
32	17	22.1	12	2 PH0771	T-cell receptor be
33	17	22.1	13	2 PH1596	Ig H chain V-D-J r
34	17	22.1	14	2 PA0109	porin por 1B - Ara
35	17	22.1	14	2 PA0045	porin por1 - Arabi
36	17	22.1	15	2 S08209	hypothetical prote
37	17	22.1	15	2 A49252	T-cell receptor be
38	17	22.1	15	2 PH1616	Ig H chain V-D-J r
39	17	22.1	15	2 PH0782	T-cell receptor al
40	16.5	21.4	13	4 I70075	glycophorin B (mis
41	16.5	21.4	14	2 PH1758	T cell receptor al
42	16.5	21.4	14	2 PH1758	T cell receptor al
43	16	20.8	9	4 I57650	hemoglobin alpha c
44	16	20.8	10	1 SPFGNK	neuromedin K - pig
45	16	20.8	10	2 S65432	angiotensin I - ho

ALIGNMENTS

RESULT 1

A35594

buccalin - California sea hare

C;Species: Aplysia californica (California sea hare)

C;Date: 14-Sep-1990 #sequence_revision 14-Sep-1990 #text_change 09-Jul-2004

C;Accession: A35594

R;Cropper, E.C.; Miller, M.W.; Tenenbaum, R.; Kolks, M.A.G.; Kupfermann, I.; Weiss, K.R

Proc. Natl. Acad. Sci. U.S.A. 85, 6177-6181, 1988

A;Title: Structure and action of buccalin: a modulatory neuropeptide localized to an id

A;Reference number: A35594; MUID:88320404; PMID:3413086

A;Accession: A35594

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <CRO>

A;Cross-references: UNIPROT:P20481

Query Match 37.7%; Score 29; DB 2; Length 11;

Best Local Similarity 60.0%; Pred. No. 56;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LDSLSPQLGL 10

Db :|||:|

2 MDLSFSGGL 11

RESULT 2

A35417

28K serine proteinase homolog - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 18-Jan-1991 #sequence_revision 18-Jan-1991 #text_change 09-Jul-2004

C;Accession: A35417

R;Ho, P.L.; Carpenter, M.R.; Smillie, L.B.; Gambarini, A.G.

Biochem. Biophys. Res. Commun. 170, 769-774, 1990

A;Title: Co-purification of proteases with basic fibroblast growth factor (FGF).

A;Reference number: A35417; MUID:90343797; PMID:2200404

A;Accession: A35417

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-15 <HOA>

A;Cross-references: UNIPROT:Q7M3G3

Query Match 31.2%; Score 24; DB 2; Length 15;

Best Local Similarity 30.8%; Pred. No. 6.2e+02;

Matches 4; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 DSLSFQLGLYLSP 14

Db :||:|

3 DSIDYRKGVTVP 15

RESULT 3

I38335

hypothetical TEL/MNI mutant fusion protein type II - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 20-Apr-2000
C:Accession: I38335
R:Buiz, A.; Sherr, S.; van Baal, S.; van Bezouw, S.; van der Plas, D.; Van Kessel, A.G.
Oncogene 10, 1511-1519, 1995
A:Title: Translocation (12;22) (p13;q11) in myeloproliferative disorders results in fusion
A:Reference number: I38031; MUID:95249265; PMID:7731705
A:Accession: I38335
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-15 <BUI>
A:Cross-references: EMBL:X85024; NID:g971471; PIDN:CAA59397.1; PID:g971472
C:Comment: This sequence is the chimeric product of a translocation mutation.
C:Genetics:
A:Gene: ETV6/MNI; TEL/MNI
A:Map position: 22q11/12p13
C:Keywords: fusion protein

Query Match 31.2%; Score 24; DB 4; Length 15;
Best Local Similarity 80.0%; Pred. No. 6.2e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 YLSPH 15
| | | | |
Db 2 YRSPH 6

RESULT 4
PH0914
T-cell receptor beta chain V-D-J region (isolate 7) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C:Accession: PH0914
R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic
A:Reference number: PH0891; MUID:92078857; PMID:1836012
A:Accession: PH0914
A:Molecule type: mRNA
A:Residues: 1-11 <GOL>
A:Experimental source: myelin basic protein-immunized lymph node
C:Keywords: T-cell receptor

Query Match 29.9%; Score 23; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. No. 6.7e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 DLSLFO 7
| | | | |
Db 5 DLSLYE 10

RESULT 5
C36201
1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) - apple tree (fragment)
C:Species: Malus domestica (apple tree)
C:Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 09-Jul-2004
C:Accession: C36201; C33103
R:Yip, W.K.; Dong, J.G.; Kenny, J.W.; Thompson, G.A.; Yang, S.P.
Proc. Natl. Acad. Sci. U.S.A. 87, 7930-7934, 1990
A:Title: Characterization and sequencing of the active site of 1-aminocyclopropane-1-car
A:Reference number: A36201; MUID:91045911; PMID:2122449
A:Accession: C36201
A:Molecule type: protein
A:Residues: 1-12 <YIP>
A:Cross-references: UNIPROT:Q9S8B01; UNIPROT:Q9SB94; UNIPROT:O24062
A:Experimental source: strain Golden delicious
C:Superfamily: 1-aminocyclopropane-1-carboxylate synthase
C:Keywords: carbon-sulfur lyase; ethylene biosynthesis; phosphoprotein; pyridoxal phosph
F:4/Binding site: pyridoxal phosphate (lys) (covalent) #status experimental

Query Match 29.9%; Score 23; DB 2; Length 12;

Best Local Similarity 75.0%; Pred. No. 7.3e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 SLSFOLGL 10
| | | | |
Db 1 SLSKDLGL 8

RESULT 6
A47628
Fc gamma receptor II (CD32) - human (fragments)
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: A47628
R:Warmerdam, P.A.M.; van de Winkel, J.G.J.; Gosselin, E.J.; Capel, P.J.A.
J. Exp. Med. 172, 19-25, 1990
A:Title: Molecular basis for a polymorphism of human Fc gamma receptor II (CD32).
A:Reference number: A47628; MUID:90293679; PMID:2141627
A:Accession: A47628
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-15 <WAR>
C:Keywords: immunoglobulin receptor

Query Match 27.3%; Score 21; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 2.1e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 GLYLSP 14
| | | | |
Db 9 GSHLSP 14

RESULT 7
PC2124
aminotransferase chimera DY376 - synthetic (fragment)
C:Species: synthetic
C:Date: 28-May-1999 #sequence_revision 28-May-1999 #text_change 28-May-1999
C:Accession: PC2124
R:Miyazawa, K.; Kawaguchi, S.; Okamoto, A.; Kato, R.; Ogawa, T.; Kuramitsu, S.
J. Biochem. 115, 568-577, 1994
A:Title: Construction of aminotransferase chimeras and analysis of their substrate speci
A:Reference number: JX0315; MUID:94334304; PMID:8056774
A:Accession: PC2124
A:Molecule type: DNA
A:Residues: 1-11 <MIY>
A:Comment: This is a chimeric enzyme of Escherichia coli aspartate aminotransferase (EC
C:Comment: The parental enzymes catalyze the reversible amino group transfer reaction be
C:Genetics:
A:Gene: aspC; tyrB
C:Keywords: aminotransferase

Query Match 26.0%; Score 20; DB 4; Length 11;
Best Local Similarity 50.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 QLGLYL 12
| | | | |
Db 6 BFGVYL 11

RESULT 8
B61497
seed protein ws-17 - winged bean (fragment)
C:Species: Psophocarpus tetragonolobus (winged bean)
C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C:Accession: B61497
R:Hirano, H.
J. Protein Chem. 8, 115-130, 1989
A:Title: Microsequence analysis of winged bean seed proteins electroblooded from two-di
A:Reference number: A61491; MUID:89351606; PMID:2765119
A:Accession: B61497
A:Status: preliminary

A:Molecule type: protein
A:Residues: 1-12 <HIR>
A:Cross-references: UNIPROT:Q7M1H9
C:Keywords: seed

Query Match 26.0%; Score 20; DB 2; Length 12;
Best Local Similarity 30.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 DLSLFQGLY 11
|:|:|:
Db 1 DTISFNFNQF 10

RESULT 9

B61597
cytochrome P450 AL-2 - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: B61597
R:Shimeno, H.; Toda, A.; Ogata, S.; Nagamatsu, A.
Drug Metab. Dispos. 19, 291-297, 1991
A:Title: Purification and aminopyrine monooxygenase activity of liver microsomal cytochrome P450AL-2 from the rat
A:Reference number: A61597; MUID:91292910; PMID:1676625
A:Accession: B61597
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-14 <SHI>
A:Cross-references: UNIPROT:Q7M047

Query Match 26.0%; Score 20; DB 2; Length 14;
Best Local Similarity 83.3%; Pred. No. 3e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 SLSFQL 8
|:|:|:
Db 6 SLSFLL 11

RESULT 10

A11483
aspartate transaminase (EC 2.6.1.1), mitochondrial - sheep (fragment)
N:Alternate names: aspartate aminotransferase, mitochondrial
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 20-Aug-1999
C:Accession: A11483
R:Campos-Cavieles, M.; Milstein, C.P.
Biochem. J. 147, 275-281, 1975
A:Title: The sequences of the coenzyme-binding peptide in the cytoplasmic and the mitochondrial aspartate transaminase from sheep
A:Reference number: A11483; MUID:76039441; PMID:1180894
A:Accession: A11483
A:Molecule type: protein
A:Residues: 1-7 <CAM>
A:Experimental source: liver
C:Keywords: aminotransferase; mitochondrion; phosphoprotein; pyridoxal phosphate
F:2/Binding site: pyridoxal phosphate (lys) (covalent) #status experimental

Query Match 24.7%; Score 19; DB 2; Length 7;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 LGLY 11
|:|:|:
Db 4 MGLY 7

RESULT 11

A30823
bothropstoxin - jararacussu (fragment)
C:Species: Bothrops jararacussu (jararacussu)
C:Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
C:Accession: A30823
R:Homsí-Brandeburgo, M.I.; Queiroz, L.S.; Santo-Neto, H.; Rodrigues-Simioni, L.; Giglio,

Toxicon 26, 615-627, 1988

A:Title: Fractionation of Bothrops jararacussu snake venom: partial chemical characterization of the venom
A:Reference number: A30823; MUID:89020120; PMID:3176051
A:Accession: A30823
A:Molecule type: protein
A:Residues: 1-10 <HOM>
A:Cross-references: UNIPROT:Q7L225

Query Match 24.7%; Score 19; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 FQLG 9
|:|:
Db 3 FZLG 6

RESULT 12

D60787
sperm-activating peptide (Ser-1, Ala-3, Gly-5 speract) - sea urchin (Hemicentrotus pulcherrimus)
C:Species: Hemicentrotus pulcherrimus
C:Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 16-Aug-2004
C:Accession: D60787
R:Suzuki, N.; Kajihara, H.; Nomura, K.; Garbers, D.L.; Yoshino, K.; Kurita, M.; Tanaka, A.
Comp. Biochem. Physiol. B 89, 687-693, 1988
A:Title: Some more speract derivatives associated with eggs of sea urchins, Pseudocentrotus striatus
A:Reference number: A60787; MUID:88242184; PMID:3378407
A:Accession: D60787
A:Molecule type: protein
A:Residues: 1-10 <SUZ>
A:Cross-references: UNIPROT:Q7M4D1
C:Comment: This oligopeptide from egg jelly is one of several from this species, all of which show some, but not absolute, species restriction.

Query Match 24.7%; Score 19; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 SFQLG 9
|:|:|:
Db 1 SFALG 5

RESULT 13

A28018
very late antigen-1 alpha chain - human (fragment)
N:Alternate names: VLA-1 alpha chain
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 12-May-1994
C:Accession: A28018
R:Takada, Y.; Strominger, J.L.; Hemler, M.E.
Proc. Natl. Acad. Sci. U.S.A. 84, 3239-3243, 1987
A:Title: The very late antigen family of heterodimers is part of a superfamily of molecules
A:Reference number: A94151; MUID:87204112; PMID:3033641
A:Accession: A28018
A:Molecule type: protein
A:Residues: 1-14 <TAK>
C:Keywords: duplication; heterodimer; membrane protein

Query Match 24.7%; Score 19; DB 2; Length 14;
Best Local Similarity 60.0%; Pred. No. 4.5e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 DLSLF 6
|:|:|:
Db 7 DSWTF 11

RESULT 14

T46625
hypothetical protein c3 - loblolly pine
C:Species: Pinus taeda (loblolly pine)
C:Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000

C:Accession: T46625
R:Chang, S.; Puryea, J.; Funkhouser, E.A.; Newton, R.J.; Cairney, J.
submitted to the EMBL Data Library, July 1995
A:Description: Cloning of a chitinase homolog which lacks chitin binding sites and is d
A:Reference number: Z23105
A:Accession: T46625

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-15 <CHA>

A:Cross-references: EMBL:U31309; NID:G974285; PID:G974290

A:Experimental source: strain sePT2xs6PT3; 8 month seedlings

Query Match 24.7%; Score 19; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.8e+03; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 QLGL 10
Db 6 QLGL 9

RESULT 15

PCI317
large granule L4 chain - horseshoe crab (Tachyplesus tridentatus) (fragment)
C:Species: Tachyplesus tridentatus
C>Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999
C:Accession: PCI317
R:Shigenaga, T.; Takayenoki, Y.; Kawasaki, S.; Seki, N.; Muta, T.; Toh, Y.; Ito, A.; Iwa
J. Biochem. 114, 307-316, 1993
A:Title: Separation of large and small granules from horseshoe crab (Tachyplesus tridenta
A:Reference number: PCI309; MUID:94110249; PMID:8282718
A:Accession: PCI317
A:Molecule type: protein
A:Residues: 1-15 <SHI>
C:Comment: This protein participates in immobilization of invading microbes.

Query Match 24.7%; Score 19; DB 2; Length 15;
Best Local Similarity 38.5%; Pred. No. 4.8e+03;
Matches 5; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 2 DSLSPQLGLYLSP 14
Db 3 DEIFPHLLXKASP 15

Search completed: November 14, 2004, 13:17:23
Job time : 18.3333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:26 ; Search time 40.0532 Seconds
(without alignments)
215.479 Million cell updates/sec

Title: US-09-831-253F-9
Perfect score: 77
Sequence: 1 LDSLSFQLGLYLSPH 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 17482

Minimum DB seq length: 0
Maximum DB seq length: 23

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	35.1	12	1	FREI_LITIN
2	27	35.1	18	2	Q38573 litoria inf
3	27	35.1	23	2	Q91CX2 bacterioph
4	27	35.1	23	2	Q91CX8 tt virus. o
5	26	33.8	15	1	ASPI_LACSN
6	26	33.8	16	2	Q91CX7 lactobacill
7	26	33.8	17	2	Q9PRU8 Q91CX7 tt virus. o
8	26	33.8	18	2	Q9QUX0 Q91CX7 tt virus. o
9	26	33.8	19	2	Q8UVW4 Q91CX7 tt virus. o
10	25	32.5	23	2	Q9SC61 Q91CX7 tt virus. o
11	25	32.5	23	2	Q9R4T0 Q91CX7 tt virus. o
12	25	32.5	22	2	Q6ZX16 Q91CX7 tt virus. o
13	25	32.5	22	2	CAG27598 Q91CX7 tt virus. o
14	25	32.5	22	2	CAG27600 Q91CX7 tt virus. o
15	25	32.5	22	2	CAG27725 Q91CX7 tt virus. o
16	25	32.5	23	2	Q64065 Q91CX7 tt virus. o
17	24	31.2	15	2	Q7M3G3 Q91CX7 tt virus. o
18	24	31.2	18	2	Q9ZYV9 Q91CX7 tt virus. o
19	24	31.2	18	2	Q6RJY6 Q91CX7 tt virus. o
20	24	31.2	18	2	AAR83863 Q91CX7 tt virus. o
21	24	31.2	22	2	Q37112 Q91CX7 tt virus. o
22	24	31.2	22	2	Q9ZYX8 Q91CX7 tt virus. o
23	24	31.2	22	2	Q45654 Q91CX7 tt virus. o
24	23	29.9	9	2	P92072 Q91CX7 tt virus. o
25	23	29.9	15	2	Q9TR52 Q91CX7 tt virus. o
26	23	29.9	16	2	Q6LBM5 Q91CX7 tt virus. o
27	23	29.9	16	2	Q7L216 Q91CX7 tt virus. o
28	23	29.9	16	2	CAA40176 Q91CX7 tt virus. o
29	23	29.9	20	1	UCRQ_EQUAR
30	23	29.9	20	2	Q9TRA1
31	23	29.9	21	2	Q9TRA9

32	23	29.9	22	2	Q9RIW6
33	23	29.9	23	1	PQQA_PSEAE
34	23	29.9	23	2	Q7RDE9
35	23	29.9	23	2	Q9T2J3
36	23	29.9	23	2	Q39633
37	23	29.9	23	2	Q53469
38	22.5	29.2	19	2	Q9TWQ6
39	22.5	29.2	22	2	Q82520
40	22.5	29.2	23	1	SODM_RANCA
41	22	28.6	12	1	CD11_LITGH
42	22	28.6	12	1	CD11_LITGI
43	22	28.6	12	1	CD11_LITSP
44	22	28.6	12	1	CD11_LITXA
45	22	28.6	15	1	TRPA_LEUMA

ALIGNMENTS

RESULT 1					
FREI_LITIN					
ID - FREI_LITIN	STANDARD;	PRT;	12 AA.		
AC P82021;					
DT 30-MAY-2000 (Rel. 39, Created)					
DT 30-MAY-2000 (Rel. 39, Last sequence update)					
DT 05-JUL-2004 (Rel. 44, Last annotation update)					
DE Frenatin 1.					
OS Litoria infrafrenata (Giant tree frog).					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;					
OC Pelodyadinae; Litoria.					
OX NCBI_TaxID=61195;					
RN [1]					
RP SEQUENCE, AND MASS SPECTROMETRY.					
RC TISSUE=Skin secretion;					
RX MEDLINE=97368637; PubMed=9225251;					
RA Raftery M.J., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;					
RT "The structures of the frenatin peptides from the skin secretion of the giant tree frog Litoria infrafrenata.";					
RL J. Pept. Sci. 2:117-124(1996).					
CC -!- FUNCTION: wide spectrum antimicrobial peptide.					
CC -!- SUBCELLULAR LOCATION: Secreted.					
CC -!- TISSUE SPECIFICITY: Expressed by the skin parotoid and/or rostral glands.					
CC -!- MASS SPECTROMETRY: MW=1140; METHOD=FAB; RANGE=1-12; NOTE=Ref.1.					
KW Amidation; Amphibian defense peptide; Antibiotic;					
KW Direct protein sequencing.					
FT MOD RES 12 12 Leucine amide.					
SQ SEQUENCE 12 AA; 1141 MW; C622550BC365B72D CRC64;					
Query Match 35.1%; Score 27; DB 1; Length 12;					
Best Local Similarity 70.0%; Pred. No. 8.9e+02;					
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;					
QY	1	LDSLSFQLGL 10			
		: :			
DB	3	LDALSGLGL 12			
RESULT 2					
Q38573					
ID Q38573	PRELIMINARY;	PRT;	18 AA.		
AC Q38573;					
DT 01-NOV-1996 (TREMREL. 01, Created)					
DT 01-NOV-1996 (TREMREL. 01, Last sequence update)					
DT 01-MAR-2004 (TREMREL. 26, Last annotation update)					
DE Coat protein (Fragment).					
OS Bacteriophage Kul.					
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;					
OC Levivirus.					
OX NCBI_TaxID=12021;					
RN [1]					
RP SEQUENCE FROM N.A.					

```

RX MEDLINE=96207403; PubMed=8615017;
RA Groeneveld H., Oudot F., van Duin J.V.;
RT "RNA phage KGI has an insertion of 18 nucleotides in the start codon
of its lysis gene.";
RL Virology 218:141-147(1996).
DR EMBL; S81763; AAD14371.1; -.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
KW Coat protein.
FT NON_TER 1
SQ SEQUENCE 18 AA; 1825 MW; 2D4092DC226D8904 CRC64;

Query Match 35.1%; Score 27; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 DLSLQGLGLY 11
DB 8 DAISQSGFY 17

RESULT 3
Q91CX2 PRELIMINARY; PRT; 23 AA.
AC Q91CX2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ORF1 (Fragment).
GN Name=ORF1;
OS TT virus.
OC Viruses; ssDNA viruses; Circoviridae; Anellovirus.
OX NCBI_TaxID=68887;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21488921; PubMed=11601907;
RA Okamoto H., Nishizawa T., Takahashi M., Asabe S., Tsuda F.,
RA Yoshikawa A.;
RT "Heterogeneous distribution of TT virus of distinct genotypes in
multiple tissues from infected humans.";
RL Virology 288:358-368(2001).
DR EMBL; AB060623; BAB69943.1; -.
FT NON_TER 1
SQ SEQUENCE 23 AA; 2710 MW; 51246068099E107F CRC64;

Query Match 35.1%; Score 27; DB 2; Length 23;
Best Local Similarity 45.5%; Pred. No. 1.8e+03;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 LSFQLGLYLSP 14
DB 7 LKTAQGVHLNP 17

RESULT 4
Q91CX8 PRELIMINARY; PRT; 23 AA.
AC Q91CX8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ORF1 (Fragment).
GN Name=ORF1;
OS TT virus.
OC Viruses; ssDNA viruses; Circoviridae; Anellovirus.
OX NCBI_TaxID=68887;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21488921; PubMed=11601907;
RA Okamoto H., Nishizawa T., Takahashi M., Asabe S., Tsuda F.,
RA Yoshikawa A.;
RT "Heterogeneous distribution of TT virus of distinct genotypes in
multiple tissues from infected humans.";

```

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RL Virology 288:358-368(2001).
DR EMBL; AB060605; BAB69928.1; -.
FT NON_TER 1
SQ SEQUENCE 23 AA; 2710 MW; 51246068099E107F CRC64;

Query Match 35.1%; Score 27; DB 2; Length 23;
Best Local Similarity 45.5%; Pred. No. 1.8e+03;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 LSFQLGLYLSP 14
DB 7 LKTAQGVHLNP 17

RESULT 5
ASPI_LACSN STANDARD; PRT; 15 AA.
ID ASPI_LACSN
AC P82648;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Acid shock protein 1 (Fragment).
OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1625;
RN [1]
RP SEQUENCE.
RX MEDLINE=2132712; PubMed=11429463;
RA De Angelis M., Bini L., Pallini V., Coconcelli P.S., Gobetti M.;
RT "The acid-stress response in Lactobacillus sanfranciscensis CBL.";
RL Microbiology 147:1863-1873(2001).
KW Direct protein sequencing.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1509 MW; 575853B4DFB030A8 CRC64;

Query Match 33.8%; Score 26; DB 1; Length 15;
Best Local Similarity 62.5%; Pred. No. 1.7e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 SFQLGLYL 12
DB 1 SPKGLFL 8

RESULT 6
Q91CX7 PRELIMINARY; PRT; 16 AA.
ID Q91CX7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ORF1 (Fragment).
GN Name=ORF1;
OS TT virus.
OC Viruses; ssDNA viruses; Circoviridae; Anellovirus.
OX NCBI_TaxID=68887;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21488921; PubMed=11601907;
RA Okamoto H., Nishizawa T., Takahashi M., Asabe S., Tsuda F.,
RA Yoshikawa A.;
RT "Heterogeneous distribution of TT virus of distinct genotypes in
multiple tissues from infected humans.";
RL Virology 288:358-368(2001).
DR EMBL; AB060615; BAB69936.1; -.
FT NON_TER 1
SQ SEQUENCE 16 AA; 1793 MW; E152327E7C679238 CRC64;

Query Match 33.8%; Score 26; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;

```


Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 7 QLGLYLSLP 14
| | | | |
Db 3 QAGLHNP 10

RESULT 7

ID Q9PRU8 PRELIMINARY; PRT; 17 AA.
AC Q9PRU8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE P130=PHOSPHOPROTEINS TIGHTLY associated with V-CRK in VIVO (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE.
RX MEDLINE=95105151; PubMed=7806494;
RA Sakai R., Iwamatsu A., Hirano N., Ogawa S., Tanaka T., Nishida J.,
RA Yazaki Y., Hirai H.;
RT "Characterization, partial purification, and peptide sequencing of
RT p130, the main phosphoprotein associated with v-Crk oncoprotein.";
RL J. Biol. Chem. 269:32740-32746(1994).
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 1861 MW; 379058CDE44F8879 CRC64;

Query Match 33.8%; Score 26; DB 2; Length 17;
Best Local Similarity 62.5%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 QLGLYLSLP 14
| | | | |
Db 2 QOGLYQAP 9

RESULT 8

ID Q9QUX0 PRELIMINARY; PRT; 18 AA.
AC Q9QUX0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE TUMORLYTIC factor (Fragment).
OS Mus sp..
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE.
RX MEDLINE=96078161; PubMed=7590903;
RA Kita E., Matsui N., Sawaki M., Mikasa K., Katsui N.;
RT "Murine tumorigenic factor, immunologically distinct from tumor
RT necrosis factor-alpha and -beta, induced in the serum of mice treated
RT with a T-cell mitogen of Corynebacterium kutscheri.";
RL Immunol. Lett. 46:101-106(1995).
SQ SEQUENCE 18 AA; 2049 MW; 3544227DA4EFD1D0 CRC64;

Query Match 33.8%; Score 26; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 2.1e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 8 LGLYLSLP 15
| | | | |
Db 8 MGLYMLTH 15

RESULT 9

ID Q8UVW4 PRELIMINARY; PRT; 19 AA.
AC Q8UVW4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE AMPA receptor subunit 2 (Fragment).
GN Name=gria2.1; Synonyms=glur2a;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21617183; PubMed=11741603;
RA Kung S.-S., Chen Y.-C., Lin W.-H., Chen C.-C., Chow W.-Y.;
RT "Q/R RNA editing of the AMPA receptor subunit 2 (GRIA2) transcript
RT evolves no later than the appearance of cartilaginous fishes.";
RL FEBS Lett. 509:277-281(2001).
DR EMBL; AF350048; AAL57190.1; -.
DR ZFIN; ZDB-GENE-020125-3; gria2.1.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 2101 MW; 19490444CB82EF5B CRC64;

Query Match 33.8%; Score 26; DB 2; Length 19;
Best Local Similarity 45.5%; Pred. No. 2.2e+03;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 DLSFOLGLYL 12
: | | | | |
Db 1 NSLWFSLGAPM 11

RESULT 10

ID Q9SC61 PRELIMINARY; PRT; 23 AA.
AC Q9SC61;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Ribonuclease H (Fragment).
GN Name=RNaseH;
OS Picea abies (Norway spruce) (Picea excelsa).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
OX NCBI_TaxID=3329;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20040041; PubMed=10571856;
RA Pearce S.R., Stuart-Rogers C.M., Knox M.R., Kumar A., Ellis N.T.,
RA Flavell A.J.;
RT "Rapid isolation of plant Tyl-copia group retrotransposon LTR
RT sequences for molecular marker studies.";
RL Plant J. 19:711-717(1999).
DR EMBL; AJ243314; CAB65328.1; -.
FT NON_TER 1
FT NON_TER 23
SQ SEQUENCE 23 AA; 2678 MW; 6C9FD7957DCFAB64 CRC64;

Query Match 33.8%; Score 26; DB 2; Length 23;
Best Local Similarity 50.0%; Pred. No. 2.7e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 LSFOLGLY 11
: | | | | |
Db 16 IQFMLGVY 23

RESULT 11

Q9R4T0 PRELIMINARY; PRT; 15 AA.
 AC Q9R4T0; DB 15 AA.
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DE Periplasmic protein 5 (Fragment)
 OS Rhodospirillum rubrum (Rhodospirillum rubrum)
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
 OC Rhodospirillaceae; Rhodospirillum
 RN NCBI_TaxID=1063;
 RX MEDLINE=95160605; PubMed=7857198;
 RA Sabaty M., Gagnon J., Vermeil A.;
 RT "Induction by nitrate of cytoplasmic and periplasmic proteins in the
 RT photodinitrifier Rhodospirillum rubrum forma sp. denitrificans under
 RT anaerobic or aerobic condition."
 RL Arch. Microbiol. 162:335-343(1994)
 SQ SEQUENCE 15 AA; 1718 MW; DA5BF4BD9AEBE157 CRC64;

Query Match 32.5%; Score 25; DB 2; Length 15;
 Best Local Similarity 55.6%; Pred. No. 2.6e+03;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 DLSLFSQGL 10

DB 4 DSETFQSGM 12

RESULT 12

Q6ZXI6 PRELIMINARY; PRT; 22 AA.
 AC Q6ZXI6;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Harpin (Fragment)
 GN Name=hrpW;
 OS Erwinia amylovora.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Erwinia.
 RN NCBI_TaxID=552;
 RX MEDLINE=95160605; PubMed=7857198;
 RA Sabaty M., Gagnon J., Vermeil A.;
 RT "Induction by nitrate of cytoplasmic and periplasmic proteins in the
 RT photodinitrifier Rhodospirillum rubrum forma sp. denitrificans under
 RT anaerobic or aerobic condition."
 RL Arch. Microbiol. 162:335-343(1994)
 SQ SEQUENCE 22 AA; 2245 MW; CC34D82FCC1BC69B CRC64;

Query Match 32.5%; Score 25; DB 2; Length 22;
 Best Local Similarity 66.7%; Pred. No. 3.9e+03;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 SFQGLGLYLS 13

DB 11 SSSLGLYQS 19

RESULT 13

CAG27598 PRELIMINARY; PRT; 22 AA.
 AC CAG27598;
 DT 10-MAY-2004 (TrEMBLrel. 27, Created)
 DT 10-MAY-2004 (TrEMBLrel. 27, Last sequence update)
 DE Harpin (Fragment)
 GN Harpin
 OS Erwinia amylovora.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Erwinia.
 RN NCBI_TaxID=552;
 RX MEDLINE=95160605; PubMed=7857198;
 RA Sabaty M., Gagnon J., Vermeil A.;
 RT "Induction by nitrate of cytoplasmic and periplasmic proteins in the
 RT photodinitrifier Rhodospirillum rubrum forma sp. denitrificans under
 RT anaerobic or aerobic condition."
 RL Arch. Microbiol. 162:335-343(1994)
 SQ SEQUENCE 22 AA; 2245 MW; CC34D82FCC1BC69B CRC64;

Query Match 32.5%; Score 25; DB 2; Length 22;
 Best Local Similarity 66.7%; Pred. No. 3.9e+03;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 SFQGLGLYLS 13

DB 11 SSSLGLYQS 19

OS Erwinia amylovora.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Erwinia.
 RN NCBI_TaxID=552;
 RX MEDLINE=95160605; PubMed=7857198;
 RA Sabaty M., Gagnon J., Vermeil A.;
 RT "Induction by nitrate of cytoplasmic and periplasmic proteins in the
 RT photodinitrifier Rhodospirillum rubrum forma sp. denitrificans under
 RT anaerobic or aerobic condition."
 RL Arch. Microbiol. 162:335-343(1994)
 SQ SEQUENCE 22 AA; 2245 MW; CC34D82FCC1BC69B CRC64;

Query Match 32.5%; Score 25; DB 2; Length 22;
 Best Local Similarity 66.7%; Pred. No. 3.9e+03;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 SFQGLGLYLS 13

DB 11 SSSLGLYQS 19

RESULT 14

CAG27600 PRELIMINARY; PRT; 22 AA.
 AC CAG27600;
 DT 10-MAY-2004 (TrEMBLrel. 27, Created)
 DT 10-MAY-2004 (TrEMBLrel. 27, Last sequence update)
 DE Harpin (Fragment)
 GN Harpin
 OS Erwinia amylovora.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Erwinia.
 RN NCBI_TaxID=552;
 RX MEDLINE=95160605; PubMed=7857198;
 RA Sabaty M., Gagnon J., Vermeil A.;
 RT "Induction by nitrate of cytoplasmic and periplasmic proteins in the
 RT photodinitrifier Rhodospirillum rubrum forma sp. denitrificans under
 RT anaerobic or aerobic condition."
 RL Arch. Microbiol. 162:335-343(1994)
 SQ SEQUENCE 22 AA; 2245 MW; CC34D82FCC1BC69B CRC64;

Query Match 32.5%; Score 25; DB 2; Length 22;
 Best Local Similarity 66.7%; Pred. No. 3.9e+03;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 SFQGLGLYLS 13

DB 11 SSSLGLYQS 19

RESULT 15

CAG27725 PRELIMINARY; PRT; 22 AA.
 AC CAG27725;
 DT 10-MAY-2004 (TrEMBLrel. 27, Created)
 DT 10-MAY-2004 (TrEMBLrel. 27, Last sequence update)
 DE Harpin (Fragment)
 GN Harpin
 OS Erwinia amylovora.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Erwinia.
 RN NCBI_TaxID=552;
 RX MEDLINE=95160605; PubMed=7857198;
 RA Sabaty M., Gagnon J., Vermeil A.;
 RT "Induction by nitrate of cytoplasmic and periplasmic proteins in the
 RT photodinitrifier Rhodospirillum rubrum forma sp. denitrificans under
 RT anaerobic or aerobic condition."
 RL Arch. Microbiol. 162:335-343(1994)
 SQ SEQUENCE 22 AA; 2245 MW; CC34D82FCC1BC69B CRC64;

Query Match 32.5%; Score 25; DB 2; Length 22;
 Best Local Similarity 66.7%; Pred. No. 3.9e+03;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 SFQGLGLYLS 13

DB 11 SSSLGLYQS 19

RP SEQUENCE FROM N.A.
RC STRAIN=PD 2915;
RA Giorgi S., Scortichini M.;
RT "Molecular characterization of Erwinia amylovora strains isolated from
RT different host plants through genomic fingerprinting and RFLP analysis
RT and sequencing of hrpN and dspA genes.";
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ698952; CAG27725.1; -.
FT NON TER 22 22
SQ SEQUENCE 22 AA; 2245 MW; CC34D82FCC1BC69B CRC64;

Query Match 32.5%; Score 25; DB 2; Length 22;
Best Local Similarity 66.7%; Pred. No. 3.9e+03;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 SFQLGLYLS 13
| | | | |
Db 11 SSSLGLYQS 19

Search completed: November 14, 2004, 12:07:38
Job time : 42.0532 secs

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OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:25 ; Search time 9.25532 Seconds
(without alignments)
155.938 Million cell updates/sec

Title: US-09-831-253F-9

Perfect score: 77

Sequence: 1 LDSLSFQLGLYLSPH 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 4495

Minimum DB seq length: 0

Maximum DB seq length: 23

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	30	39.0	20	2 S10876	hypothetical prote
2	29	37.7	11	2 A35594	buccalin - Califor
3	27	35.1	19	2 B53145	high conductance c
4	25	32.5	16	2 PH1634	Ig H chain V-D-J r
5	24	31.2	15	2 A35417	28K serine protein
6	24	31.2	15	4 I38335	hypothetical TEL/M
7	24	31.2	22	2 S29326	hypothetical prote
8	23	29.9	11	2 PH0914	T-cell receptor be
9	23	29.9	12	2 C36201	1-aminocyclopropan
10	23	29.9	16	2 A42411	myosin light chain
11	23	29.9	17	2 A58946	formylmethanofuran
12	23	29.9	23	2 PQ0690	photosystem I 8.0K
13	23	29.9	23	2 A83397	pyrroloquinoline q
14	23	29.9	23	2 T10123	probable catalase
15	22.5	29.2	19	2 FC1309	small granule S2 c
16	22	28.6	19	2 A39729	gene hMLH1 protein
17	22	28.6	19	2 I52721	amylase (EC 3.2.1.
18	22	28.6	23	1 S20453	pyrroloquinoline q
19	21	27.3	15	2 A47628	Pc gamma receptor
20	21	27.3	18	2 S55501	thrombospondin pre
21	21	27.3	18	4 I39461	anti-angiogenesis,
22	21	27.3	20	2 A61576	insulin-like growt
23	21	27.3	21	2 S03504	T-cell receptor al
24	20	26.0	11	4 PC2124	aminotransferase c
25	20	26.0	12	2 B61497	seed protein ws-17
26	20	26.0	14	2 B61597	cytochrome P450 AL
27	20	26.0	16	2 S11290	matrix protein M1
28	20	26.0	16	2 S51057	ribosomal protein
29	20	26.0	17	2 JH0785	DNA-directed RNA p

30	20	26.0	18	2 S09087	proteasome chain 6
31	20	26.0	19	2 PS0332	phospholipase A2 (
32	20	26.0	20	2 S00774	kinase-related tra
33	20	26.0	20	2 A56900	chymotrypsin I (EC
34	20	26.0	20	2 S03505	T-cell receptor al
35	20	26.0	21	2 JQ2196	hypothetical 2.5K
36	20	26.0	22	2 S09021	carboxylesterase (
37	20	26.0	22	2 T45268	hypothetical prote
38	19	24.7	7	2 A11483	aspartate transami
39	19	24.7	10	2 A30823	bothropstoxin - ja
40	19	24.7	10	2 D60787	sperm-activating p
41	19	24.7	14	2 A28018	very late antigen-
42	19	24.7	15	2 T46625	hypothetical prote
43	19	24.7	15	2 PC1317	large granule L4 c
44	19	24.7	15	2 B45115	peptidylprolyl iso
45	19	24.7	15	2 C32521	hexokinase (EC 2.7

ALIGNMENTS

RESULT 1

S10876

hypothetical protein - human

C;Species: Homo sapiens (man)

C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 18-Nov-1994

C;Accession: S10876

R;Assouline, Z.; Kerbirou-Nabias, D.M.; Pietu, G.; Thomas, N.; Bahnak, B.R.; Meyer, D.

Biochem. Biophys. Res. Commun. 153, 1159-1166, 1988

A;Title: The human gene for von Willebrand factor. Identification of repetitive Alu seq

A;Reference number: S10876; MUID:88268889; PMID:3260493

A;Accession: S10876

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-20 <ASS>

A;Cross-references: EMBL:X07258

Query Match 39.0%; Score 30; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 70;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 QLGLYL 12

DB 3 QLGLYL 8

RESULT 2

A35594

buccalin - California sea hare

C;Species: Aplysia californica (California sea hare)

C;Date: 14-Sep-1990 #sequence_revision 14-Sep-1990 #text_change 09-Jul-2004

C;Accession: A35594

R;Cropper, E.C.; Miller, M.W.; Tenenbaum, R.; Kolks, M.A.G.; Kupfermann, I.; Weiss, K.R.

Proc. Natl. Acad. Sci. U.S.A. 85, 6177-6181, 1988

A;Title: Structure and action of buccalin: a modulatory neuropeptide localized to an id

A;Reference number: A35594; MUID:88320404; PMID:3413086

A;Accession: A35594

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <CRO>

A;Cross-references: UNIPROT:P20481

Query Match 37.7%; Score 29; DB 2; Length 11;

Best Local Similarity 60.0%; Pred. No. 56;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LDSLSFQLGL 10

DB 2 MDSLAFSGGL 11

RESULT 3

B53145

high conductance calcium-activated potassium channel, maxi-K channel - bovine (fragment)
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C:Accession: B53145

R;Knaus, H.G.; Garcia-Calvo, M.; Kaczorowski, G.J.; Garcia, M.L.
 J. Biol. Chem. 269, 3921-3924, 1994

A;Title: Subunit composition of the high conductance calcium-activated potassium channel
 A;Reference number: A35145; MUID:94140798; PMID:7508434

A;Accession: B53145

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-19 <KNA>

A;Cross-references: UNIPROT:Q28204; UNIPROT:Q9TS86

A;Note: sequence extracted from NCBI backbone (NCBIP:144547)

C;Superfamily: fruit fly calcium-activated potassium channel slo

Query Match 35.1%; Score 27; DB 2; Length 19;

Best Local Similarity 41.7%; Pred. No. 2.3e+02;

Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 LSFQLGLYLSPH 15

DB 5 VEFYQGSVLNPH 16

|||

|||

RESULT 4

PH1634

I9 H chain V-D-J region (clone B-less 213) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999

C:Accession: PH1634

R;Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
 A;Reference number: PH1580; MUID:93301609; PMID:8315387

A;Accession: PH1634

A;Molecule type: DNA

A;Residues: 1-16 <LEV>

A;Experimental source: bone marrow pre-B lymphocyte

C;Keywords: immunoglobulin

Query Match 32.5%; Score 25; DB 2; Length 16;

Best Local Similarity 80.0%; Pred. No. 4.4e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 YLSPH 15

DB 6 YVSPH 10

|||

|||

RESULT 5

A35417

28K serine proteinase homolog - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C>Date: 18-Jan-1991 #sequence_revision 18-Jan-1991 #text_change 09-Jul-2004

C:Accession: A35417

R;Ho, P.L.; Carpenter, M.R.; Smillie, L.B.; Gambarini, A.G.

Biochem. Biophys. Res. Commun. 170, 769-774, 1990

A;Title: Co-purification of proteases with basic fibroblast growth factor (FGF).

A;Reference number: A35417; MUID:90343797; PMID:2200404

A;Accession: A35417

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-15 <HOA>

A;Cross-references: UNIPROT:Q7M3G3

Query Match 31.2%; Score 24; DB 2; Length 15;

Best Local Similarity 30.8%; Pred. No. 6.2e+02;

Matches 4; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 DSLSFQLGLYLSPH 14

DB 3 DSIDYRKGVVTP 15

|||

|||

RESULT 6

I38335

hypothetical TEL/MNI mutant fusion protein type II - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 20-Apr-2000

C:Accession: I38335

R;Bulj, A.; Sherr, S.; van Baal, S.; van Bezouw, S.; van der Plas, D.; Van Kessel, A.G.

Oncogene 10, 1511-1519, 1995

A;Title: Translocation (12;22) (p13;q11) in myeloproliferative disorders results in fus;

A;Reference number: I38031; MUID:95249265; PMID:7731705

A;Accession: I38335

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-15 <BUI>

A;Cross-references: EMBL:X85024; NID:971471; PIDN:CAA59397.1; PID:971472

C;Comment: This sequence is the chimeric product of a translocation mutation.

C;Genetics:

A;Gene: ETV6/MNI; TEL/MNI

A;Map position: 22q11/12p13

C;Keywords: fusion protein

Query Match 31.2%; Score 24; DB 4; Length 15;

Best Local Similarity 80.0%; Pred. No. 6.2e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 YLSPH 15

DB 2 YRSPH 6

|||

|||

RESULT 7

S29326

hypothetical protein 22, psbA 5'-region - Japanese black pine chloroplast

C:Species: chloroplast Pinus thunbergiana (Japanese black pine)

C>Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 09-Jul-2004

C:Accession: S29326; T07427

R;Tsudzuki, J.; Nakashima, K.; Tsudzuki, T.; Hirtsuka, J.; Shibata, M.; Wakasugi, T.; S

Mol. Gen. Genet. 232, 206-214, 1992

A;Title: Chloroplast DNA of black pine retains a residual inverted repeat lacking rRNA

A;Reference number: S20449; MUID:92212283; PMID:1557027

A;Accession: S29326

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-22 <TSU>

A;Cross-references: UNIPROT:Q37112; EMBL:D11467; NID:9344007; PIDN:BAA02023.1; PID:93440

R;Wakasugi, T.; Tsudzuki, J.; Ito, S.; Nakashima, K.; Tsudzuki, T.; Sugiura, M.

Proc. Natl. Acad. Sci. U.S.A. 91, 9794-9798, 1994

A;Title: Loss of all ndh genes as determined by sequencing the entire chloroplast genom

A;Reference number: Z16030; MUID:95024047; PMID:7937893

A;Accession: T07427

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-22 <WAK>

A;Cross-references: EMBL:D17510; NID:9529643; PIDN:BAA04307.1; PID:91262588

C;Genetics:

A;Genome: chloroplast

C;Keywords: chloroplast

Query Match 31.2%; Score 24; DB 2; Length 22;

Best Local Similarity 50.0%; Pred. No. 9.3e+02;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 SFQLGLYL 12

DB 9 SIECGIYL 16

|||

|||

RESULT 8

PH0914

T-cell receptor beta chain V-D-J region (isolate 7) - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0914
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0914
A;Molecule type: mRNA
A;Residues: 1-11 <GO>
A;Experimental source: myelin basic protein-immunized lymph node
C;Keywords: T-cell receptor

Query Match 29.9%; Score 23; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. No. 6.7e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 DLSLFQ 7
|||:
5 DLSLYE 10

Db

RESULT 9
C36201
l-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) - apple tree (fragment)
C;Species: Malus domestica (apple tree)
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 09-Jul-2004
C;Accession: C36201; C33103
R;Yip, W.K.; Dong, J.G.; Kenny, J.W.; Thompson, G.A.; Yang, S.F.
Proc. Natl. Acad. Sci. U.S.A. 87, 7930-7934, 1990
A;Title: Characterization and sequencing of the active site of l-aminocyclopropane-1-car
A;Reference number: A36201; MUID:91045911; PMID:2122449
A;Accession: C36201
A;Molecule type: protein
A;Residues: 1-12 <YIP>
A;Cross-references: UNIPROT:Q9PUC3; UNIPROT:Q9SB01; UNIPROT:Q9SB94; UNIPROT:Q24062
A;Experimental source: strain Golden delicious
C;Superfamily: l-aminocyclopropane-1-carboxylate synthase
C;Keywords: carbon-sulfur lyase; ethylene biosynthesis; phosphoprotein; pyridoxal phosph
F;4/Binding site: pyridoxal phosphate (Lys) (covalent) #status experimental

Query Match 29.9%; Score 23; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 7.3e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 SLSFQLGL 10
|||:
1 SLSKDLGL 8

Db

RESULT 10
A42411
myosin light chain kinase - chicken
C;Species: Gallus gallus (chicken)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A42411
R;Leachman, S.A.; Gallagher, P.J.; Herring, B.P.; McPhaul, M.J.; Stull, J.T.
J. Biol. Chem. 267, 4930-4938, 1992
A;Title: Biochemical properties of chimeric skeletal and smooth muscle myosin light chain
A;Reference number: A42411; MUID:92185861; PMID:1371510
A;Accession: A42411
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid; protein
A;Residues: 1-16 <LEA>
A;Cross-references: UNIPROT:Q7LZ16
A;Experimental source: skeletal muscle
A;Note: sequence extracted from NCBI backbone (NCBIP:84332)

Query Match 29.9%; Score 23; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LSPH 15
|||

Db 13 LSPH 16

RESULT 11
A58946
formylmethanofuran dehydrogenase (EC 1.2.99.5) (molybdenum) chain C - Methanobacterium
N;Alternate names: formylmethanofuran dehydrogenase (molybdenum) chain B [misidentifica
C;Species: Methanobacterium thermoautotrophicum
C;Date: 16-Apr-1999 #sequence_revision 16-Apr-1999 #text_change 04-Feb-2000
C;Accession: A58946
R;Hochheimer, A.; Schmitz, R.A.; Thauer, R.K.; Hedderich, R.
Eur. J. Biochem. 234, 910-920, 1995
A;Title: The tungsten formylmethanofuran dehydrogenase from Methanobacterium thermoauto
A;Reference number: S63519; MUID:96163477; PMID:8575452
A;Accession: A58946
A;Molecule type: protein
A;Residues: 1-17 <HOC>
A;Note: the authors identify this peptide as the amino terminus of chain B, but it appe
C;Keywords: iron-sulfur protein; metalloprotein; molybdenum; molybdopterin; oxidoreduct

Query Match 29.9%; Score 23; DB 2; Length 17;
Best Local Similarity 80.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 FQLGL 10
|||:
10 FQIGL 14

Db

RESULT 12
PQ0690
photosystem I 8.0 K chain - common tobacco (fragment)
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 17-Mar-1999
C;Accession: PQ0690
R;Obokata, J.; Mikami, K.; Hayashida, N.; Nakamura, M.; Sugitara, M.
Plant Physiol. 102, 1259-1267, 1993
A;Title: Molecular heterogeneity of photosystem I. psaD, psaE, psaF, psaH and psaL are
A;Reference number: PQ0667; MUID:94105345; PMID:8278548
A;Accession: PQ0690
A;Molecule type: protein
A;Residues: 1-23 <ORO>
C;Superfamily: photosystem I chain V
C;Keywords: chloroplast; photosynthesis; photosystem I; thylakoid

Query Match 29.9%; Score 23; DB 2; Length 23;
Best Local Similarity 60.0%; Pred. No. 1.5e+03;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 SLSFQLGLYL 12
|||:
9 SLSTGLSLFL 18

Db

RESULT 13
A83397
pyrroloquinoline quinone biosynthesis protein A PA1985 [imported] - Pseudomonas aerugin
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: A83397
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: A83397
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-23 <STO>
A;Cross-references: UNIPROT:Q9ZAA0; GB:AE004625; GB:AE0047983; PIDN:AA0505
A;Experimental source: strain PA01
C;Genetics:

A;Gene: pqQA; PA1985

Query Match 29.9%; Score 23; DB 2; Length 23;
Best Local Similarity 40.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 3; Mismatches 0; Gaps 0;

QY 4 LSFQLGLYLS 13
| | | | |
Db 12 LGFEVTLYFA 21

RESULT 14

T10123
probable catalase (EC 1.11.1.6) - cucumber (fragment)
C;Species: Cucumis sativus (cucumber)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T10123
R;Toyama, T.; Teramoto, H.; Takeba, G.; Tsuji, H.
Plant Cell Physiol. 36, 1349-1359, 1995
A;Title: Cytokinin induces a rapid decrease in the levels of mRNAs for catalase, 3-hydroxyisovaleryl-CoA synthetase, and isochlorogenic acid synthase
A;Reference number: Z16946; MUID:96104306; PMID:8564304
A;Accession: T10123
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-23 <TOY>
A;Cross-references: UNIPROT:Q39633; EMBL:D63385; NID:g1199475; PIDN:BAA09701.1; PID:g1199475
A;Experimental source: seedling; cotyledons
C;Keywords: oxidoreductase

Query Match 29.9%; Score 23; DB 2; Length 23;
Best Local Similarity 50.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 8 LGLYLSPH 15
| | | | |
Db 9 VGQKLAPH 16

RESULT 15

PC1309
small granule S2 chain - horseshoe crab (Tachyplesus tridentatus) (fragment)
C;Species: Tachyplesus tridentatus
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 09-Jul-2004
C;Accession: PC1309
R;Shigenaga, T.; Takayanoki, Y.; Kawasaki, S.; Seki, N.; Muta, T.; Toh, Y.; Ito, A.; Iwa
J. Biochem. 114, 307-316, 1993
A;Title: Separation of large and small granules from horseshoe crab (Tachyplesus tridentatus)
A;Reference number: PC1309; MUID:94110249; PMID:8282718
A;Accession: PC1309
A;Molecule type: protein
A;Residues: 1-19 <SHI>
A;Cross-references: UNIPROT:Q9TW06
C;Comment: This protein contributes to a self-defense system against invaders.

Query Match 29.2%; Score 22.5; DB 2; Length 19;
Best Local Similarity 54.5%; Pred. No. 1.5e+03;
Matches 6; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 4 LSFQLGLYLS 14
| | | | |
Db 2 LAFKXGRY-SP 11

Search completed: November 14, 2004, 12:03:15
Job time : 10.2553 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:25 ; Search time 43.4043 Seconds
(without alignments)
123.973 Million cell updates/sec

Title: US-09-831-253F-9

Perfect score: 77
Sequence: 1 LDSLSFQLGLYLSPH 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 718658

Minimum DB seq length: 0
Maximum DB seq length: 23

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	77	100.0	15	3 AAY93106	Aay93106 Transform
2	77	100.0	15	3 AAY92953	Aay92953 Transform
3	33	42.9	20	8 ADM29169	Adm29169 Hepatitis
4	32	41.6	16	4 AAB68433	Aab68433 Peptide d
5	32	41.6	20	2 AAR82557	Aar82557 Bovine PL
6	31	40.3	10	4 AAG83462	Aag83462 Arabidops
7	31	40.3	15	5 ABP58975	Abp58975 Human I k
8	30	39.0	15	5 AAM47809	Aam47809 Miniature
9	30	39.0	17	6 ABP82548	Abp82548 G protein
10	30	39.0	21	2 AAW17133	Aaw17133 Rabbit 3-
11	30	39.0	23	4 AAE09350	Aae09350 Human ion
12	30	39.0	23	4 AAE10097	Aae10097 Human ion
13	30	39.0	23	6 ABU97358	Abu97358 Amino aci
14	30	39.0	23	6 ABO12018	Abol12018 Human zin
15	30	39.0	23	7 ADE92976	Ade92976 Novel hum
16	29.5	38.3	16	5 ABP46134	Abp46134 Human Bly
17	29.5	38.3	16	7 ADG96961	Adg96961 scFv VHCD
18	29	37.7	11	8 ADN03302	Adn03302 Exemplary
19	29	37.7	12	3 AAB07274	Aab07274 Human pep
20	29	37.7	12	6 ABR00682	Abr00682 HCV nonst
21	29	37.7	13	6 ABR00699	Abr00699 HCV nonst
22	29	37.7	13	6 ABR00693	Abr00693 HCV nonst
23	29	37.7	14	4 AAM97619	Aam97619 Human pep
24	29	37.7	14	6 ABR00703	Abr00703 HCV nonst
25	29	37.7	14	6 ABR00706	Abr00706 HCV nonst

26	29	37.7	15	6 ABR00715	Abr00715 HCV nonst
27	29	37.7	15	6 ABR00714	Abr00714 HCV nonst
28	29	37.7	16	6 ABR00725	Abr00725 HCV nonst
29	29	37.7	16	6 ABR00726	Abr00726 HCV nonst
30	29	37.7	17	2 AAR91038	Aar91038 V8 protea
31	29	37.7	17	6 ABR00732	Abr00732 HCV nonst
32	29	37.7	17	6 ABR00731	Abr00731 HCV nonst
33	29	37.7	18	6 ABR00733	Abr00733 HCV nonst
34	29	37.7	18	6 ABR00735	Abr00735 HCV nonst
35	29	37.7	19	6 ABR00739	Abr00739 HCV nonst
36	29	37.7	19	6 ABR00741	Abr00741 HCV nonst
37	29	37.7	20	6 ABR00742	Abr00742 HCV nonst
38	29	37.7	20	6 ABR00743	Abr00743 HCV nonst
39	29	37.7	21	6 ABR00745	Abr00745 HCV nonst
40	29	37.7	21	6 ABR00746	Abr00746 HCV nonst
41	29	37.7	22	6 ABR00594	Abr00594 HCV nonst
42	29	37.7	23	2 AAY27698	Aay27698 Human sec
43	29	37.7	23	6 ABO14129	Abol14129 Novel hum
44	29	37.7	23	8 ADG78536	Adg78536 Human sec
45	29	37.7	23	8 ADN60827	Adn60827 Human sec

ALIGNMENTS

RESULT 1

AAAY93106
ID AAY93106 standard; peptide; 15 AA.

XX AC AAY93106;

XX DT 08-NOV-2000 (first entry)

XX DE Transforming growth factor inhibitory peptide P152.

XX XX Hepatotrophic; antagonist; transforming growth factor betaf; TGF-b1;

KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;

KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.

XX OS Homo sapiens.

XX PN WO200031135-A1.

XX PD 02-JUN-2000.

XX PF 23-NOV-1999; 99WO-ES000375.

XX PR 24-NOV-1998; 98ES-00002465.

(CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.

PI Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
PI Borrás Cuesta F;

XX WPI; 2000-411935/35.

PT Peptides that antagonize binding of transforming growth factor betaf.
PT useful for treatment of liver disease, especially cirrhosis, are partial
PT sequences of the factor or its receptors.

PS Disclosure; Page 33; 86pp; Spanish.

XX CC The invention relates to synthetic peptides that antagonise the binding
XX of transforming growth (TGF) factor betaf (TGF-b1) to its receptor in
XX vivo which have partial amino acid sequences identical, or similar, with
XX those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
XX examples of the peptides of the invention. The peptides act by
XX competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
XX they are inhibitors of stimulation of collagen synthesis in liver cells
XX and inhibitors of synthesis of proteolytic enzymes able to degrade the
XX extracellular matrix. The peptides, their mimetopes and/or DNA (or
XX expression systems) encoding the peptides are used for treatment of liver
XX disease, specifically cirrhosis

```

XX
SQ      Sequence 15 AA;
      Query Match      100.0%; Score 77; DB 3; Length 15;
      Best Local Similarity 100.0%; Pred. No. 5e-07;
      Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDSLSFQLGLYLSPH 15
      |||||
Db      1 LDSLSFQLGLYLSPH 15
      |||||

RESULT 2
AAY92953
ID      AAY92953 standard; peptide; 15 AA.
XX
AC      AAY92953;
XX
DT      08-NOV-2000 (first entry)
XX
DE      Transforming growth factor inhibitory peptide #9.
XX
KW      Hepatotrophic; antagonist; transforming growth factor betal; TGF-b1;
KW      competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW      extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX
OS      Homo sapiens.
XX
PN      WO200031135-A1.
XX
PD      02-JUN-2000.
XX
PF      23-NOV-1999; 99WO-ES000375.
XX
PR      24-NOV-1998; 98ES-00002465.
XX
PA      (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
XX
PI      Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
PI      Borrás Cuesta F;
XX
WPI; 2000-411935/35.
XX
PT      Peptides that antagonize binding of transforming growth factor betal,
PT      useful for treatment of liver disease, especially cirrhosis, are partial
PT      sequences of the factor or its receptors.
XX
PS      Claim 10; Page 82; 86pp; Spanish.
XX
CC      The invention relates to synthetic peptides that antagonise the binding
CC      of transforming growth (TGF) factor betal (TGF-b1) to its receptor in
CC      vivo which have partial amino acid sequences identical, or similar, with
CC      those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
CC      examples of the peptides of the invention. The peptides act by
CC      competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
CC      they are inhibitors of stimulation of collagen synthesis in liver cells
CC      and inhibitors of synthesis of proteolytic enzymes able to degrade the
CC      extracellular matrix. The peptides, their mimetopes and/or DNA (or
CC      expression systems) encoding the peptides are used for treatment of liver
CC      disease, specifically cirrhosis
XX
SQ      Sequence 15 AA;
      Query Match      100.0%; Score 77; DB 3; Length 15;
      Best Local Similarity 100.0%; Pred. No. 5e-07;
      Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDSLSFQLGLYLSPH 15
      |||||
Db      1 LDSLSFQLGLYLSPH 15
      |||||

RESULT 3
AAY92953
ID      AAY92953 standard; peptide; 15 AA.
XX
AC      AAY92953;
XX
DT      08-NOV-2000 (first entry)
XX
DE      Transforming growth factor inhibitory peptide #9.
XX
KW      Hepatotrophic; antagonist; transforming growth factor betal; TGF-b1;
KW      competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW      extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX
OS      Homo sapiens.
XX
PN      WO200031135-A1.
XX
PD      02-JUN-2000.
XX
PF      23-NOV-1999; 99WO-ES000375.
XX
PR      24-NOV-1998; 98ES-00002465.
XX
PA      (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
XX
PI      Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
PI      Borrás Cuesta F;
XX
WPI; 2000-411935/35.
XX
PT      Peptides that antagonize binding of transforming growth factor betal,
PT      useful for treatment of liver disease, especially cirrhosis, are partial
PT      sequences of the factor or its receptors.
XX
PS      Claim 10; Page 82; 86pp; Spanish.
XX
CC      The invention relates to synthetic peptides that antagonise the binding
CC      of transforming growth (TGF) factor betal (TGF-b1) to its receptor in
CC      vivo which have partial amino acid sequences identical, or similar, with
CC      those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
CC      examples of the peptides of the invention. The peptides act by
CC      competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
CC      they are inhibitors of stimulation of collagen synthesis in liver cells
CC      and inhibitors of synthesis of proteolytic enzymes able to degrade the
CC      extracellular matrix. The peptides, their mimetopes and/or DNA (or
CC      expression systems) encoding the peptides are used for treatment of liver
CC      disease, specifically cirrhosis
XX
SQ      Sequence 15 AA;
      Query Match      100.0%; Score 77; DB 3; Length 15;
      Best Local Similarity 100.0%; Pred. No. 5e-07;
      Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDSLSFQLGLYLSPH 15
      |||||
Db      1 LDSLSFQLGLYLSPH 15
      |||||

RESULT 4
AAB68433
ID      AAB68433 standard; peptide; 16 AA.
XX
AC      AAB68433;
XX
DT      23-JUL-2001 (first entry)
XX
DE      Peptide derived from human G-protein coupled receptor HG67.
XX

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ADM29169
ID      ADM29169 standard; peptide; 20 AA.
XX
AC      ADM29169;
XX
DT      01-JUL-2004 (first entry)
XX
DE      Hepatitis C virus cellular immune response related peptide.
XX
KW      DNA vaccine; vaccine; antigen gene; antigen; hepatitis C virus; HCV;
KW      recombinant adenovirus vaccine; adenovirus; HCV infection;
KW      hepatitis C virus infection; infection; virucide.
XX
OS      Hepatitis C virus.
OS      Synthetic.
XX
PN      WO2004028563-A1.
XX
PD      08-APR-2004.
XX
PF      24-SEP-2003; 2003WO-KR001951.
XX
PR      27-SEP-2002; 2002KR-00058712.
PR      06-NOV-2002; 2002KR-00068496.
XX
PA      (GENE-) GENEXINE INC.
PA      (POST-) POSTECH FOUND.
PA      (DONG-) DONG-A PHARM CO LTD.
PA      (DAEW-) DAEWOO CO LTD.
PA      (POSC-) POSCO.
XX
PI      Sung YC, Youn J, Yang S, Park S, Lee CG;
XX
WPI; 2004-305120/28.
XX
PT      New DNA vaccine comprising plasmid containing 2-6 kb of the total antigen
PT      gene of hepatitis C virus (HCV), useful in treating or preventing HCV
PT      infection.
XX
PS      Disclosure; Fig 20e; 165pp; English.
XX
CC      The present invention describes a DNA vaccine which comprises a plasmid
CC      containing 2-6 kb of the total antigen gene of hepatitis C virus (HCV).
CC      Also described: (1) a recombinant adenovirus vaccine including an
CC      adenovirus containing 2-6 kb of total antigen gene of HCV; (2) a vaccine
CC      administering method; and (3) a method for treating or preventing HCV
CC      infection. The DNA vaccine has virucide activity. The DNA vaccine is
CC      useful in treating or preventing HCV infection. The present sequence
CC      represents a peptide from the HCV peptide pool used for the investigation
CC      of cellular immune response in the exemplification of the present
CC      invention.
XX
SQ      Sequence 20 AA;
      Query Match      42.9%; Score 33; DB 8; Length 20;
      Best Local Similarity 66.7%; Pred. No. 90;
      Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      2 DLSLSPQLGL 10
      |||||
Db      11 DEVSPQVGL 19
      |||||

RESULT 4
AAB68433
ID      AAB68433 standard; peptide; 16 AA.
XX
AC      AAB68433;
XX
DT      23-JUL-2001 (first entry)
XX
DE      Peptide derived from human G-protein coupled receptor HG67.
XX

```

KW G-protein coupled receptor; HG67; MCH-R2; weight loss; obesity; stress;
 KW melanin concentrating hormone receptor; cancer; pain; sexual dysfunction;
 KW weight gain; hypertension; dyslipidemia; cardiovascular disease;
 KW gall stone; osteoarthritis; cancer; diabetes; anorexia; AIDS; wasting;
 KW cachexia.

XX Synthetic.
 OS Homo sapiens.

XX WO200136479-A1.

XX PD 25-MAY-2001.

XX PF 14-NOV-2000; 2000WO-US031240.

XX PR 16-NOV-1999; 99US-0165871P.

XX PR 13-MAR-2000; 2000US-0188977P.

XX PR 18-APR-2000; 2000US-0198029P.

XX (MERI) MERCK & CO INC.

XX PA (BANY) BANYU PHARM CO LTD.

XX PI Liu Q, McDonald TP, Howard AD, Iwaasa H, Sano H;

XX WPI; 2001-355618/37.

XX New G-protein coupled receptor, designated MCH-R2, is a receptor for
 PT melanin-concentrating hormone and is useful to provide treatment for
 PT weight disorders including obesity.

XX Claim 3; Page 32; 32pp; English.

XX AAB68429-33 represent peptides derived from a human G-protein coupled
 CC receptor, designated HG67 or MCH-R2. HG67 is a melanin concentrating
 CC hormone receptor. Modulators of HG67 can be used to treat a patient,
 CC particularly to reduce weight, particularly in obesity, or to treat
 CC stress. These modulators can also be used to treat cancer, reduce pain,
 CC treat sexual dysfunction or to produce weight gain. Bringing about weight
 CC loss can be used to reduce the likelihood of hypertension, diabetes,
 CC dyslipidemia, cardiovascular disease, gall stones, osteoarthritis or
 CC certain forms of cancers. Increasing weight can be useful in the
 CC treatment of anorexia, AIDS, wasting, cachexia and frail elderly
 CC patients, or those undergoing chemotherapy or radiation therapy

XX Sequence 16 AA;

Query Match 41.6%; Score 32; DB 4; Length 16;

Best Local Similarity 54.5%; Pred. No. 1.1e+02;

Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 SLSFQLGLYLS 13

Db 5 TLAFYGVGYLS 15

RESULT 5

AAR82557

ID AAR82557 standard; peptide; 20 AA.

XX AAR82557;

DT 17-MAY-1996 (first entry)

XX Bovine PVP peptide 71-90.

XX Myelin basic protein; MBP; multiple sclerosis; MS; bystander antigen;
 KW non-interferon polypeptide; Th2-enhancing cytokine activity.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1

/note= "Indicated in the specification as COOH-Pro"

FT Modified-site 20
 FT /note= "Indicated in the specification as Cys-NH2"

XX WO9527500-A1.

XX PD 19-OCT-1995.

XX PF 07-APR-1995; 95WO-US004512.

XX PR 08-APR-1994; 94US-00225372.

XX PR 31-OCT-1994; 94US-00332524.

XX (BGHM) BRIGHAM & WOMENS HOSPITAL.

XX PI Weiner HL, Chen Y;

XX WPI; 1995-366229/47.

XX Use of oral tolerisation and/or Th2-enhancing cytokine(s) - to treat
 PT auto-immune diseases such as multiple sclerosis.

XX Example 1; Page 33; 49pp; English.

XX The sequences given in AAR82556-57 are myelin basic protein (MBP) derived
 CC peptides which were used in the method of the invention for the treatment
 CC of multiple sclerosis. These peptides act as bystander antigens and act
 CC in combination with an amount of a non- interferon polypeptide having Th2
 CC -enhancing cytokine activity

XX Sequence 20 AA;

Query Match 41.6%; Score 32; DB 2; Length 20;

Best Local Similarity 33.3%; Pred. No. 1.4e+02;

Matches 4; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 4 LSFQLGLYLSPH 15

Db 2 LAYTIGVFKDPH 13

RESULT 6

AAG83462

ID AAG83462 standard; peptide; 10 AA.

XX AAG83462;

DT 11-SEP-2001 (first entry)

XX Arabidopsis thaliana peptide ligand #102.

XX Plant; peptide pesticide; peptide herbicide; agricultural research.

XX Arabidopsis thaliana.

XX WO200142279-A2.

XX PD 14-JUN-2001.

XX PF 13-DEC-2000; 2000WO-GB004781.

XX PR 13-DEC-1999; 99GB-00029469.

XX (PROT-) PROTEOM LTD.

XX Roberts GW, Heal JR;

XX WPI; 2001-381629/40.

XX A set of peptide ligands for agricultural research and development of
 PT therapeutic agents comprise specific complementary peptides to proteins
 PT encoded by genes of plant genomes.

XX Example 4; Page 45; 201pp; English.

XX The present invention relates to a set of peptide ligands consisting of
 CC specific complementary peptides to proteins encoded by genes of plant
 CC genomes. The present sequence is one such peptide from Arabidopsis
 CC thaliana. The peptides of the present invention are useful in an assay to
 CC identify a peptide, especially a peptide pesticide or herbicide. The
 CC peptides are also useful for tools for agricultural research and
 CC development
 XX
 SQ Sequence 10 AA;

Query Match 40.3%; Score 31; DB 4; Length 10;
 Best Local Similarity 70.0%; Pred. No. 98;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 SLSFQLGLYL 12
 DB 1 SLTFQLLFL 10
 ||||| |

RESULT 7
 ABP58975
 ID ABP58975 standard; peptide; 15 AA.
 XX
 AC ABP58975;
 XX

XX 14-APR-2003 (first entry)
 DT

DE Human I kappa B kinase inhibitor 37.40 N-terminal peptide.

XX Human; I kappa B kinase inhibitor 37.40; recombinant production;
 KW gene therapy; cancer; tumor; angiocardiopathy; cardiovascular disorder;
 KW neurological disorder; immune disorder; inflammatory condition;
 KW cytostatic; antiinflammatory; immunomodulator; N-terminal peptide;
 KW enzyme linked immunosorbent assay; ELISA.

XX Homo sapiens.

XX CN1361264-A.

XX 31-JUL-2002.

XX 26-DEC-2000; 2000CN-00136306.

XX 26-DEC-2000; 2000CN-00136306.

XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.

XX Mao Y, Xie Y;

XX WPI; 2002-751595/82.

XX Human inhibitor molecule I kappa B kinase 37.40 polypeptides and
 PT polynucleotides encoding this polypeptide.

XX Example 5; Page 18 (disclosure); 33pp; Chinese.

XX The invention relates to human I kappa B kinase inhibitor 37.40
 CC (ABP58974) and nucleic acids encoding it (ABZ70827). The protein has a
 CC molecular weight of 37.4 kD. The invention also relates to a method for
 CC the recombinant production of the protein, an antagonist of the protein,
 CC and the use of the protein, gene and antagonist in therapeutic
 CC applications. I kappa B kinase inhibitor 37.40 can be used in the
 CC treatment of a variety of diseases such as cancer, angiocardiopathy,
 CC neurological disorders, immune disorders and inflammatory conditions. The
 CC present sequence represents the 15 N-terminal amino acids of human I
 CC kappa B kinase inhibitor 37.40 used in ELISA (enzyme linked immunosorbent
 CC assay) in an exemplification of the invention

XX Sequence 15 AA;

Query Match 40.3%; Score 31; DB 5; Length 15;
 Best Local Similarity 75.0%; Pred. No. 1.5e+02;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 FOLGLYLS 13
 DB 5 FLLGLYIS 12
 ||||| |

RESULT 8
 AAM47809
 ID AAM47809 standard; peptide; 15 AA.
 XX

XX AAM47809;

DT 15-FEB-2002 (first entry)

XX Miniature protein 9.

XX Avian pancreatic polypeptide; alpha helix domain; modulate transcription;
 KW miniature protein.

XX Synthetic.

XX WO200181375-A2.

XX 01-NOV-2001.

XX 24-APR-2001; 2001WO-US013023.

XX 24-APR-2000; 2000US-0199408P.

XX 16-OCT-2000; 2000US-0240566P.

XX 30-JAN-2001; 2001US-0265099P.

XX 23-FEB-2001; 2001US-0271368P.

XX (UYVA) UNIV YALE.

XX Schepartz Shrader A, Chin JWK, Zutshi R, Rutledge SE;
 PI Kehbeck Martin JD, Zondlo NJ;

XX WPI; 2002-041395/05.

XX Polypeptide scaffold e.g. an avian pancreatic polypeptide that comprises
 PT modification by substitution of an amino acid residue, that is exposed on
 PT the alpha helix domain of the polypeptide is useful for screening for
 PT drugs.

XX Example 17; Fig 5; 81pp; English.

XX The invention relates to an avian pancreatic polypeptide, modified by
 CC substitution of at least one amino acid residue, where the residue is
 CC being exposed on the alpha helix domain of the polypeptide when the
 CC polypeptide is in a tertiary form. The polypeptide is useful for
 CC screening drugs to identify agents capable of binding to the same binding
 CC site as the avian pancreatic polypeptide. It is also useful for
 CC diagnostic purposes to identify the presence and/or detect the levels of
 CC DNA or protein that binds to the polypeptide, in treatment of diseases
 CC associated with the presence of a particular DNA or protein, where the
 CC polypeptide can be used to bind to DNA to promote or inhibit
 CC transcription and for identifying binding partners. The present sequence
 CC is that of a miniature protein of the invention used to modulate the
 CC interaction between a known protein and another molecule

XX Sequence 15 AA;

Query Match 39.0%; Score 30; DB 5; Length 15;
 Best Local Similarity 85.7%; Pred. No. 2.3e+02;

- Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 FOLGLYL 12
 DB 6 FOLGWYL 12
 ||||| |

RESULT 9

ABP82548
ID ABP82548 standard; peptide; 17 AA.

AC ABP82548;

DT 04-MAR-2003 (first entry)

DE G protein-coupled receptor (GPCR) antigenic peptide SEQ ID NO:1221.

KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer.

OS Homo sapiens.

PN WO200261087-A2.

XX 08-AUG-2002.

PF 19-DEC-2001; 2001WO-US050107.

PR 19-DEC-2000; 2000US-0257144P.

XX (LIFE-) LIFESPAN BIOSCIENCES INC.

PA Burner GC, Roush CL, Brown JP;

PI WPI; 2003-046718/04.

DR New isolated antigenic peptides e.g., for G protein-coupled receptors
(GPCR), useful for diagnosing and designing drugs for treating conditions
in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
autoimmune diseases.

XX Claim 1; Fig 2; 523pp; English.

XX The present invention describes antigenic peptides (I) comprising: (a)
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular G
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity or
CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related disease, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention

XX Sequence 17 AA;

SQ Query Match 39.0%; Score 30; DB 6; Length 17;

Best Local Similarity 45.5%; Pred. No. 2.7e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 SFOLGLYLSPH 15

DB 2 SFOKSPYINAH 12

RESULT 10

AAW71733

ID AAW71733 standard; peptide; 21 AA.

XX AAW71733;

DT 10-DEC-1998 (first entry)

DE Rabbit 3-phosphoinositide dependent protein kinase peptide #5.

XX Protein kinase B-alpha; 3-phosphoinositide-dependent protein kinase;
KW diabetes; cancer; cell proliferation; phosphorylation.

OS Oryctolagus cuniculus.

PN WO9841638-A1.

XX 24-SEP-1998.

PF 16-MAR-1998; 98WO-GB000777.

PR 17-MAR-1997; 97GB-00005462.

PR 19-JUN-1997; 97GB-00012826.

PR 15-AUG-1997; 97GB-00017253.

PR 03-OCT-1997; 97US-00943667.

PA (WED-) MEDICAL RES COUNCIL.

XX Alessi DR;

WPI; 1998-531572/45.

PT New isolated 3-phosphoinositide-dependent protein kinase - which
phosphorylates and activates protein kinase B-alpha, used to develop
products for treating diabetes or cancers or for enhancing cell
proliferation.

XX Example 2; Page 57; 120pp; English.

XX A pure 3-phosphoinositide-dependent protein kinase (3PDPK) that
phosphorylates and activates PK B-alpha has been isolated. The present
sequence represents a rabbit 3-phosphoinositide dependent protein kinase
peptide. Products from the present invention (e.g. 3PDPK, nucleotide
sequence encoding 3PDPK, antibodies against 3PDPK) can be used to
identify compounds which modulate the PK activity e.g. for treating
diabetes or cancers or for enhancing cell proliferation in the
regeneration of nerves or in wound healing

SQ Sequence 21 AA;

Query Match 39.0%; Score 30; DB 2; Length 21;

Best Local Similarity 70.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LDSLSFQLGL 10

DB 12 LDSNSFELD 21

RESULT 11

AAE09350

ID AAE09350 standard; protein; 23 AA.

XX AAE09350;

DT 19-NOV-2001 (first entry)
XX Human ion-10 protein.
XX Human; ion channel-10; ion-10; schizophrenia; depression; anxiety;
KW attention deficit hyperactivity disorder; ADHD; migraine; stroke;
KW ischaemia; respiratory disease; asthma; neurodegenerative disease;
KW Alzheimer's disease; Parkinson's disease; arrhythmia; cancer;
KW macular degeneration; cardiovascular disease; endocrine disorder;
KW congestive heart failure; thyroid disorder; inflammatory condition;
KW epilepsy; muscular disorder; autoimmune disorder; mood disorder;
XX Gene therapy.
XX Homo sapiens.
XX OS
XX WO200160864-A2.
PN
XX
XX 23-AUG-2001.
PD
XX
XX 14-FEB-2001; 2001WO-US004644.
PF
XX
XX 14-FEB-2000; 2000US-0182325P.
PR
XX
XX (PHAA) PHARMACIA & UPJOHN CO.
PA
XX
XX Roberds SL, Karnovsky AM, Ruble CL;
PI WPI; 2001-536567/59.
DR N-PSDB; AAD16151.
DR
XX
XX New ion channel polypeptides and polynucleotides encoding them, for
PT treating e.g. schizophrenia, depression, anxiety, attention deficit
PT hyperactivity disorder, migraine, stroke, ischemia, respiratory diseases.
XX
XX Claim 35; Page 67; 108pp; English.
PS
XX
XX The present sequence is human ion channel-10 (ion-10) protein. The
CC invention relates to human ion channel polypeptides and nucleic acid
CC molecules encoding such polypeptides. The ion channel proteins are useful
CC targets for discovering ligands or drugs to treat disorders or defects,
CC including schizophrenia, depression, anxiety, attention deficit
CC hyperactivity disorder (ADHD), migraine, stroke, ischaemia, respiratory
CC diseases (e.g. asthma), brain injury, neurodegenerative diseases such as
CC Alzheimer's disease, Parkinson's disease, glaucoma and macular
CC degeneration. Compounds which modulate ion channel proteins are used in
CC the treatment of cardiovascular diseases including congestive heart
CC failure, arrhythmia, high blood pressure, restenosis, endocrine disorders
CC (e.g. thyroid disorder), epilepsy, proliferative disorders (e.g. cancer),
CC bipolar and other mood disorders, inflammatory conditions, autoimmune
CC disorders, muscular disorders, obesity and retinal degeneration. The ion
CC channel proteins are used as research tools for identification, the ion
CC characterisation and purification of interacting regulatory proteins. Ion
CC channel cDNAs are used in gene therapy
XX
XX Sequence 23 AA;
SQ
Query Match 39.0%; Score 30; DB 4; Length 23;
Best Local Similarity 50.0%; Pred. No. 3.8e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 LBSLSFQLGLYL 12
|||:|:|:
Db 9 LDLVSCVLGIYI 20
RESULT 12
AAE10097
ID AAE10097 standard; protein; 23 AA.
XX
XX AAE10097;
AC
XX
XX 29-NOV-2001 (first entry)
DT
XX

DE Human ion channel-72 (ion72) protein.
XX
XX Human; ion channel-72; ion72; antiinflammatory; immunosuppressive;
KW analgesic; nootropic; neuroprotective; antidepressant; cardiant;
KW cytostatic; antiviral; human immunodeficiency virus; HIV; anorectic;
KW antitaxial; thyroid disorder; thyrotoxicosis; myxoedema; renal failure;
KW Crohn's disease; rheumatoid arthritis; autoimmune disorder; pain; stroke;
KW Crohn's disease; neurologic disorder; anxiety; dyskinesia;
KW Huntington's disease; degenerative disorder; Parkinson's disease;
KW schizophrenia; Alzheimer's disease; cardiovascular disease; cancer;
KW metabolic disorder; anorexia; obesity; mental disorder.
XX
XX Homo sapiens.
XX OS
XX WO200168849-A2.
PN
XX
XX 20-SEP-2001.
PD
XX
XX 09-MAR-2001; 2001WO-US007503.
PF
XX
XX 10-MAR-2000; 2000US-0188400P.
PR
XX
XX 10-MAR-2000; 2000US-0188517P.
PR
XX
XX 10-MAR-2000; 2000US-0188518P.
PR
XX
XX 05-JUL-2000; 2000US-0215815P.
PR
XX
XX 06-JUL-2000; 2000US-0216481P.
PR
XX
XX (PHAA) PHARMACIA & UPJOHN CO.
PA
XX
XX Wood LS, Vogeli G, Karnovsky AM, Ruble CL, Linske-O'connell LI;
PI Wang J, Liu D;
PI WPI; 2001-565795/63.
DR N-PSDB; AAD17149.
DR
XX
XX New ion channel polynucleotides and polypeptides, useful for
PT identification of ion channel modulators and treatment of mental
PT disorders, infections, cancer and autoimmune diseases.
XX
XX Claim 31; Page 93; 188pp; English.
PS
XX
XX The patent discloses novel human ion channel polypeptides and their
CC corresponding polynucleotides. The ion channel sequences and their
CC modulators are used for the treatment of viral infections (e.g. human
CC immunodeficiency virus (HIV)) thyroid disorders (e.g., thyrotoxicosis,
CC myxoedema), renal failure, inflammatory conditions (e.g., Crohn's
CC disease), rheumatoid arthritis, autoimmune disorders, pain, stroke,
CC psychotic and neurological disorders (e.g. anxiety, depression and
CC schizophrenia), dyskinesias (e.g. Huntington's disease), degenerative
CC disorders (e.g., Parkinson's disease, Alzheimer's disease), cardio-
CC vascular diseases, cancer, metabolic disorders (e.g. anorexia, obesity)
CC and mental disorders. The present sequence is ion channel-72 (ion72)
CC protein from human
XX
XX Sequence 23 AA;
SQ
Query Match 39.0%; Score 30; DB 4; Length 23;
Best Local Similarity 50.0%; Pred. No. 3.8e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 LBSLSFQLGLYL 12
|||:|:|:
Db 9 LDLVSCVLGIYI 20
RESULT 13
ABU97358
ID ABU97358 standard; peptide; 23 AA.
XX
XX ABU97358;
AC
XX
XX 29-JUL-2003 (first entry)
DT
XX

KW antiarteriosclerotic; antiinflammatory; antidepressant; antiarthritic;
KW ophthalmological; cytotetic; hypertensive; hypotensive; vasotropic;
KW antinigraine; analgesic; antiparkinsonian; thrombolytic; antithyroid;
KW ion channel; ion-x; brain disorder; mental disorder; schizophrenia;
KW depression; anxiety; attention deficit hyperactivity disorder; migraine;
KW stroke; neurodegenerative disease; Alzheimer's disease;
KW Parkinson's disease; glaucoma; macular degeneration;
KW cardiovascular disease; ischaemia; congestive heart failure; arrhythmia;
KW high blood pressure; restenosis; thyroid disorder; renal failure;
KW inflammatory condition; autoimmune disorder; rheumatoid arthritis;
KW movement disorder; central nervous system disorder; infection;
KW eating disorder; cardiovascular disorder; thrombosis; atherosclerosis;
KW proliferative disorder; cancer; hormonal disorder; sexual dysfunction.
XX
OS Homo sapiens.
XX
XX US2003190714-A1.
XX
XX
XX 09-OCT-2003.
XX
XX 09-MAR-2001; 2001US-00802668.
XX
XX 10-MAR-2000; 2000US-0188400P.
XX 10-MAR-2000; 2000US-0188484P.
XX 10-MAR-2000; 2000US-0188517P.
XX 10-MAR-2000; 2000US-0188518P.
XX 10-MAR-2000; 2000US-0188519P.
XX 05-JUL-2000; 2000US-0215815P.
XX 06-JUL-2000; 2000US-0216481P.
XX
XX (ROBE/) ROBERTS S L.
XX (BENJ/) BENJAMIN C W.
XX (KARN/) KARNOVSKY A M.
XX (RUBL/) RUBLE C L.
XX (LINS/) LINSKE-O'CONNELL L I.
XX (WANG/) WANG.
XX (LIUD/) LIU D.
XX
XX Roberts SL, Benjamin CW, Karnovsky AM, Ruble CL;
PI Linske-O'connell LI, Wang J, Liu D;
XX
XX WPI; 2003-875311/81.
XX N-PSDB; ADE29225.
XX
XX New nucleic acid sequences encoding ion channels are useful to detect and
PT treat human diseases and conditions, particularly of the brain,
PT especially mental disorders.
XX
XX Claim 31; SEQ ID NO 79; 105pp; English.
XX
XX The invention describes an isolated nucleic acid comprising a sequence
CC encoding at least a portion of an ion channel (ion-x). The invention is
CC useful to detect and treat diseases and conditions of the brain,
CC particularly mental disorders, including schizophrenia, depression,
CC anxiety, attention deficit hyperactivity disorder, migraine, stroke, and
CC neurodegenerative diseases such as Alzheimer's disease, Parkinson's
CC disease, glaucoma and macular degeneration, cardiovascular diseases such
CC as ischaemia, congestive heart failure, arrhythmia, high blood pressure
CC and restenosis. The invention may also be used to detect or treat thyroid
CC disorders, renal failure, inflammatory conditions, autoimmune disorders
CC including rheumatoid arthritis, movement disorders, central nervous
CC system disorders, infections, eating disorders, cardiovascular disorders
CC including thrombosis and atherosclerosis, and proliferative disorders such
CC as cancers, hormonal disorders and sexual dysfunction. This is the amino
CC acid sequence of a novel ion channel.
XX
SQ Sequence 23 AA;

Query Match 39.0%; Score 30; DB 7; Length 23;
Best Local Similarity 50.0%; Pred. No. 3.8e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 LBSLSFQLGLYL 12

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OM protein - protein search, using sw model

Run on: November 14, 2004, 12:03:21 ; Search time 35.4255 Seconds
(without alignments)
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Title: US-09-831-253F-9
Perfect score: 77
Sequence: 1 LDSLSFQLGLYLSPH 15

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 1568699 seqs, 353819137 residues

Total number of hits satisfying chosen parameters: 294451

Minimum DB seq length: 0
Maximum DB seq length: 23

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	40.3	10	10	US-09-572-270A-102
2	30	39.0	15	15	US-10-682-420-55
3	30	39.0	15	15	US-10-682-420-55
4	30	39.0	15	15	US-10-409-613-55
5	30	39.0	15	15	US-10-409-613-55
6	30	39.0	15	15	US-10-442-180-55
7	30	39.0	15	15	US-10-442-180-55
8	30	39.0	17	14	US-10-225-567A-1221
9	30	39.0	21	14	US-10-150-012-12
10	30	39.0	23	10	US-09-802-668-79
11	30	39.0	23	14	US-10-243-475-79
12	29.5	38.3	16	10	US-09-880-748-2145
13	29.5	38.3	16	14	US-10-293-418-2145

14	29	37.7	11	14	US-10-197-954-26	Sequence 26, Appl
15	29	37.7	23	10	US-09-974-879-297	Sequence 297, App
16	29	37.7	23	10	US-09-305-736-297	Sequence 297, App
17	29	37.7	23	10	US-09-818-683-297	Sequence 297, App
18	29	37.7	23	11	US-09-818-683-297	Sequence 297, App
19	29	37.7	23	15	US-10-424-599-180905	Sequence 180905
20	29	37.7	23	15	US-10-621-401-297	Sequence 297, App
21	28	36.4	9	14	US-10-119-536A-101	Sequence 101, App
22	28	36.4	10	15	US-10-462-452-757	Sequence 757, App
23	28	36.4	10	15	US-10-601-953-60	Sequence 60, Appl
24	28	36.4	10	16	US-10-322-266-758	Sequence 758, App
25	28	36.4	14	10	US-09-820-649-319	Sequence 319, App
26	28	36.4	14	14	US-10-160-162-319	Sequence 319, App
27	28	36.4	15	15	US-10-682-420-99	Sequence 99, Appl
28	28	36.4	15	15	US-10-409-613-99	Sequence 99, Appl
29	28	36.4	15	15	US-10-442-180-99	Sequence 99, Appl
30	28	36.4	20	14	US-10-225-567A-2058	Sequence 2058, Ap
31	28	36.4	23	14	US-10-225-567A-2062	Sequence 2062, Ap
32	27	35.1	9	14	US-10-163-499-12	Sequence 12, Appl
33	27	35.1	10	10	US-09-572-404B-1179	Sequence 1179, Ap
34	27	35.1	10	10	US-09-572-270A-100	Sequence 100, App
35	27	35.1	15	13	US-10-103-395-264	Sequence 264, App
36	27	35.1	15	14	US-10-163-499-31	Sequence 31, Appl
37	27	35.1	15	15	US-10-296-734-808	Sequence 808, App
38	27	35.1	19	14	US-10-237-852-49	Sequence 49, Appl
39	27	35.1	20	14	US-10-280-066-326	Sequence 326, App
40	27	35.1	20	15	US-10-186-229-28	Sequence 28, Appl
41	27	35.1	21	10	US-09-962-756-611	Sequence 611, App
42	27	35.1	21	14	US-10-097-896-3	Sequence 3, Appli
43	27	35.1	21	14	US-10-253-471-611	Sequence 611, App
44	27	35.1	21	15	US-10-253-493-611	Sequence 611, App
45	27	35.1	21	16	US-10-685-105-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-572-270A-102
; Sequence 102, Application US/09572270A
; Publication No. US20030148368A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Inter- complementary peptide listing
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/572,270A
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 1144
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 102
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Arabidopsis Thaliana
; OTHER INFORMATION: Sequence located in ILL2. at 8-17 and may interact with
US-09-572-270A-102

Query Match 40.3%; Score 31; DB 10; Length 10;
Best Local Similarity 70.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy

3 SLSFQLGLVL 12

Db

1 SLTFQLLLFL 10

RESULT 2

US-10-682-420-55
; Sequence 55, Application US/10682420
; Publication No. US20040062775A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre

```

; APPLICANT: BLANCHARD, Phillipe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS
; TITLE OF INVENTION: DISEASE (PWD)
; FILE REFERENCE: 065691/0176
; CURRENT APPLICATION NUMBER: US/10/682,420
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US/10/637,011
; PRIOR FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: US/09/514,245B
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 55
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Type B PWD circovirus
US-10-682-420-55

Query Match          39.0%; Score 30; DB 15; Length 15;
Best Local Similarity 35.7%; Pred. No. 2.8e+02;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 LDLSFQGLGYLSP 14
Db 2 VNELRFNIGQFLPP 15

RESULT 3
US-10-682-420-98
; Sequence 98, Application US/10682420
; Publication No. US20040062775A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Phillipe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS
; TITLE OF INVENTION: DISEASE (PWD)
; FILE REFERENCE: 065691/0176
; CURRENT APPLICATION NUMBER: US/10/682,420
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US/10/637,011
; PRIOR FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: US/09/514,245B
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 98
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Type A PWD circovirus
US-10-682-420-98

Query Match          39.0%; Score 30; DB 15; Length 15;
Best Local Similarity 35.7%; Pred. No. 2.8e+02;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

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QY 1 LDLSFQGLGYLSP 14
Db 2 VNELRFNIGQFLPP 15

RESULT 4
US-10-409-613-55
; Sequence 55, Application US/10409613
; Publication No. US20040076635A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Phillipe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS
; TITLE OF INVENTION: DISEASE (PWD)
; FILE REFERENCE: 065691/0176
; CURRENT APPLICATION NUMBER: US/10/409,613
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US/09/514,245B
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 55
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Type B PWD circovirus
US-10-409-613-55

Query Match          39.0%; Score 30; DB 15; Length 15;
Best Local Similarity 35.7%; Pred. No. 2.8e+02;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 LDLSFQGLGYLSP 14
Db 2 VNELRFNIGQFLPP 15

RESULT 5
US-10-409-613-98
; Sequence 98, Application US/10409613
; Publication No. US20040076635A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Phillipe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS
; TITLE OF INVENTION: DISEASE (PWD)
; FILE REFERENCE: 065691/0176
; CURRENT APPLICATION NUMBER: US/10/409,613
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US/09/514,245B
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 98

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; LENGTH: 15
; TYPE: PRT
; ORGANISM: Type A PWD circovirus
US-10-409-613-98

Query Match      39.0%; Score 30; DB 15; Length 15;
Best Local Similarity 35.7%; Pred. No. 2.8e+02;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 LDSLSFQGLGLSP 14
   ::|||::|
Db 2 VNELRFNIGQLP 15

RESULT 6
US-10-442-180-55
; Sequence 55, Application US/10442180
; Publication No. US20040091502A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Philippe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS
; TITLE OF INVENTION: DISEASE (PWD)
; FILE REFERENCE: 065691/0176
; CURRENT APPLICATION NUMBER: US/10/442,180
; CURRENT FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: US/09/514,245
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 55
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Type B PWD circovirus
US-10-442-180-55

Query Match      39.0%; Score 30; DB 15; Length 15;
Best Local Similarity 35.7%; Pred. No. 2.8e+02;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 LDSLSFQGLGLSP 14
   ::|||::|
Db 2 VNELRFNIGQLP 15

RESULT 7
US-10-442-180-98
; Sequence 98, Application US/10442180
; Publication No. US20040091502A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Philippe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS
; TITLE OF INVENTION: DISEASE (PWD)
; FILE REFERENCE: 065691/0176
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; CURRENT APPLICATION NUMBER: US/10/442,180
; CURRENT FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: US/09/514,245
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 98
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Type A PWD circovirus
US-10-442-180-98

Query Match      39.0%; Score 30; DB 15; Length 15;
Best Local Similarity 35.7%; Pred. No. 2.8e+02;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 LDSLSFQGLGLSP 14
   ::|||::|
Db 2 VNELRFNIGQLP 15

RESULT 8
US-10-225-567A-1221
; Sequence 1221, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1221
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-1221

Query Match      39.0%; Score 30; DB 14; Length 17;
Best Local Similarity 45.5%; Pred. No. 3.2e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 SFQGLGLSP 15
   |||||::|
Db 2 SFQKSFYNH 12

RESULT 9
US-10-190-012-12
; Sequence 12, Application US/10190012
; Publication No. US20030108971A1
; GENERAL INFORMATION:
; APPLICANT: Alessi, Dario R
; TITLE OF INVENTION: ENZYME
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jaeckle Fleischmann & Mugel, LLP
; STREET: 39 State Street
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14614-1310
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/10/190,012
FILING DATE: 05-JUL-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/943,667
FILING DATE: 03-OCT-1997
APPLICATION NUMBER: GB 9705462.1
FILING DATE: 17-MAR-1997
APPLICATION NUMBER: GB 9712826.8
FILING DATE: 19-JUN-1997
APPLICATION NUMBER: GB 9717253.0
FILING DATE: 15-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Braman, Susan J
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 87792.97R421
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-262-3640
TELEFAX: 716-262-4133
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-190-012-12

Query Match 39.0%; Score 30; DB 14; Length 21;
Best Local Similarity 70.0%; Pred. No. 4e+02; 2; Indels 0; Gaps 0;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LDSLSFQLGL 10
|||:|:|:
DB 12 LDSNSPELDL 21

RESULT 10
US-09-802-668-79
; Sequence 79, Application US/09802668
; Publication No. US20030190714A1
; GENERAL INFORMATION:
; APPLICANT: Wood, Linda
; APPLICANT: Vogel, Gabriel
; APPLICANT: Karnovsky, Alla
; APPLICANT: Linske-O'Connell, Lisa I.
; APPLICANT: Wang, Jun
; APPLICANT: Liu, Derong
; TITLE OF INVENTION: Human Ion Channels
; FILE REFERENCE: 00069US1
; CURRENT APPLICATION NUMBER: US/09/802,668
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,517
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 79
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-802-668-79

Query Match 39.0%; Score 30; DB 10; Length 23;
Best Local Similarity 50.0%; Pred. No. 4.4e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 LDSLSFQLGLYL 12
||:|:|:|:
DB 9 LDLVSCVLGIYI 20

RESULT 11
US-10-243-475-79
; Sequence 79, Application US/10243475
; Publication No. US20030194720A1
; GENERAL INFORMATION:
; APPLICANT: Roberts, Steven L.
; APPLICANT: Benjamin, Christopher W.
; APPLICANT: Karnovsky, Alla M.
; APPLICANT: Ruble, Cara L.
; TITLE OF INVENTION: Human Ion Channels
; FILE REFERENCE: PHRM0039-100
; CURRENT APPLICATION NUMBER: US/10/243,475
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: 60/403,254
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 60/318,733
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 79
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-243-475-79

Query Match 39.0%; Score 30; DB 14; Length 23;
Best Local Similarity 50.0%; Pred. No. 4.4e+02; 3; Mismatches 3; Indels 0; Gaps 0;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 LDSLSFQLGLYL 12
||:|:|:|:
DB 9 LDLVSCVLGIYI 20

RESULT 12
US-09-880-748-2145
; Sequence 2145, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2145
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2145

Query Match 38.3%; Score 29.5; DB 10; Length 16;
Best Local Similarity 61.5%; Pred. No. 3.6e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 2 DSL-SFQLGLYLS 13
|:|:|:|:|:|:|

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Db      4 DTLTSYVLGYL 16

RESULT 13
US-10-293-418-2145
; Sequence 2145, Application US/10293418
; Publication No. US2003022396A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523p2
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2145
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2145

Query Match      38.3%; Score 29.5; DB 14; Length 16;
Best Local Similarity 61.5%; Pred. No. 3.6e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Qy      2 DSL-SFQGLYL 13
       |:|:|:|:|
Db      4 DTLTSYVLGYL 16

RESULT 14
US-10-197-954-26
; Sequence 26, Application US/10197954
; Publication No. US20030119021A1
; GENERAL INFORMATION:
; APPLICANT: K'ster, Hubert
; APPLICANT: Siddiqi, Suhail
; APPLICANT: Little, Daniel
; TITLE OF INVENTION: Capture Compounds, Collections Thereof
; TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: 24743-2305
; CURRENT APPLICATION NUMBER: US/10/197,954
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 60/306,019
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/314,123
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/363,433
; PRIOR FILING DATE: 2002-03-11
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: AMIDATION

Query Match      37.7%; Score 29; DB 10; Length 23;
Best Local Similarity 41.7%; Pred. No. 6.6e+02;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy      3 SLSPQLGLYLP 14
       |:|:|:|
Db      12 SVKSLGIFLGP 23

; LOCATION: 11
US-10-197-954-26

Query Match      37.7%; Score 29; DB 14; Length 11;
Best Local Similarity 60.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      1 LDLSLQGL 10
       |:|:|
Db      2 MDLSLQGL 11

RESULT 15
US-09-974-879-297
; Sequence 297, Application US/09974879
; Publication No. US20030028003A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 125 Human Secreted Proteins
; FILE REFERENCE: P2020P2
; CURRENT APPLICATION NUMBER: US/09/974,879
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/239,893
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US 09/818,683
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 09/305,736
; PRIOR FILING DATE: 1999-05-05
; PRIOR APPLICATION NUMBER: PCT/US98/23435
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 60/064,911
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,912
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,983
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,900
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,988
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,987
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,908
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,984
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/064,985
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: US 60/066,094
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 60/066,100
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 60/066,089
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 60/066,095
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: US 60/066,090
; PRIOR FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 611
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 297
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-974-879-297

Query Match      37.7%; Score 29; DB 10; Length 23;
Best Local Similarity 41.7%; Pred. No. 6.6e+02;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy      3 SLSPQLGLYLP 14
       |:|:|:|
Db      12 SVKSLGIFLGP 23
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Search completed: November 14, 2004, 12:27:00
Job time : 35.4255 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:26 ; Search time 11.8085 Seconds
(without alignments)
84.242 Million cell updates/sec

Title: US-09-831-253F-9
Perfect score: 77
Sequence: 1 LDSLSFQLGLYLSPH 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 202416

Minimum DB seq length: 0
Maximum DB seq length: 23

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pcp.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pcp.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pcp.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pcp.*
5: /cgn2_6/ptodata/1/iaa/PTGis COMB.pcp.*
6: /cgn2_6/ptodata/1/iaa/bagfilesi.pcp.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	41.6	16	4	US-09-712-368-9
2	30	39.0	15	4	US-09-514-245-55
3	30	39.0	15	4	US-09-514-245-98
4	30	39.0	21	4	US-08-943-667-12
5	29	37.7	13	4	US-08-753-7508-64
6	29	37.7	17	3	US-08-523-373-18
7	28	36.4	15	4	US-09-514-245-99
8	28	36.4	17	3	US-09-025-769B-240
9	28	36.4	17	4	US-09-490-070A-240
10	28	36.4	17	4	US-09-490-153-240
11	28	36.4	20	1	US-07-990-893-9
12	27	35.1	7	4	US-09-463-239-29
13	27	35.1	9	4	US-09-239-043D-1855
14	27	35.1	10	3	US-08-159-339A-458
15	27	35.1	10	4	US-09-239-043D-620
16	27	35.1	11	4	US-09-239-043D-1944
17	27	35.1	11	4	US-09-239-043D-467
18	27	35.1	11	4	US-09-239-043D-580
19	27	35.1	11	4	US-09-239-043D-1867
20	27	35.1	15	1	US-08-102-738-20
21	27	35.1	15	4	US-09-009-953-264
22	27	35.1	15	4	US-09-239-043D-2188
23	27	35.1	20	1	US-09-618-592-7
24	27	35.1	20	2	US-08-797-842-7
25	27	35.1	23	4	US-09-423-097-7
26	26.5	34.4	12	3	US-09-298-924-19
27	26	33.8	8	3	US-08-913-842-28

28	26	33.8	9	4	US-09-311-784A-271	Sequence 271, App
29	26	33.8	9	4	US-09-601-729-70	Sequence 70, Appl
30	26	33.8	10	3	US-08-159-339A-472	Sequence 472, App
31	26	33.8	10	3	US-08-159-339A-503	Sequence 503, App
32	26	33.8	12	4	US-09-407-687-34	Sequence 34, Appl
33	26	33.8	14	1	US-07-914-280-14	Sequence 14, Appl
34	26	33.8	14	5	PCT-US93-06625-14	Sequence 14, Appl
35	26	33.8	15	4	US-09-148-712-7	Sequence 7, Appl
36	26	33.8	22	3	US-09-439-313-557	Sequence 557, App
37	26	33.8	23	4	US-09-511-204B-10	Sequence 10, Appl
38	25	32.5	8	3	US-08-444-818-557	Sequence 557, App
39	25	32.5	9	1	US-08-336-618-2	Sequence 2, Appl
40	25	32.5	12	4	US-09-389-956-52	Sequence 52, Appl
41	25	32.5	15	1	US-08-049-783-11	Sequence 11, Appl
42	25	32.5	15	1	US-08-158-232-22	Sequence 22, Appl
43	25	32.5	15	1	US-08-304-626-22	Sequence 22, Appl
44	25	32.5	15	1	US-08-316-301A-23	Sequence 23, Appl
45	25	32.5	15	2	US-08-611-928-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-09-712-368-9
; Sequence 9, Application US/09712368
; Patent No. 6593108
; GENERAL INFORMATION:
; APPLICANT: Liu, Qingyun
; APPLICANT: McDonald, Terrence P.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Iwaasa, Hisashi
; APPLICANT: Sano, Hideki
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: 20579Y
; CURRENT APPLICATION NUMBER: US/09/712,368
; CURRENT FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: 60/165,871
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/188,977
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/198,029
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MCH-R2 Segment
US-09-712-368-9

Query Match 41.6%; Score 32; DB 4; Length 16;
Best Local Similarity 54.5%; Pred. No. 10;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Oy 3 SLSFQLGLYLS 13
Db 5 TLAFYVGYLS 15

RESULT 2
US-09-514-245-55
; Sequence 55, Application US/09514245
; Patent No. 6703023
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Philippe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire

```
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS DISEASE
; FILE REFERENCE: 065691/0176
; CURRENT APPLICATION NUMBER: US/09/514,245
; CURRENT FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 55
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Type B PWD circovirus
US-09-514-245-55

Query Match          39.0%; Score 30; DB 4; Length 15;
Best Local Similarity 35.7%; Pred. No. 23;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 LDSLSPQLGLYLSLP 14
   : : : : : : : :
Db 2 VNELRFNIGQFLPP 15

RESULT 3
US-09-514-245-98
; Sequence 98, Application US/09514245
; Patent No. 6703023
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Philippe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS DISEASE
; FILE REFERENCE: 065691/0176
; CURRENT APPLICATION NUMBER: US/09/514,245
; CURRENT FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 98
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Type A PWD circovirus
US-09-514-245-98

Query Match          39.0%; Score 30; DB 4; Length 15;
Best Local Similarity 35.7%; Pred. No. 23;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 LDSLSPQLGLYLSLP 14
   : : : : : : : :
Db 2 VNELRFNIGQFLPP 15

RESULT 4
US-08-943-667-12
; Sequence 12, Application US/08943667
; Patent No. 6734001
; GENERAL INFORMATION:
; APPLICANT: Alessi, Dario R
; TITLE OF INVENTION: ENZYME
; NUMBER OF SEQUENCES: 35
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jaesckle Fleischmann & Mugel, LLP
; STREET: 39 State Street
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14614-1310
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,667
; FILING DATE: 03-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9705462.1
; FILING DATE: 17-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9712826.8
; FILING DATE: 19-JUN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9717253.0
; FILING DATE: 15-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Braman, Susan J
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 87792.97R421
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-262-3640
; TELEFAX: 716-262-4133
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-943-667-12

Query Match          39.0%; Score 30; DB 4; Length 21;
Best Local Similarity 70.0%; Pred. No. 36;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LDSLSPQLGL 10
   : : : : : : :
Db 12 LDSNSFELDL 21

RESULT 5
US-08-753-750B-64
; Sequence 64, Application US/08753750B
; Patent No. 6610506
; GENERAL INFORMATION:
; APPLICANT: Lo, Reggie Y.C.
; APPLICANT: Schryvers, Anthony B.
; APPLICANT: Potter, Andrew A.
; TITLE OF INVENTION: TRANSFERRIN BINDING PROTEINS OF
; FILE REFERENCE: PASTEURILLA HAEMOLYTICA AND VACCINES CONTAINING THE SAME
; CURRENT APPLICATION NUMBER: US/08/753,750B
; CURRENT FILING DATE: 1996-11-29
; PRIOR APPLICATION NUMBER: CA 2,164,274
; PRIOR FILING DATE: 1995-12-01
; PRIOR APPLICATION NUMBER: 60/008,569
; PRIOR FILING DATE: 1995-12-01
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64
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; LENGTH: 13
; TYPE: PRT
; ORGANISM: Escherichia coli
US-08-753-750B-64

Query Match 37.7%; Score 29; DB 4; Length 13;
Best Local Similarity 66.7%; Pred. No. 31;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 SLSFQLGLY 11
| : : : :
Db 4 SESWELGLY 12

RESULT 6
US-08-523-373-18
; Sequence 18, Application US/08523373
; Patent No. 6037145
; GENERAL INFORMATION:
; APPLICANT: Yabuta, Masayuki
; APPLICANT: Ohsuye, Kazuhiro
; TITLE OF INVENTION: PROCESS FOR PRODUCTION OF PROTEIN
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESSES:
; ADDRESSES: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314-3187

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/523,373
FILING DATE: 05-SEP-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 6-238595

FILING DATE: 07-SEP-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 6-296028

FILING DATE: 07-NOV-1994

ATTORNEY/AGENT INFORMATION:

NAME: Meuth, Donna M.

REGISTRATION NUMBER: 36,607

REFERENCE/DOCKET NUMBER: 001560-251

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-836-6620

TELEFAX: 703-836-2021

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: peptide

FRAGMENT TYPE: C-terminal

US-08-523-373-18

Query Match 37.7%; Score 29; DB 3; Length 17;
Best Local Similarity 33.3%; Pred. No. 43;
Matches 5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 LDSLSFQLGLYSPH 15
: : : : :
Db 2 IEDHIFELRYRRHH 16

RESULT 7

US-09-514-245-99

; Sequence 99, Application US/09514245
; Patent No. 6703023
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Philippe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois

; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS DISEASES
; FILE REFERENCE: 065691/0176
; CURRENT APPLICATION NUMBER: US/09/514,245
; CURRENT FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 99
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Type A PWD circovirus
US-09-514-245-99

Query Match 36.4%; Score 28; DB 4; Length 15;
Best Local Similarity 45.5%; Pred. No. 58;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 LSFQLGLYSLP 14
| : : : :
Db 1 LRFNIGQLFPP 11

RESULT 8

US-09-025-769B-240

; Sequence 240, Application US/09025769B

; Patent No. 6300064

; GENERAL INFORMATION:

APPLICANT: Knappik, Achim

APPLICANT: Pack, Peter

APPLICANT: Ilag, Vic

APPLICANT: Ge, Liming

APPLICANT: Moroney, Simon

APPLICANT: Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B

FILING DATE: 18-FEB-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)596-9000

TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 240:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-09-025-769B-240

Query Match 36.4%; Score 28; DB 3; Length 17;
Best Local Similarity 55.6%; Pred. No. 67;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 QLGLYLSPH 15
DB 3 RLQAYLKPH 11

RESULT 9
US-09-490-070A-240
Sequence 240, Application US/09490070A
Patent No. 6696248
GENERAL INFORMATION:

APPLICANT: Knappik, Achim

Ge, Liming
Ilag, Vic

Moroney, Simon
Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
White & McAuliffe

STREET: 1666 K Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20006

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,070A

FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: Colin G. Sandercock, Esq.

REGISTRATION NUMBER: 31,298

REFERENCE/DOCKET NUMBER: 37629-0005

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 912-2000

TELEFAX: (202) 912-2020

INFORMATION FOR SEQ ID NO: 240:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 240:

US-09-490-070A-240

Query Match 36.4%; Score 28; DB 4; Length 17;
Best Local Similarity 55.6%; Pred. No. 67;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 QLGLYLSPH 15
DB 3 RLQAYLKPH 11

RESULT 10
US-09-490-153-240
Sequence 240, Application US/09490153
Patent No. 6706484
GENERAL INFORMATION:

APPLICANT: Knappik, Achim

Ge, Liming

Ilag, Vic

Moroney, Simon

Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,153

FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769B

FILING DATE: 18-FEB-1998

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)596-9000

TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 240:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 240:

US-09-490-153-240

Query Match 36.4%; Score 28; DB 4; Length 17;
Best Local Similarity 55.6%; Pred. No. 67;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 QLGLYLSPH 15
DB 3 RLQAYLKPH 11

RESULT 11
US-07-990-893-9
Sequence 9, Application US/07990893
Patent No. 5547841
GENERAL INFORMATION:
APPLICANT: Marotta, Charles A.
APPLICANT: Zain, Sayeeda

;; TITLE OF INVENTION: Genetic Sequences Coding For Alzheimer
;; TITLE OF INVENTION: Amyloid From Brain
;; NUMBER OF SEQUENCES: 18
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Sterne, Kesler, Goldstein & Fox
;; STREET: 1225 Connecticut Avenue
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: U.S.A.
;; ZIP: 20036
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/990,893
;; FILING DATE: 19921215
;; CLASSIFICATION: 536
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Esmond, Robert W.
;; REGISTRATION NUMBER: 32,893
;; REFERENCE/DOCKET NUMBER: 0932.0250003
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 466-0800
;; TELEFAX: (202) 833-8716
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 amino acids
;; TYPE: AMINO ACID
;; TOPOLOGY: both
US-07-990-893-9

Query Match 36.4%; Score 28; DB 1; Length 20;
Best Local Similarity 41.7%; Pred. No. 83;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LDSLSPQLGLYL 12
| : |||:::
Db 5 LNREPFQGLIFV 16

RESULT 12
US-09-463-239-29
; Sequence 29, Application US/09463239
; Patent No. 6700039
; GENERAL INFORMATION:
; APPLICANT: Jepson, Ian
; APPLICANT: Ebner, Marcus
; APPLICANT: Sonnewald, Uwe
; TITLE OF INVENTION: Genetic Method for Controlling Sprouting
; FILE REFERENCE: 109846.178
; CURRENT APPLICATION NUMBER: US/09/463,239
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: PCT/GB98/02023
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: EP 97113118.0
; PRIOR FILING DATE: 1997-07-30
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 29
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence encoding MOT isolated from potato.
US-09-463-239-29

Query Match 35.1%; Score 27; DB 4; Length 7;
Best Local Similarity 85.7%; Pred. No. 3.8e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 FQLGLYL 12

Db 1 FQLGLNL 7

RESULT 13
US-09-239-043D-1855
; Sequence 1855, Application US/09239043D
; Patent No. 6689363
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Vitello, Maria A.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Chesnut, Robert
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; FILE REFERENCE: 2060.0060007
; CURRENT APPLICATION NUMBER: US/09/239,043D
; CURRENT FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/978,291
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: US 08/820,360
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,363
; PRIOR FILING DATE: 1996-03-13
; PRIOR APPLICATION NUMBER: US 08/461,603
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23
; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/197,484
; PRIOR FILING DATE: 1994-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2579
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1855
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Orthohepadnaviridae hepatitis B virus
US-09-239-043D-1855

Query Match 35.1%; Score 27; DB 4; Length 9;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LGLYLSPH 15
| : |||:::
Db 1 LGLHLPN 8

RESULT 14
US-08-159-339A-458
; Sequence 458, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses

NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-005030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX:
INFORMATION FOR SEQ ID NO: 458:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-159-339A-458

Query Match 35.1%; Score 27; DB 3; Length 10;
Best Local Similarity 50.0%; Pred. No. 55;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 8 LGLYLSPH 15
||:|:|:
DB 2 LGIHLNPN 9

RESULT 15

US-09-239-043D-620
Sequence 620, Application US/09239043D
Patent No. 6689363
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Vitello, Maria A.
APPLICANT: Livingston, Brian D.
APPLICANT: Celis, Esteban
APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Chesnut, Robert
APPLICANT: Epimmune Inc.
TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
FILE OF INVENTION: Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.006007
CURRENT APPLICATION NUMBER: US/09/239,043D
CURRENT FILING DATE: 1999-01-27
PRIOR APPLICATION NUMBER: US 09/189,702
PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: US 08/978,291

PRIOR FILING DATE: 1997-11-25
PRIOR APPLICATION NUMBER: US 08/820,360
PRIOR FILING DATE: 1997-03-12
PRIOR APPLICATION NUMBER: US 60/013,363
PRIOR FILING DATE: 1996-03-13
PRIOR APPLICATION NUMBER: US 08/461,603
PRIOR FILING DATE: 1995-06-05
PRIOR APPLICATION NUMBER: US 08/347,610
PRIOR FILING DATE: 1994-12-01
PRIOR APPLICATION NUMBER: US 08/344,824
PRIOR FILING DATE: 1994-11-23
PRIOR APPLICATION NUMBER: US 08/278,634
PRIOR FILING DATE: 1994-07-21
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/197,484
PRIOR FILING DATE: 1994-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2579
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 620
LENGTH: 10
TYPE: PRT
ORGANISM: Orthohepadnaviridae hepatitis B virus
US-09-239-043D-620
Query Match 35.1%; Score 27; DB 4; Length 10;
Best Local Similarity 50.0%; Pred. No. 55;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 8 LGLYLSPH 15
||:|:|:
DB 2 LGIHLNPN 9
Search completed: November 14, 2004, 12:08:51
Job time : 12.8085 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2004, 12:45:35 ; Search time 37 Seconds
(without alignments)
31.205 Million cell updates/sec

Title: US-09-831-253F-3
Perfect score: 63
Sequence: 1 TSLDATMIWTMM 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1582

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR.79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	38.1	11	2 PQ0731	unidentified 5.7/3
2	22	34.9	7	2 PH1602	Ig H chain V-D-J r
3	20	31.7	10	2 S69159	cystathionine gamm
4	19	30.2	7	2 PT0586	T-cell receptor be
5	18	28.6	10	2 D61440	polygalacturonase
6	18	28.6	12	2 S69123	proton-translocati
7	17	27.0	6	2 I49808	D-SP2.5 region - m
8	17	27.0	6	2 PT0519	T-cell receptor be
9	17	27.0	6	2 PT0650	T-cell receptor be
10	17	27.0	9	2 SI3889	phosphoenolpyruvat
11	17	27.0	12	2 A29169	phospholipase A2 (
12	16	25.4	4	2 PT0661	T-cell receptor be
13	16	25.4	7	2 S09652	hypothetical prote
14	16	25.4	7	2 PX0008	glucuronosyltransf
15	16	25.4	7	4 I55382	hypothetical pepti
16	16	25.4	9	2 A43848	cell surface adhes
17	16	25.4	9	2 G85802	hypothetical prote
18	16	25.4	10	2 C39191	hypothetical prote
19	16	25.4	10	2 PQ0753	beta-fructofuranos
20	16	25.4	10	2 PT0310	Ig heavy chain CRD
21	16	25.4	11	2 S05002	corazonin - Americ
22	16	25.4	12	2 PN0581	tyrosine 3-monooxy
23	16	25.4	12	2 PN0580	tyrosine 3-monooxy
24	16	25.4	12	2 PN0579	tyrosine 3-monooxy
25	16	25.4	12	2 PN0577	tyrosine 3-monooxy
26	16	25.4	12	2 PN0578	tyrosine 3-monooxy
27	16	25.4	12	2 PT0274	Ig heavy chain CRD
28	16	25.4	12	2 177529	estrogen receptor
29	16	25.4	12	2 177529	estrogen receptor

30 16 25.4 12 2 PQ0776 NADH2 dehydrogenas
31 15 23.8 5 2 PT0624 T-cell receptor be
32 15 23.8 6 2 S66195 alcohol dehydrogen
33 15 23.8 6 2 PT0587 T-cell receptor be
34 15 23.8 7 2 S09066 globulin IV alpha
35 15 23.8 8 2 PT0588 neuromodulatory pe
36 15 23.8 8 2 S33246 T-cell receptor be
37 15 23.8 10 2 C41946 T-cell receptor ga
38 15 23.8 11 1 LFTWWE probable trpEG lea
39 15 23.8 11 2 S66196 alcohol dehydrogen
40 15 23.8 11 2 CS3652 rhnr protein - pse
41 15 23.8 11 2 D41946 T-cell receptor ga
42 15 23.8 12 2 I64829 gene HEXA protein
43 15 23.8 12 2 S16204 6-phosphofructokin
44 15 23.8 12 2 A28955 polysialologlycoprot
45 15 23.8 12 2 A61503 sterol carrier pro

ALIGNMENTS

RESULT 1
PQ0731
unidentified 5.7/35K protein [imported] - rice (fragment)
C;Species: Oryza sativa (rice)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: PQ0731
R;Komatsu, S.; Kajiwara, H.; Hirano, H.
Theor. Appl. Genet. 86, 935-942, 1993
A;Title: A rice protein library; a data-file of rice proteins separated by two-dimensio
A;Reference number: PQ0696
A;Accession: PQ0731
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <KOM>
A;Cross-references: UNIPROT:Q7M1U2

Query Match 38.1%; Score 24; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 ATMIW 9
DB 1 ATVW 5

RESULT 2
PH1602
Ig H chain V-D-J region (wild-type clone 313) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PH1602
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mic
A;Reference number: PH1580; MUID:93301609; PMID:8315387
A;Accession: PH1602
A;Molecule type: DNA
A;Residues: 1-7 <LEV>
A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin

Query Match 34.9%; Score 22; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATMIWT 10
DB 2 ASSLWT 7

RESULT 3
S69159

cystathionine gamma-synthase - spinach (fragment)
 C:Species: Spinacia oleracea (spinach)
 C:Date: 12-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
 C:Accession: S69159
 R:Ravanel, S.; Droux, M.; Douce, R.
 Arch. Biochem. Biophys. 316, 572-584, 1995
 A:Title: Methionine biosynthesis in higher plants. I. Purification and characterization
 A:Reference number: S69159; MUID:95142682; PMID:7840669
 A:Accession: S69159
 A:Molecule type: protein
 A:Residues: 1-10 <RAV>
 A:Cross-references: UNIPROT:Q7MLJ3
 C:Keywords: chloroplast

Query Match 31.7%; Score 20; DB 2; Length 10;
 Best Local Similarity 50.0%; Pred. No. 6.9e+02;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 TSLDATMI 8
 DB 2 TAVDAAAI 9

RESULT 4

PT0586
 T-cell receptor beta chain V-D-J region (141-1CN) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PT0586; PT0592
 R:Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A:Reference number: PT0509; MUID:91277601; PMID:1711558
 A:Accession: PT0586
 A>Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-7 <FEE>
 A:Experimental source: day 19 fetal thymus, strain BALB/c (clones 141-1CN and 141-1CD)
 C:Keywords: T-cell receptor

Query Match 30.2%; Score 19; DB 2; Length 7;
 Best Local Similarity 60.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATMIW 9
 DB 1 ASSIW 5

RESULT 5

D61440
 polygalacturonase (EC 3.2.1.15) IV - Aspergillus sp. (fragment)
 C:Species: Aspergillus sp.
 C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
 C:Accession: D61440
 R:Stratilova, E.; Markovic, O.; Skrovinova, D.; Rexova-Benkova, L.; Jornvall, H.
 J. Protein Chem. 12, 15-22, 1993
 A:Title: Pectinase Aspergillus sp. polygalacturonase: multiplicity, divergence, and structure
 A:Reference number: D61440; MUID:93151962; PMID:8427629
 A:Accession: D61440
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-10 <STR>
 A:Cross-references: UNIPROT:Q7M501
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 28.6%; Score 18; DB 2; Length 10;
 Best Local Similarity 80.0%; Pred. No. 1.7e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TSLDA 5
 DB 6 TSADA 10

RESULT 6

S69123
 proton-translocating transhydrogenase - Rhodospirillum rubrum (fragment)
 C:Species: Rhodospirillum rubrum
 C:Date: 10-Mar-1998 #sequence_revision 24-Apr-1998 #text_change 24-Apr-1998
 C:Accession: S69123
 R:Diggle, C.; Hutton, M.; Jones, G.R.; Thomas, C.M.; Jackson, J.B.
 Eur. J. Biochem. 228, 719-726, 1995
 A:Title: Properties of the soluble polypeptide of the proton-translocating transhydrogenase
 A:Reference number: S69123; MUID:95255277; PMID:7737169
 A:Accession: S69123
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-12 <DIG>

Query Match 28.6%; Score 18; DB 2; Length 12;
 Best Local Similarity 40.0%; Pred. No. 2.1e+03;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATMIW 9
 DB 2 ADVVW 6

RESULT 7

I49808
 D-SP2.5 region - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
 C:Accession: I49808
 R:Kurosawa, Y.; Tonegawa, S.
 J. Exp. Med. 155, 201-218, 1982
 A:Title: Organization, structure, and assembly of immunoglobulin heavy chain diversity I
 A:Reference number: I49808; MUID:82099938; PMID:6798155
 A:Accession: I49808
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-6 <RES>
 A:Cross-references: GB:J00432; NID:gl94370; PIDN:AAA37904.1; PID:9450452
 C:Genetics:
 A:Gene: Igh

Query Match 27.0%; Score 17; DB 2; Length 6;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATMIWT 10
 DB 1 STMVTT 6

RESULT 8

PT0519
 T-cell receptor beta chain V-D-J region (100-4C) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PT0519
 R:Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A:Reference number: PT0509; MUID:91277601; PMID:1711558
 A:Accession: PT0519
 A>Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-6 <FEE>
 A:Experimental source: adult thymus, strain BALB/c
 C:Keywords: T-cell receptor

Query Match 27.0%; Score 17; DB 2; Length 6;
 Best Local Similarity 40.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATMIW 9
| : : |
Db 1 ASSIW 5

RESULT 9

PT0650
T-cell receptor beta chain V-D-J region (121-3BF) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0650
R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0650
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-6 <FE>
A;Experimental source: day 4 postnatal thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 27.0%; Score 17; DB 2; Length 6;
Best Local Similarity 80.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 SLDAT 6
| : : |
Db 2 SSDAT 6

RESULT 10

S13889
Phosphoenolpyruvate carboxylase (EC 4.1.1.31) - maize

C;Species: Zea mays (maize)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S13889
R;Jiao, J.; Chollet, R.

Arch. Biochem. Biophys. 283, 300-305, 1990
A;Title: Regulatory phosphorylation of serine-15 in maize phosphoenolpyruvate carboxylase
A;Reference number: S13889; MUID:91112741; PMID:2148863

A;Accession: S13889
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <JIA>
A;Cross-references: UNIPROT:Q43267; UNIPROT:Q41197
C;Keywords: carbon-carbon lyase; carboxy-lyase

Query Match 27.0%; Score 17; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 SLDATM 7
| : : |
Db 3 SIDAQL 8

RESULT 11

A29169

phospholipase A2 (EC 3.1.1.4) precursor - sheep (fragment)

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 16-Aug-2004
C;Accession: A29169

R;Dutilh, C.E.; Van Doren, P.J.; Verheul, F.E.A.M.; De Haas, G.H.

Eur. J. Biochem. 53, 91-97, 1975
A;Title: Isolation and properties of phospholipase A2 from ox and sheep pancreas.
A;Reference number: A94661

A;Accession: A29169
A;Molecule type: protein
A;Residues: 1-12 <DUT>

A;Cross-references: UNIPROT:Q7M3E5
C;Superfamily: Phospholipase A2

C;Keywords: carboxylic ester hydrolase; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 27.0%; Score 17; DB 2; Length 12;
Best Local Similarity 28.6%; Pred. No. 3.2e+03;
Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 LDATMIW 9
| : : |
Db 4 LNSRALW 10

RESULT 12

PT0661

T-cell receptor beta chain V-D-J region (121-1BV) - mouse (fragment)

C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C;Accession: PT0661
R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0661
A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-4 <FE>

A;Cross-references: UNIPROT:Q8BZQ7; UNIPROT:Q8CCN5

A;Experimental source: day 4 postnatal thymus, strain BALB/c

C;Keywords: T-cell receptor

Query Match 25.4%; Score 16; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 WT 10
| : : |
Db 3 WT 4

RESULT 13

S09652

hypothetical protein (aacC2 3' region) - Enterobacter cloacae (fragment)

C;Species: Enterobacter cloacae
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 08-Oct-1999
C;Accession: S09652

R;Vlieghehart, J.S.; Ketelaar-van Gaalen, P.A.G.; van de Klundert, J.A.M.

Antimicrob. Agents Chemother. 33, 1153-1159, 1989

A;Title: Nucleotide sequence of the aacC2 gene, a gentamicin resistance determinant inv

A;Reference number: S09651; MUID:90024972; PMID:2552900

A;Accession: S09652

A;Molecule type: DNA

A;Residues: 1-7 <VLI>

A;Cross-references: EMBL:X51534; NID:g40878; PIDN:CAA35914.1; PID:g581034

Query Match 25.4%; Score 16; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 MIW 9
| : : |
Db 2 IIW 4

RESULT 14

PX0008

glucuronosyltransferase (EC 2.4.1.17), hepatic - rat (fragment)

N;Alternate names: UDP-glucuronyltransferase

C;Species: Rattus norvegicus (Norway rat)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 07-Feb-1997

C;Accession: PX0008

R;Yokota, H.; Yuasa, A.; Sato, R.

J. Biochem. 104, 531-536, 1988

A;Title: Purification and properties of a form of UDP-glucuronyltransferase from liver

A;Reference number: PX0008; MUID:89197852; PMID:3149280
A;Accession: PX0008
A;Molecule type: protein
A;Residues: 1-7 <YOK>
C;Keywords: glycosyltransferase; hexosyltransferase; liver

Query Match 25.4%; Score 16; DB 2; Length 7;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 MW 9
Db 4 LWN 6

RESULT 15

I55382
hypothetical peptide PA11 promoter region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 16-Apr-1999 #sequence_revision 16-Apr-1999 #text_change 20-Apr-2000
C;Accession: I55382
R;Dawson, S.J.; Wiman, B.; Hamsten, A.; Green, F.; Humphries, S.; Henney, A.M.
J. Biol. Chem. 268, 10739-10745, 1993
A;Title: The two allele sequences of a common polymorphism in the promoter of the plasminogen activator gene
A;Reference number: I55382; MUID:93266509; PMID:8388372
A;Accession: I55382
A;Status: translation not shown; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-7 <DAW>
A;Cross-references: GB:M91557; NID:g190020; PIDN:AAA60110.1; PID:g190021
C;Comment: This is the hypothetical translation of a sequence from the PA11 gene promoter
C;Genetics:
A;Gene: GDB:PA11
A;Cross-references: GDB:120297; OMIM:173360
A;Map position: 7q21.3-7q22

Query Match 25.4%; Score 16; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 WT 10
Db 1 WT 2

Search completed: November 14, 2004, 12:55:21
Job time : 38 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2004, 13:16:33 ; Search time 79.6667 Seconds
(without alignments)
66.619 Million cell updates/sec

Title: US-09-831-253F-8

Perfect score: 80

Sequence: 1 EAVLILQGPVYSWL 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1568699 seqs, 353819137 residues

Total number of hits satisfying chosen parameters: 238011

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubaa/US06_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubaa/US09_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	33	41.2	14	14	US-10-083-768-39
2	33	41.2	14	14	US-10-083-768-216
3	33	41.2	14	15	US-10-609-217-67
4	33	41.2	14	15	US-10-632-388-67
5	33	41.2	14	15	US-10-651-723-67
6	33	41.2	14	15	US-10-645-761-67
7	33	41.2	14	15	US-10-666-696-67
8	33	41.2	14	15	US-10-653-048-67
9	32	40.0	14	14	US-10-083-768-37
10	31	38.8	6	15	US-10-243-613-25
11	31	38.8	9	15	US-10-428-335-69
12	31	38.8	12	10	US-09-990-832C-71
13	31	38.8	15	9	US-09-760-397-6

14	31	38.8	15	14	US-10-324-182-6	Sequence 6, Appli
15	30	37.5	9	10	US-09-077-439A-13	Sequence 13, Appl
16	30	37.5	9	13	US-10-205-150-9	Sequence 9, Appli
17	30	37.5	9	14	US-10-079-167-66	Sequence 66, Appl
18	30	37.5	9	14	US-10-360-836-66	Sequence 66, Appl
19	30	37.5	9	15	US-10-057-475B-10639	Sequence 10639, A
20	30	37.5	9	15	US-10-057-475B-10660	Sequence 10660, A
21	30	37.5	9	15	US-10-057-475B-10715	Sequence 10715, A
22	30	37.5	9	15	US-10-154-884B-10639	Sequence 10639, A
23	30	37.5	9	15	US-10-154-884B-10660	Sequence 10660, A
24	30	37.5	9	15	US-10-154-884B-10715	Sequence 10715, A
25	30	37.5	9	15	US-10-367-580-146	Sequence 146, App
26	30	37.5	9	15	US-10-367-593-146	Sequence 146, App
27	30	37.5	9	15	US-10-367-594-146	Sequence 146, App
28	30	37.5	9	15	US-10-367-654-146	Sequence 146, App
29	30	37.5	9	15	US-10-367-658-146	Sequence 146, App
30	30	37.5	9	15	US-10-367-668-146	Sequence 146, App
31	30	37.5	9	16	US-10-367-674-146	Sequence 146, App
32	30	37.5	9	16	US-10-653-624-66	Sequence 66, Appl
33	30	37.5	9	16	US-10-833-439-66	Sequence 66, Appl
34	30	37.5	9	17	US-10-833-745-66	Sequence 66, Appl
35	30	37.5	9	17	US-10-833-744-66	Sequence 66, Appl
36	30	37.5	9	17	US-10-686-943-66	Sequence 66, Appl
37	30	37.5	12	16	US-10-654-623-3	Sequence 3, Appli
38	29	36.2	9	9	US-09-915-543-8	Sequence 8, Appli
39	29	36.2	9	14	US-10-322-579-8	Sequence 8, Appli
40	29	36.2	9	15	US-10-664-859-8	Sequence 8, Appli
41	29	36.2	9	15	US-10-398-104-140	Sequence 140, App
42	29	36.2	11	15	US-10-449-829A-35	Sequence 35, Appl
43	29	36.2	11	15	US-10-398-104-280	Sequence 280, App
44	29	36.2	11	16	US-10-652-334-12	Sequence 12, Appl
45	29	36.2	12	15	US-10-328-916-47	Sequence 47, Appl

ALIGNMENTS

RESULT 1
US-10-083-768-39
; Sequence 39, Application US/10083768
; Publication No. US20030158116A1
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; Barrett, Ronald W.
; Cwirla, Steven E.
; Duffin, David J.
; Gates, Christian
; Haselden, Sherril S.
; Mattheakis, Larry C.
; Schatz, Peter J.
; Wagstrom, Christopher R.
; Wrighton, Nicholas C.
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
; THROMBOPOIETIN RECEPTOR
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glaxo Wellcome
; STREET: Five Moore Drive, P.O. Box 13398
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/083,768
; FILING DATE: 27-Feb-2002
; ATTORNEY/AGENT INFORMATION:
; NAME: Hrubiec, Robert T.
; REGISTRATION NUMBER: 36,392

REFERENCE/DOCKET NUMBER: PK3065USW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-10-083-768-39

Query Match 41.2%; Score 33; DB 14; Length 14;
Best Local Similarity 60.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LQPPPVSWL 15
| | | : | | |
DB 3 LVGPSSLMSWL 12

RESULT 2
US-10-083-768-216
; Sequence 216, Application US/10083768
; Publication No. US20030158116A1
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; Barrett, Ronald W.
; Cwiria, Steven E.
; Duffin, David J.
; Gates, Christian
; Haselden, Sherril S.
; Mattheakis, Larry C.
; Schatz, Peter J.
; Wagstrom, Christopher R.
; Wrighton, Nicholas C.
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glaxo Wellcome
; STREET: Five Moore Drive, P.O. Box 13398
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/083,768
; FILING DATE: 27-Feb-2002
; ATTORNEY/AGENT INFORMATION:
; NAME: Hrubiec, Robert T.
; REGISTRATION NUMBER: 36,392
; REFERENCE/DOCKET NUMBER: PK3065USW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-248-1000
; INFORMATION FOR SEQ ID NO: 216:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 216:
US-10-083-768-216

Query Match 41.2%; Score 33; DB 14; Length 14;
Best Local Similarity 60.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LQPPPVSWL 15
| | | : | | |
DB 3 LVGPSSLMSWL 12

RESULT 3
US-10-609-217-67
; Sequence 67, Application US/10609217
; Publication No. US20040044188A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/609,217
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 67
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TPO-MIMETIC PEPTIDE
US-10-609-217-67

Query Match 41.2%; Score 33; DB 15; Length 14;
Best Local Similarity 60.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LQPPPVSWL 15
| | | : | | |
DB 3 LVGPSSLMSWL 12

RESULT 4
US-10-632-388-67
; Sequence 67, Application US/10632388
; Publication No. US20040053845A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/632,388
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 67
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TPO-MIMETIC PEPTIDE
US-10-632-388-67

Query Match 41.2%; Score 33; DB 15; Length 14;
Best Local Similarity 60.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LOGPPYVSWL 15
| | | : | | |
Db 3 LVGPSLMSWL 12

RESULT 5

US-10-651-723-67
; Sequence 67, Application US/10651723
; Publication No. US20040057953A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/651,723
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TPO-MIMETIC PEPTIDE
US-10-651-723-67

Query Match 41.2%; Score 33; DB 15; Length 14;
Best Local Similarity 60.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LOGPPYVSWL 15
| | | : | | |
Db 3 LVGPSLMSWL 12

RESULT 6

US-10-645-761-67
; Sequence 67, Application US/10645761
; Publication No. US20040071712A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/645,761
; CURRENT FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TPO-MIMETIC PEPTIDE
US-10-645-761-67

Query Match 41.2%; Score 33; DB 15; Length 14;
Best Local Similarity 60.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LOGPPYVSWL 15
| | | : | | |
Db 3 LVGPSLMSWL 12

RESULT 7

US-10-666-696-67
; Sequence 67, Application US/10666696
; Publication No. US20040077022A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; APPLICANT: GUDAS, JEAN MARIE
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527A
; CURRENT APPLICATION NUMBER: US/10/666,696
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/563,286C
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/428,082
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1157
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TPO-mimetic peptide
US-10-666-696-67

Query Match 41.2%; Score 33; DB 15; Length 14;
Best Local Similarity 60.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LOGPPYVSWL 15
| | | : | | |
Db 3 LVGPSLMSWL 12

RESULT 8

US-10-653-048-67
; Sequence 67, Application US/10653048
; Publication No. US20040087778A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/653,048
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TPO-MIMETIC PEPTIDE
US-10-653-048-67

Query Match 41.2%; Score 33; DB 15; Length 14;
Best Local Similarity 60.0%; Pred. No. 3.5e+02;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LOGPPVSWL 15
| | | | |
Db 3 LVGPSLMSWL 12

RESULT 9

US-10-083-768-37
; Sequence 37, Application US/10083768
; Publication No. US20030158116A1

GENERAL INFORMATION:

APPLICANT: Dower, William J.
; Barrett, Ronald W.
; Cwirle, Steven E.
; Duffin, David J.
; Gases, Christian
; Haselden, Sherril S.
; Matheakis, Larry C.
; Schatz, Peter J.
; Wagstrom, Christopher R.
; Wrighton, Nicholas C.
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
; THROMBOPOIETIN RECEPTOR
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glaxo Wellcome
; STREET: Five Moore Drive, P.O. Box 13398
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/083,768
; FILING DATE: 27-Feb-2002
; ATTORNEY/AGENT INFORMATION:
; NAME: Hrubiec, Robert T.
; REGISTRATION NUMBER: 36,392
; REFERENCE/DOCKET NUMBER: PK3065USW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-248-1000

INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-10-083-768-37

Query Match 40.0%; Score 32; DB 14; Length 14;
Best Local Similarity 55.6%; Pred. No. Se+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 OGPPVSWL 15
| | | | |
Db 3 OGPTLTAWL 11

RESULT 10

US-10-243-613-25
; Sequence 25, Application US/10243613
; Publication No. US20040053823A1

GENERAL INFORMATION:

APPLICANT: Smith, Jeffrey W.
; APPLICANT: Chen, Emily I.
; APPLICANT: Kridel, Steven J.

; TITLE OF INVENTION: Selective Substrates for Matrix
; TITLE OF INVENTION: Metalloproteinases
; FILE REFERENCE: P-LJ 5432
; CURRENT APPLICATION NUMBER: US/10/243,613
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 09/953,592
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-243-613-25

Query Match 38.8%; Score 31; DB 15; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 PYVSWL 15
| | | | |
Db 1 PYVIWL 6

RESULT 11

US-10-428-335-69
; Sequence 69, Application US/10428335
; Publication No. US20040009186A1
; GENERAL INFORMATION:
; APPLICANT: BAE Joo-eun
; APPLICANT: KLINGEMANN, Hans G.
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES
; FILE REFERENCE: 047940-0128
; CURRENT APPLICATION NUMBER: US/10/428,335
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 10/138,469
; PRIOR FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 69
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-428-335-69

Query Match 38.8%; Score 31; DB 15; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 PPVSWL 15
| | | | |
Db 3 PPIFSWL 9

RESULT 12

US-09-990-832C-71
; Sequence 71, Application US/0990832C
; Publication No. US20030149235A1
; GENERAL INFORMATION:
; APPLICANT: University Court of the University of Glasgow
; TITLE OF INVENTION: Targeting peptides
; FILE REFERENCE: PC/MC/JM/PI1910US
; CURRENT APPLICATION NUMBER: US/09/990,832C
; CURRENT FILING DATE: 2003-01-27
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

OTHER INFORMATION: Targeting peptide sequence
US-09-990-832C-71

Query Match 38.8%; Score 31; DB 10; Length 12;
Best Local Similarity 44.4%; Pred. No. 6.2e+02;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 4 LILQGPYPV 12
|::|::|::|::|
DB 4 LLIEYPPYI 12

RESULT 13
US-09-760-397-6
; Sequence 6, Application US/09760397
; Patent No. US20020009781A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Gavitt, Patrick D.
; TITLE OF INVENTION: Improved Methods for Recombinant Peptide Production
; FILE REFERENCE: 1103/11041US01
; CURRENT APPLICATION NUMBER: US/09/760,397
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/271,970
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Human
US-09-760-397-6

Query Match 38.8%; Score 31; DB 9; Length 15;
Best Local Similarity 71.4%; Pred. No. 7.6e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 PPYVSWL 15
|||
DB 2 PPKVGWL 8

RESULT 14
US-10-324-182-6
; Sequence 6, Application US/10324182
; Publication No. US20030194782A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Gavitt, Patrick D.
; TITLE OF INVENTION: Improved Methods for Recombinant Peptide Production
; FILE REFERENCE: 1103/11041US01
; CURRENT APPLICATION NUMBER: US/10/324,182
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US/09/271,970
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Human
US-10-324-182-6

Query Match 38.8%; Score 31; DB 14; Length 15;
Best Local Similarity 71.4%; Pred. No. 7.6e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 PPYVSWL 15
|||
DB 2 PPKVGWL 8

RESULT 15

US-09-077-439A-13
; Sequence 13, Application US/09077439A
; Publication No. US20030202989A1
; GENERAL INFORMATION:
; APPLICANT: Collier, R. John
; APPLICANT: Blanke, Steven R.
; APPLICANT: Milne, Jill C.
; APPLICANT: Benson, Ericka L.
; APPLICANT: Ballard, Jimmy D.
; APPLICANT: Starnbach, Michael N.
; TITLE OF INVENTION: Use of Toxin Peptides and/or Affinity
; TITLE OF INVENTION: Handles for Delivering Compounds into Cells
; FILE REFERENCE: 00246/187002
; CURRENT APPLICATION NUMBER: US/09/077,439A
; CURRENT FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: PCT/US96/20463
; PRIOR FILING DATE: 1996-12-13
; PRIOR APPLICATION NUMBER: US 60/019,275
; PRIOR FILING DATE: 1996-06-07
; PRIOR APPLICATION NUMBER: US 60/008,518
; PRIOR FILING DATE: 1995-12-13
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-077-439A-13

Query Match 37.5%; Score 30; DB 10; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 PYVSWL 15
|||
DB 2 PYLWGL 7

Search completed: November 14, 2004, 13:36:59
Job time : 80.6667 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2004, 12:55:26 ; Search time 93.3333 Seconds
(without alignments)
57.653 Million cell updates/sec

Title: US-09-831-253F-8

Perfect score: 80
Sequence: 1 EAVLILQGPVYVSWL 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 605831

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_23Sep04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	80	100.0	15	3 AAY92952	Aay92952 Transform
2	80	100.0	15	3 AAY93104	Aay93104 Transform
3	33	41.2	14	2 AAW09483	Aaw09483 Thrombopo
4	33	41.2	14	2 AAW36634	Aaw36634 Thrombopo
5	33	41.2	14	2 AAW36767	Aaw36767 Thrombopo
6	33	41.2	14	3 AAB17011	Aab17011 TPO-mimet
7	33	41.2	14	4 AAU25853	Aau25853 Human thr
8	33	41.2	14	5 ABB72897	Abb72897 TPO mimet
9	33	41.2	14	7 ADJ73048	Adj73048 TPO mimet
10	33	41.2	14	8 ADJ52683	Adj52683 CHI delet
11	33	41.2	14	8 ADJ51644	Adj51644 CHI delet
12	33	41.2	15	5 ABB05646	Abb05646 Human thy
13	32	40.0	9	8 ADK03181	Adk03181 Hepatitis
14	32	40.0	10	8 ADK03184	Adk03184 Hepatitis
15	32	40.0	11	2 AAW83368	Aaw83368 PpGI met
16	32	40.0	14	2 AAW09481	Aaw09481 Thrombopo
17	32	40.0	14	2 AAW36632	Aaw36632 Thrombopo
18	32	40.0	14	4 AAU25851	Aau25851 Human thr
19	32	40.0	15	5 AAU97014	Aau97014 Human coa
20	31.5	39.4	14	4 AAM96969	Aam96969 Human pep
21	31	38.8	6	6 ABR55023	Abr55023 MMP-2 sel
22	31	38.8	6	6 ADK14204	Adk14204 Matrix me
23	31	38.8	9	2 AAW37010	Aaw37010 TRP-2 der
24	31	38.8	9	8 ADN28269	Adn28269 Human CD3
25	30	37.5	8	2 AAW25563	Aaw25563 Synthetic

26	30	37.5	8	2 AAW25562	Aaw25562 Synthetic
27	30	37.5	8	2 AAW25561	Aaw25561 Synthetic
28	30	37.5	8	2 AAR29768	Aar29768 PIA TRA a
29	30	37.5	9	2 AAR63674	Aar63674 Antigenic
30	30	37.5	9	2 AAR63152	Aar63152 PIA tumou
31	30	37.5	9	2 AAR82990	Aar82990 MAGE tumo
32	30	37.5	9	2 AAR89158	Aar89158 Peptide P
33	30	37.5	9	2 AAW29251	Aaw29251 Immunomod
34	30	37.5	9	2 AAW22041	Aaw22041 Antigenic
35	30	37.5	9	2 AAW68309	Aaw68309 MHC bindi
36	30	37.5	9	2 AAY41263	Aay41263 H-2Ld-res
37	30	37.5	9	2 AAY03653	Aay03653 PIA tummo
38	30	37.5	9	2 AAY22128	Aay22128 PIATRA an
39	30	37.5	9	4 AAG66423	Aag66423 Mouse mas
40	30	37.5	9	4 AAG78821	Aag78821 P815AB pe
41	30	37.5	9	5 AAU76804	Aau76804 MHC class
42	30	37.5	9	6 AAE35597	Aae35597 PIA prote
43	30	37.5	9	6 ABE58361	Abp58361 Mastocyto
44	30	37.5	9	6 ABR44537	Abr44537 PIA-1 pep
45	30	37.5	9	6 AAO23280	Aao23280 PIA (35-4

ALIGNMENTS

RESULT 1
AAY92952
ID AAY92952 standard; peptide; 15 AA.
XX
AC AAY92952;
XX
DT 08-NOV-2000 (first entry)
XX
DE Transforming growth factor inhibitory peptide #8.
XX
KW Hepatotrophic; antagonist; transforming growth factor betaf; TGF-b1;
KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW extracellular matrix degradation inhibitor; mimetops; cirrhosis.
XX
OS Homo sapiens.
XX
PN WO200031135-A1.
XX
PD 02-JUN-2000.
XX
PF 23-NOV-1999; 99WO-ES000375.
XX
PR 24-NOV-1998; 98ES-00002465.
(CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
Ezquerro Saenz JJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
Borras Cuesta F;
WPI; 2000-411935/35.
Peptides that antagonize binding of transforming growth factor betaf,
useful for treatment of liver disease, especially cirrhosis, are partial
sequences of the factor or its receptors.
Claim 9; Page 82; 86pp; Spanish.
The invention relates to synthetic peptides that antagonise the binding
of transforming growth (TGF) factor betaf (TGF-b1) to its receptor in
vivo which have partial amino acid sequences identical, or similar, with
those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
examples of the peptides of the invention. The peptides act by
competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
they are inhibitors of stimulation of collagen synthesis in liver cells
and inhibitors of synthesis of proteolytic enzymes able to degrade the
extracellular matrix. The peptides, their mimetops and/or DNA (or
expression systems) encoding the peptides are used for treatment of liver
disease, specifically cirrhosis

```

XX SQ Sequence 15 AA;
Query Match 100.0%; Score 80; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EAVLLIQGPPYVSWL 15
Db 1 EAVLLIQGPPYVSWL 15

RESULT 2
AAY93104
ID AAY93104 standard; peptide; 15 AA.
XX AC AAY93104;
XX DT 08-NOV-2000 (first entry)
XX DE Transforming growth factor inhibitory peptide P150.
XX KW Hepatotropic; antagonist; transforming growth factor betaf; TGF-b1;
XX KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
XX KW extracellular matrix degradation inhibitor; mimotope; cirrhosis.
XX OS Homo sapiens.
XX PN WO200031135-A1.
XX PD 02-JUN-2000.
XX PF 23-NOV-1999; 99WO-ES000375.
XX PR 24-NOV-1998; 98ES-00002465.
XX PA (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
XX PI Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
PI Borrás Cuesta F;
XX WPI; 2000-411935/35.
XX PT Peptides that antagonize binding of transforming growth factor betaf.
XX PT useful for treatment of liver disease, especially cirrhosis, are partial
XX PT sequences of the factor or its receptors.
XX PS Disclosure; Page 33; 86pp; Spanish.
XX CC The invention relates to synthetic peptides that antagonise the binding
XX CC of transforming growth (TGF) factor betaf (TGF-b1) to its receptor in
XX CC vivo which have partial amino acid sequences identical, or similar, with
XX CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
XX CC examples of the peptides of the invention. The peptides act by
XX CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
XX CC they are inhibitors of stimulation of collagen synthesis in liver cells
XX CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
XX CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
XX CC expression systems) encoding the peptides are used for treatment of liver
XX CC disease, specifically cirrhosis
XX SQ Sequence 15 AA;
Query Match 100.0%; Score 80; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EAVLLIQGPPYVSWL 15
Db 1 EAVLLIQGPPYVSWL 15

RESULT 3
AAW09483
ID AAW09483 standard; protein; 14 AA.
XX AC AAW09483;
XX DT 10-SEP-1997 (first entry)
XX DE Thrombopoietin receptor binding peptide.
XX KW Haematology; thrombocytopenia; TPO; TR; proliferation;
XX KW bone marrow transfusion; chemotherapy; radiation therapy.
XX OS Synthetic.
XX PN WO9640189-A1.
XX PD 19-DEC-1996.
XX PF 05-JUN-1996; 96WO-US008998.
XX PR 07-JUN-1995; 95US-00472371.
XX PR 07-JUN-1995; 95US-00473604.
XX PR 07-JUN-1995; 95US-00476168.
XX PR 07-JUN-1995; 95US-00478128.
XX PR 07-JUN-1995; 95US-00484090.
XX PR 07-JUN-1995; 95US-00485301.
XX PA (GLAX ) GLAXO GROUP LTD.
XX PI Dower WJ, Barrett RW, Cwirla SE, Duffin DJ, Gates CM, Johnson SS;
XX PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
XX WPI; 1997-051883/05.
XX PT Thrombopoietin receptor-binding/activating peptide(s) and peptide
XX PT mimetic(s) - useful in treatment of haematological disorders, esp.
XX PT thrombocytopenia resulting from chemotherapy, etc.
XX PS Disclosure; Page 26; 106pp; English.
XX CC The present sequence is a peptide which binds to thrombopoietin (TPO)
XX CC receptor (TR). The compound can be used for treating patients suffering
XX CC from haematological disorders and thrombocytopenia resulting from
XX CC chemotherapy, radiation therapy or bone marrow transfusions. The peptide
XX CC may also be used to maintain the proliferation and growth of TPO-
XX CC dependent cell lines and for use in biological research, for detecting
XX CC TPO receptors on living cells
XX SQ Sequence 14 AA;
Query Match 41.2%; Score 33; DB 2; Length 14;
Best Local Similarity 60.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LQGPYVSWL 15
Db 3 LVGPSLMSWL 12

RESULT 4
AAW36634
ID AAW36634 standard; peptide; 14 AA.
XX AC AAW36634;
XX DT 11-MAR-1998 (first entry)
XX DE Thrombopoietin receptor binding peptide.
XX KW Thrombopoietin receptor; binding peptide; treatment; agonist;
XX KW haematological disorder; thrombocytopenia; chemotherapy;
XX KW radiation therapy; bone marrow transfusion; diagnosis;
XX KW signal transduction; receptor activation; cell culture.

```


XX OS Synthetic.
 XX PN WO9640750-A1.
 XX PD 19-DEC-1996.
 XX PF 07-JUN-1996; 96WO-US009623.
 XX PR 07-JUN-1995; 95US-00478128.
 XX PR 07-JUN-1995; 95US-00485301.
 XX PA (GLAX) GLAXO GROUP LTD.
 XX PI Dower WJ, Barret RW, Cwirla SE, Duffin DJ, Gates CM, Johnson SS;
 PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
 XX WPI; 1997-052226/05.
 XX PT Peptides and peptide mimetics which bind to and activate the
 PT thrombopoietin receptor - useful in treatment of haematological
 PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
 XX XX Disclosure; Page 26; 106pp; English.
 XX CC The present peptide, which binds the thrombopoietin receptor (TR), can be
 CC used to treat disorders which are susceptible to treatment with a
 CC thrombopoietin agonist, preferably haematological disorders and
 CC thrombocytopenia resulting from chemotherapy, radiation therapy or bone
 CC marrow transfusions. It can also be used diagnostically, e.g. to
 CC investigate the mechanism of thrombopoietin signal transduction and
 CC receptor activation, or to maintain the proliferation and growth of
 CC thrombopoietin dependent cell lines
 XX SQ Sequence 14 AA;
 Query Match 41.2%; Score 33; DB 2; Length 14;
 Best Local Similarity 60.0%; Pred. No. 2.4e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 6 LQGPYPVSWL 15
 | | | : | | |
 Db 3 LVGPSLMSWL 12
 RESULT 5
 AAW36767 AAW36767 standard; peptide; 14 AA.
 XX AC AAW36767;
 XX DT 11-MAR-1998 (first entry)
 XX DE Thrombopoietin receptor binding peptide.
 XX KW Thrombopoietin receptor; binding peptide; treatment; agonist;
 KW haematological disorder; thrombocytopenia; chemotherapy;
 KW radiation therapy; bone marrow transfusion; diagnosis;
 KW signal transduction; receptor activation; cell culture.
 XX OS Synthetic.
 XX PH Key Location/Qualifiers
 FT Disulfide-bond 1. 14
 FT Modified-site 14
 FT /note= "NH2-Cys"
 XX PN WO9640750-A1.
 XX PD 19-DEC-1996.
 XX PR 07-JUN-1996; 96WO-US009623.
 XX

PR 07-JUN-1995; 95US-00478128.
 PR 07-JUN-1995; 95US-00485301.
 XX (GLAX) GLAXO GROUP LTD.
 XX PI Dower WJ, Barret RW, Cwirla SE, Duffin DJ, Gates CM, Johnson SS;
 PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
 XX WPI; 1997-052226/05.
 XX PT Peptides and peptide mimetics which bind to and activate the
 PT thrombopoietin receptor - useful in treatment of haematological
 PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.
 XX XX Example 9; Page 75; 106pp; English.
 XX CC The present peptide, which binds the thrombopoietin receptor (TR), can be
 CC used to treat disorders which are susceptible to treatment with a
 CC thrombopoietin agonist, preferably haematological disorders and
 CC thrombocytopenia resulting from chemotherapy, radiation therapy or bone
 CC marrow transfusions. It can also be used diagnostically, e.g. to
 CC investigate the mechanism of thrombopoietin signal transduction and
 CC receptor activation, or to maintain the proliferation and growth of
 CC thrombopoietin dependent cell lines
 XX SQ Sequence 14 AA;
 Query Match 41.2%; Score 33; DB 2; Length 14;
 Best Local Similarity 60.0%; Pred. No. 2.4e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 6 LQGPYPVSWL 15
 | | | : | | |
 Db 3 LVGPSLMSWL 12
 RESULT 6
 AAB17011 AAB17011 standard; peptide; 14 AA.
 XX AC AAB17011;
 XX DT 31-OCT-2000 (first entry)
 XX DE TPO-mimetic peptide sequence SEQ ID NO:67.
 XX KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
 KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
 KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KW vascular endothelial growth factor; matrix metalloproteinase; asthma;
 KW thrombosis; pharmaceutical.
 XX OS Synthetic.
 XX PN WO200024782-A2.
 XX PD 04-MAY-2000.
 XX PF 25-OCT-1999; 99WO-US025044.
 XX PR 23-OCT-1998; 98US-0105371P.
 XX PR 22-OCT-1999; 99US-00428082.
 XX PA (AMGE-) AMGEN INC.
 XX PI Feige U, Liu C, Cheetham J, Boone TC;
 XX WPI; 2000-350702/30.
 XX PT Novel composition of matter comprising an Fc domain and pharmacologically
 PT active peptides, useful for treating cancer and autoimmune diseases.

XX PS Claim 19; Page 217; 608pp; English.

XX CC The present invention describes composition of matter (I) comprising an

CC FC domain, pharmacologically active peptides, and linkers. Where (I) is:

CC (X1)a-F1-(X2)b, where: F1 = an FC domain; X1 and X2 = are each

CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-

CC (L2)d-P2-(L3)e-P³, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,

CC P3, and P4 = are each independently sequences of pharmacologically active

CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,

CC c, d, e, and f = are each independently 0 or 1, provided that at least 1

CC of a and b is 1. The composition can have cytostatic, antiasthmatic,

CC thrombolytic and immunosuppressive activities. DNAs, vectors and host

CC cells from the present invention can be used for producing pharmaceutical

CC compositions. The compositions are useful for treating cancer, asthma,

CC thrombosis, or autoimmune diseases. The use of an FC domain (rather than

CC a Fab domain) can provide a longer half-life or incorporate functions

CC such as FC receptor binding, protein A binding, complement fixation, and

CC possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to

CC AAB18003 represent nucleotide and amino acid sequences used in the

CC exemplification of the present invention

XX SQ Sequence 14 AA;

Query Match 41.2%; Score 33; DB 3; Length 14;

Best Local Similarity 60.0%; Pred. No. 2.4e+02;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LQGPYVSWL 15

Db 3 LVGPSLSMSWL 12

RESULT 7

AAU25853

ID AAU25853 standard; peptide; 14 AA.

AC AAU25853;

XX DT 17-DEC-2001 (first entry)

XX DE Human thrombopoietin receptor (TPO-R) activator peptide #39.

XX KW Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;

XX KW haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA;

XX KW bone marrow transplantation; haematological disorder; platelet disorder;

XX KW enzyme-linked immunosorbent assay; in situ staining; biological fluid;

XX KW tissue homogenate; fluorescence-activated cell sorting; Western blotting;

XX KW in vitro expansion; megakaryocyte; Headpiece Dimer gene; lacI gene.

XX OS Homo sapiens.

XX US6251864-B1.

XX 26-JUN-2001.

XX 01-MAR-2000; 2000US-00516704.

XX 07-JUN-1995; 95US-00478128.

XX 07-JUN-1995; 95US-00485301.

XX 07-JUN-1996; 96WO-US009623.

XX 15-AUG-1996; 96US-00699027.

XX (GLAX) GLAXO GROUP LTD.

XX Dower WJ, Barrett RW, Cwirila SE, Gates CM, Schatz PJ;

PI Balasubramanian P, Wagstrom CR, Hendren RW, Deprince RB, Podduturi S;

PI Yin Q;

XX WPI; 2001-564142/63.

XX Activating thrombopoietin receptors in cells, used to treat

PT thrombocytopenia and hematological disorders, comprises contacting cells

PT with peptides and peptide mimetics attached to hydrophilic polymers.

XX PS Disclosure; Col 20; 128pp; English.

XX CC Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that

CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods

CC of activating thrombopoietin receptors in cells comprise contacting the

CC cells with effective amounts of peptides and peptide mimetics attached to

CC hydrophilic polymers. The methods are used to treat thrombocytopenia such

CC as that due to chemotherapy, radiation therapy or bone-marrow

CC transplantation and to prevent thrombocytopenia in patients at risk. The

CC sequences are used to treat and prevent haematological disorders

CC including thrombocytopenia and platelet disorders. They are used in vitro

CC as unique tools for understanding the biological role of thrombopoietin

CC (TPO) and to develop other compounds that bind to and activate the TPO

CC receptor. The peptides can be used to detect TPO receptors on living

CC cells and fixed cells, in biological fluids, in tissue homogenates, and

CC in purified or natural biological materials. They may also be used for in

CC situ staining, fluorescence-activated cell sorting, Western blotting and

CC enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can

CC be used for in vitro expansion of megakaryocytes and their committed

CC progenitors alone or in conjunction with additional cytokines

XX SQ Sequence 14 AA;

Query Match 41.2%; Score 33; DB 4; Length 14;

Best Local Similarity 60.0%; Pred. No. 2.4e+02;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LQGPYVSWL 15

Db 3 LVGPSLSMSWL 12

RESULT 8

ABB72897

ID ABB72897 standard; peptide; 14 AA.

XX AC ABB72897;

XX DT 05-APR-2002 (first entry)

XX DE TPO mimetic peptide SEQ ID NO:67.

XX KW Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IGG; EPO;

XX KW erythropoietin; TPO; tumour necrosis factor alpha inhibitor;

XX KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;

XX KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;

XX KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;

XX KW cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;

XX KW antianaemic; anorectic; antiinfertility; haemostatic; dermatological;

XX KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;

XX KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;

XX KW sleep disorder; neurological degenerative disease; anaemia;

XX KW thrombocytopenia; metastatic tumour; systemic lupus erythematosus;

XX KW Fanconi's syndrome.

XX OS Homo sapiens.

OS Synthetic.

XX WO200183525-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US014310.

XX 03-MAY-2000; 2000US-00563286.

XX (AMGE-) AMGEN INC.

XX Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;

XX WPI; 2002-130313/17.

XX Novel vehicle-peptide molecule or its multimers useful for treating
PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
PT diabetic retinopathy, obesity, sleep disorders and infertility.
XX
XX Claim 39; Page 44; 176pp; English.
XX
XX The present invention describes a vehicle-peptide molecule (I) or its
CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
CC antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
CC neuroprotective activities. (I) can be used as a therapeutic or
CC prophylactic agent as well as for screening purposes. (I) is useful for
CC diagnosing diseases characterised by dysfunction of their associated
CC protein of interest, for identifying normal or abnormal proteins of
CC interest, as a part of diagnostic kit to detect the presence of their
CC proteins of interest in a biological sample. Additionally, (I) is useful
CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC infertility, and neurological degenerative diseases. (I), comprising EPO-
CC mimetic compounds are useful for treating disorders characterised by low
CC red blood cell levels such as anaemia. The TPO-mimetic comprising
CC compounds are useful for treating conditions that involve an existing
CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
CC represent amino acid and nucleic acid sequences used in the
CC exemplification of the present invention
XX
XX Sequence 14 AA;
SQ

Query Match 41.2%; Score 33; DB 5; Length 14;
Best Local Similarity 60.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LQGPYPVSWL 15
Db 3 LVGPSLMSWL 12
| | | : | | |
| | | : | | |

RESULT 9
ADJ73048
ID ADJ73048 standard; peptide; 14 AA.
XX
XX AC ADJ73048;
XX
XX DT 06-MAY-2004 (first entry)
XX
XX DE TPO mimetic peptide sequence SeqID 502.
XX
XX KW mimetic; CDR mimetibody; gene therapy; transgenic; immune;
KW cardiovascular; infectious; malignant; neurologic disease; anaemia;
KW immunomodulator; cardiant; antimicrobial; cytostatic; neuroprotective;
KW TPO.
XX
XX OS Synthetic.
XX
XX PN WO2003084477-A2.
XX
XX PD 16-OCT-2003.
XX
XX PF 24-MAR-2003; 2003WO-US009139.
XX
XX PR 29-MAR-2002; 2002US-0368791P.
XX
XX PA (CENZ) CENTOCOR INC.
XX
XX PI Heavner GA, Knight DM, Scallion BJ, Ghayeb J;
XX
XX DR WPI; 2003-804237/75.
XX
XX PT New CDR mimetibody comprising a portion of a heavy or light chain

PT variable region comprising human framework or ligand binding region,
PT useful for preparing a composition for treating e.g., immune,
PT cardiovascular or neurologic disease.
XX
XX Disclosure; SEQ ID NO 502; 97pp; English.
XX
XX This invention relates to novel mammalian CDR mimetibodies, specific
CC portions or variants thereof. Specifically, it refers to an antibody
CC fragment where a protein has been inserted into, or replaces a portion
CC of, one or more CDR regions, such that each CDR mimetibody comprises at
CC least one portion of a heavy chain or light chain variable region, which
CC itself comprises at least one human framework region and at least one
CC ligand binding region (LBR). The present invention describes human
CC mimetibodies, including modified immunoglobulins and cleavage products
CC that can be useful in gene therapy and the generation of transgenic
CC plants and animals. Furthermore, the CDR mimetibody is useful for
CC preparing compositions for modulating, treating or reducing the symptoms
CC of immune, cardiovascular, infectious, malignant and/or neurologic
CC diseases, as well as anaemia. Accordingly, they exhibit immunomodulator,
CC cardiant, antimicrobial, cytostatic and neuroprotective activities. This
CC peptide sequence is a TPO mimetic peptide sequence used to make a
CC mimetibody of the invention.
XX
XX Sequence 14 AA;
SQ

Query Match 41.2%; Score 33; DB 7; Length 14;
Best Local Similarity 60.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LQGPYPVSWL 15
Db 3 LVGPSLMSWL 12
| | | : | | |
| | | : | | |

RESULT 10
ADJ52683
ID ADJ52683 standard; peptide; 14 AA.
XX
XX AC ADJ52683;
XX
XX DT 06-MAY-2004 (first entry)
XX
XX DE CH1 deleted mimetibody-related peptide SeqID502.
XX
XX KW CH1 deleted mimetibody; immunosuppressive; cardiovascular; cardiant;
KW hypotensive; neuroprotective; nootropic; antibacterial; virucide;
KW fungicide; gene therapy; immune disorder; cardiovascular disease;
KW arrhythmia; hypertension; heart failure; neurodegenerative;
KW multiple sclerosis; dementia; Alzheimer's disease; anaemia;
KW cancerous condition; infectious disease; bacterial infection;
KW viral infection; fungal infection.
XX
XX OS Unidentified.
XX
XX OS Synthetic.
XX
XX PN WO2004002417-A2.
XX
XX PD 08-JAN-2004.
XX
XX PF 27-JUN-2003; 2003WO-US020347.
XX
XX PR 28-JUN-2002; 2002US-0392431P.
XX
XX PA (CENZ) CENTOCOR INC.
XX
XX PI Heavner GA, Knight DM, Ghayeb J, Scallion BJ, Nesspor TC;
XX
XX PI Kutloski KA;
XX
XX DR WPI; 2004-082870/08.
XX
XX PT New CH1-deleted mimetibody polypeptides and nucleic acids, useful for
PT modulating, treating, alleviating, preventing an immune, cardiovascular,
PT or neurodegenerative disease or disorder, anemia, cancer, or infectious

PT diseases.
 XX Claim 2; SEQ ID NO 502; 129pp; English.
 XX This invention relates to CHI deleted mimetibodies (and the DNA sequences
 CC which encode them), compositions, methods and uses. The invention may be
 CC useful for the development of compounds with an immunosuppressive,
 CC cardiovascular, cardiant, hypotensive, neuroprotective, nootropic,
 CC antibacterial, virucide or fungicide activity. In addition, the disclosed
 CC sequences may prove useful for gene therapy. The CHI-deleted mimetibody
 CC is useful for diagnosing or treating a disease condition in a cell,
 CC tissue, organ or animal, specifically for modulating, treating,
 CC alleviating, preventing the incidence for reducing the symptoms of an
 CC immune, cardiovascular (for example arrhythmia, hypertension or heart
 CC failure), or neurodegenerative (for example multiple sclerosis, dementia
 CC or Alzheimer's disease) diseases or disorders, anaemia, cancerous
 CC conditions, or infectious diseases (for example bacterial, viral or
 CC fungal infection). The present sequence is that of a peptide which may be
 CC used during the creation of a mimetibody of the invention.
 XX SQ Sequence 14 AA;
 Query Match 41.2%; Score 33; DB 8; Length 14;
 Best Local Similarity 60.0%; Pred. No. 2.4e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 6 LOGPPYVSWL 15
 Db | | | | |
 3 LVGPSLSMSWL 12
 RESULT 11
 ADJ51644
 ID ADJ51644 standard; peptide; 14 AA.
 XX ADJ51644;
 AC
 DT 06-MAY-2004 (first entry)
 XX CHI deleted mimetibody-related peptide SeqID502.
 DE
 XX CHI deleted mimetibody; osteopathic; cardiovascular-Gen;
 KW dermatological-Gen; auditory; endocrine-Gen; gastrointestinal-Gen;
 KW gynaecological-Gen; hepatotropic; haemostatic; immunomodulator;
 KW antiallergic; muscular-Gen; cytostatic; antiinflammatory; neuroleptic;
 KW ophthalmological; nephrotropic; respiratory-Gen; tumour necrosis factor;
 KW TNF; cytokine; bone disorder; joint disorder; cardiovascular disorder;
 KW dental disorder; oral disorder; dermatological disorder; ear disorder;
 KW nose disorder; throat disorder; endocrine disorder; metabolic disorder;
 KW gastrointestinal disorder; gynaecological disorder; hepatic disorder;
 KW obstetric disorder; haematologic disorder; immunological disorder;
 KW allergic disorder; infectious disorder; musculoskeletal disorder;
 KW oncological disorder; neurological disorder; nutritional disorder;
 KW ophthalmologic disorder; pediatric disorder; psychiatric disorder;
 KW renal disorder; pulmonary disorder.
 XX
 OS Unidentified.
 OS Synthetic.
 XX WO2004002424-A2.
 XX
 PN
 PD 08-JAN-2004.
 XX
 PF 30-JUN-2003; 2003WO-US020495.
 XX
 PR 28-JUN-2002; 2002US-0392431P.
 PR 19-SEP-2002; 2002US-0412144P.
 XX
 XX (CENZ) CENTOCOR INC.
 PA Heavner GA, Knight DM, Grayeb J, Scallon BJ, Neseppor TC;
 PI Kutoloski KA;
 XX

DR WPI; 2004-082872/08.
 XX New CHI deleted mimetibody polypeptide and nucleic acid, useful for
 PT diagnosing, preventing or treating cardiovascular, dermatologic,
 PT endocrine, gastrointestinal, gynecologic, infectious, neurologic and
 PT nutritional disorders.
 XX Claim 15; SEQ ID NO 502; 123pp; English.
 PS This invention relates to CHI deleted mimetibodies (and the DNA sequences
 CC which encode them), compositions, methods and uses. The invention may be
 CC useful for the development of compounds with an osteopathic,
 CC cardiovascular-Gen, dermatological-Gen, auditory, endocrine-Gen,
 CC gastrointestinal-Gen, gynaecological-Gen, hepatotropic, haemostatic,
 CC immunomodulator, antiallergic, muscular-Gen, cytostatic,
 CC antiinflammatory, neuroleptic, ophthalmological, nephrotropic or
 CC respiratory-Gen activity acting as a tumour necrosis factor (TNF)-
 CC modulator or cytokine-agonist. The methods and compositions of the
 CC present invention are useful for the diagnosis, prevention and/or
 CC treatment of diseases or conditions associated with aberrant expression
 CC or activity of the CHI deleted mimetibody, such as a bone or joint,
 CC cardiovascular, dental or oral, dermatological, ear, nose or throat,
 CC endocrine, metabolic, gastrointestinal, gynaecological, hepatic,
 CC obstructive, haematologic, immunological, allergic, infectious,
 CC musculoskeletal, oncological, neurological, nutritional, ophthalmologic,
 CC pediatric, psychiatric renal or pulmonary disorders. The present
 CC sequence is that of a peptide which may be used during the creation of a
 CC mimetibody of the invention.
 XX SQ Sequence 14 AA;
 Query Match 41.2%; Score 33; DB 8; Length 14;
 Best Local Similarity 60.0%; Pred. No. 2.4e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 6 LOGPPYVSWL 15
 Db | | | | |
 3 LVGPSLSMSWL 12
 RESULT 12
 ABB05646
 ID ABB05646 standard; peptide; 15 AA.
 AC ABB05646;
 XX 29-APR-2002 (first entry)
 DT Human thyroglobulin 38 protein N-terminal peptide SEQ ID NO:7.
 XX Human thyroglobulin 38; cytostatic; antiinflammatory; simple goitre;
 KW thyroiditis; hyperthyroidism; hypothyroidism; thyroid tumour;
 KW nodular goitre.
 XX Homo sapiens.
 OS
 XX CN1321665-A.
 PN
 XX 14-NOV-2001.
 PD
 XX 29-APR-2000; 2000CN-00115532.
 PF
 XX 29-APR-2000; 2000CN-00115532.
 PR
 XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.
 PA Mao Y, Xie Y;
 PI
 XX WPI; 2002-140635/19.
 DR Novel human thyroglobulin 38 and polynucleotide for coding this
 PT polypeptide, useful for treating diseases such as simple goiter,
 PT thyroiditis, hyperthyroidism, hypothyroidism, thyroid tumor and nodular

PT goiter.
 XX
 PS Example 5; Page 18 (Disclosure); 33pp; Chinese.
 XX
 CC The present invention describes human thyroglobulin 38 protein (I). (I)
 CC has cytostatic and antiinflammatory activities. (I) and the
 CC polynucleotide (II) encoding it can be used in the treatment of diseases
 CC such as simple goitre, thyroiditis, hyperthyroidism, hypothyroidism,
 CC thyroid tumour and nodular goitre. The present sequence represents the N-
 CC terminal peptide of human thyroglobulin 38, which is used in an example
 CC from the present invention
 XX
 XX Sequence 15 AA;

Query Match 41.2%; Score 33; DB 5; Length 15;
 Best Local Similarity 45.5%; Pred. No. 2.6e+02;
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 4 LILQPPYVSW 14
 :||| |||
 Db 5 MMLQDKPYPDW 15

RESULT 13
 ADK03181
 ID ADK03181 standard; peptide; 9 AA.
 XX
 AC ADK03181;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Hepatitis C virus CTL epitope peptide #1011.
 XX
 KW pathogenic virus; alternative reading frame; antigenic determinant;
 KW virucide; vaccine; therapeutic agent; infection; epitope peptide;
 KW HLA-allele; CTL.
 XX
 OS Hepatitis C virus.
 XX
 PN WO2004011650-A2.
 XX
 PD 05-FEB-2004.
 XX
 PF 24-JUL-2003; 2003WO-EP008112.
 XX
 PR 24-JUL-2002; 2002AT-00001124.
 PR 11-JUL-2003; 2003EP-00450171.
 XX
 PA (INTE-) INTERCELL AG.
 XX
 PI Mattner F, Schmidt W, Habel A;
 XX
 DR WPI; 2004-169243/16.
 XX

XX New polypeptide encoded by an alternative reading frame of a pathogenic
 PT virus comprising an antigenic determinant, useful for treating or
 PT preventing an infection with the pathogenic virus.
 XX
 PS Claim 14; Page 70; 220pp; English.
 XX
 CC This invention relates to a novel polypeptide encoded by an alternative
 CC reading frame of a pathogenic virus, where the polypeptide starts with a
 CC methionine amino acid residue, which comprises an antigenic determinant
 CC and more than 7 amino acid residues. The invention may be useful for the
 CC production of compounds with a virucide activity or the development of a
 CC vaccine. The polypeptide or its fragments may be useful as a therapeutic
 CC agent. It is also useful for the manufacture of a medicament for treating
 CC or preventing an infection with the pathogenic virus. The present
 CC sequence is that of a hepatitis C virus CTL epitope peptide of the
 CC invention.
 XX
 XX Sequence 9 AA;

Query Match 40.0%; Score 32; DB 8; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.7e+06;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 7 QQPPYVSWL 15
 :||| |||
 Db 1 QQPPLVWNL 9

RESULT 14
 ADK03184
 ID ADK03184 standard; peptide; 10 AA.
 XX
 AC ADK03184;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Hepatitis C virus CTL epitope peptide #1014.
 XX
 KW pathogenic virus; alternative reading frame; antigenic determinant;
 KW virucide; vaccine; therapeutic agent; infection; epitope peptide;
 KW HLA-allele; CTL.
 XX
 OS Hepatitis C virus.
 XX
 PN WO2004011650-A2.
 XX
 PD 05-FEB-2004.
 XX
 PF 24-JUL-2003; 2003WO-EP008112.
 XX
 PR 24-JUL-2002; 2002AT-00001124.
 PR 11-JUL-2003; 2003EP-00450171.
 XX
 PA (INTE-) INTERCELL AG.
 XX
 PI Mattner F, Schmidt W, Habel A;
 XX
 DR WPI; 2004-169243/16.
 XX
 PT New polypeptide encoded by an alternative reading frame of a pathogenic
 PT virus comprising an antigenic determinant, useful for treating or
 PT preventing an infection with the pathogenic virus.
 XX
 PS Claim 14; Page 70; 220pp; English.

XX This invention relates to a novel polypeptide encoded by an alternative
 CC reading frame of a pathogenic virus, where the polypeptide starts with a
 CC methionine amino acid residue, which comprises an antigenic determinant
 CC and more than 7 amino acid residues. The invention may be useful for the
 CC production of compounds with a virucide activity or the development of a
 CC vaccine. The polypeptide or its fragments may be useful as a therapeutic
 CC agent. It is also useful for the manufacture of a medicament for treating
 CC or preventing an infection with the pathogenic virus. The present
 CC sequence is that of a hepatitis C virus CTL epitope peptide of the
 CC invention.
 XX
 XX Sequence 10 AA;

Query Match 40.0%; Score 32; DB 8; Length 10;
 Best Local Similarity 66.7%; Pred. No. 2.4e+02;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 7 QQPPYVSWL 15
 :||| |||
 Db 2 QQPPLVWNL 10

RESULT 15
 AAW83368
 ID AAW83368 standard; peptide; 11 AA.
 XX
 AC AAW83368;
 XX

```

XX 11-FEB-1999 (first entry)
DT
XX
DE PspGI methylase motif IV peptide.
XX
XX PspGI; type II restriction endonuclease; Pyrococcus; methylase;
KW recombinant.
XX
XX Pyrococcus sp.
OS
XX WO9851783-A1.
PN
XX 19-NOV-1998.
PD
XX
XX 31-MAR-1998; 98WO-US006332.
PF
XX 15-MAY-1997; 97US-00856663.
PR
XX (NEWE ) NEW ENGLAND BIOLABS INC.
PA
XX Morgan RD, Chang Z;
PI
XX WPI; 1999-009770/01.
DR
XX
XX New Type II restriction endonuclease from Pyrococcus species G-I-H - and
PT DNA coding for the endonuclease, optionally with its methylase for
PT recombinant production of the restriction enzyme.
XX
PS Example; Page 32; 47pp; English.
XX
XX The present invention describes a type II restriction endonuclease,
CC designated PspGI, from Pyrococcus species G-I-H. The endonuclease,
CC recognises and cleaves the following base sequence before the first C at
CC the 5' end, to give a five base overhang at the 5' end: 5'-CC(A/T)GG-3'.
CC Also described are: (1) isolated DNA (I) obtainable from Pyrococcus
CC species G-I-H and coding for the PspGI restriction endonuclease; (2)
CC isolated DNA (II) obtainable from ATCC No. 98435 and coding for the PspGI
CC restriction endonuclease and methylase; (3) a recombinant DNA vector into
CC which (I) is inserted; (4) a cloning vector comprising (II); and (5) a
CC host cell transformed with the vector as in (3) or (4). The endonuclease
CC can be isolated using conventional protein purification techniques from
CC Pyrococcus sp. G-I-H. Alternatively, the endonuclease, along with its
CC corresponding methylase can be obtained using recombinant DNA techniques.
CC Restriction endonuclease PspGI is useful in genetic engineering. The DNA,
CC vectors and host cells are all useful for recombinantly producing the
CC endonuclease in commercial quantities. The present sequence represents
CC motif IV from the PspGI methylase
XX
SQ Sequence 11 AA;

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Query Match 40.0%; Score 32; DB 2; Length 11;
Best Local Similarity 75.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

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QY 4 LILQGPY 11
   ||| |||
Db 2 LILTSPY 9

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Search completed: November 14, 2004, 13:11:17
Job time : 95.3333 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2004, 12:56:07 ; Search time 100 Seconds
(without alignments)
86.306 Million cell updates/sec

Title: US-09-831-253F-8

Perfect score: 80

Sequence: 1 EAVLILQGPVYVSWL 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 7754

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	38.8	13	2 Q95925	Q95925 porphyra pu
2	29	36.2	13	2 Q95808	Q95808 gracilaria op
3	28	35.0	13	1 SOVO SEPOF	P83567 sepiia offic
4	27	33.8	8	1 ALL5 CALVO	P41841 calliphora
5	27	33.8	13	1 PROX-ORYSA	P83647 oryza sativ
6	25	31.2	14	2 Q26075	Q26075 psammechinu
7	24	30.0	15	1 SODM STRGR	P80733 streptomyce
8	23	28.7	12	2 Q7M1H0	Q7M1H0 leonurus ar
9	23	28.7	13	2 Q04220	Q04220 plasmid p30
10	23	28.7	14	1 CALI CALGI	P20728 calotropis
11	23	28.7	14	2 P81801	P81801 streptomyce
12	23	28.7	15	2 Q9S8Z0	Q9S8Z0 hordeum vul
13	22.5	28.1	13	2 Q9R3R3	Q9R3R3 borrelia bu
14	22.5	28.1	15	2 Q8GL28	Q8GL28 borrelia bu
15	22	27.5	8	1 ACI THUAL	P18691 thunnus alb
16	22	27.5	8	1 LCK7 LEUMA	P19889 leucophaea
17	22	27.5	8	2 Q8GTG5	Q8GTG5 lycopersico
18	22	27.5	9	2 Q9H326	Q9H326 homo sapien
19	22	27.5	9	2 Q7M2M9	Q7M2M9 bos taurus
20	22	27.5	10	2 Q76MK9	Q76MK9 eurypharynx
21	22	27.5	10	2 Q76MM5	Q76MM5 eurypharynx
22	22	27.5	10	2 BAB87140	BAB87140 euryphary
23	22	27.5	10	2 BAB87148	BAB87148 euryphary
24	22	27.5	10	2 BAB87156	BAB87156 euryphary
25	22	27.5	10	2 BAB87164	BAB87164 euryphary
26	22	27.5	11	2 Q8GL19	Q8GL19 borrelia bu
27	22	27.5	11	2 Q8GL24	Q8GL24 borrelia bu
28	22	27.5	13	2 O61340	O61340 panulirus i
29	22	27.5	14	1 LPW_ECOLI	P03053 escherichia
30	22	27.5	15	2 Q9R3E1	Q9R3E1 legionella
31	22	27.5	15	2 Q9RQ22	Q9RQ22 salmonella

32 21 26.2 8 1 CCKN_MACEU P30369 macropus eu
33 21 26.2 8 1 LCK1_LEUMA P21140 leucophaea
34 21 26.2 8 1 LCK2_LEUMA P21141 leucophaea
35 21 26.2 8 1 LCK8_LEUMA P19990 leucophaea
36 21 26.2 8 1 PK1_PERAM P82685 periplaneta
37 21 26.2 8 1 PK3_PERAM P82687 periplaneta
38 21 26.2 8 1 PK5_PERAM P82689 periplaneta
39 21 26.2 9 2 Q99193 Q99193 pseudomonas
40 21 26.2 10 2 Q7PHS9 Q7PHS9 anopheles g
41 21 26.2 10 2 Q7M2N0 Q7M2N0 bos taurus
42 21 26.2 10 2 O6EX62 O6EX62 hyptis suav
43 21 26.2 10 2 Q7LZC5 Q7LZC5 kassina mac
44 21 26.2 12 2 Q7LZ10 Q7LZ10 vipera lebe
45 21 26.2 15 1 UE15_HORVU P34938 hordeum vul

ALIGNMENTS

RESULT 1

Q95925 PRELIMINARY; PRT; 13 AA.
AC Q95925;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cytochrome oxidase subunit 3 (Fragment).
GN Names-cox3;
OS Porphyra purpurea.
OG Mitochondrion.
OC Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra.
OX NCBI_TaxID=2787;
RN [1]
RP SEQUENCE FROM N.A.
RA Lang B.Franz., Goff L.J., Gray M.W.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U59763; AAB17951.1; -;
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 13 AA; 1522 MW; 0831666D0E8C65B0 CRC64;

Query Match 38.8%; Score 31; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 3.9e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 PPVSW 14
| | | |
Db 3 PDYISW 8

RESULT 2

Q95808 PRELIMINARY; PRT; 13 AA.
ID Q95808;
AC Q95808;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome oxidase subunit 3 (Fragment).
GN Names-cox3;
OS Gracilariopsis lemaneiformis.
OG Mitochondrion.
OC Eukaryota; Rhodophyta; Florideophyceae; Gracilariiales; Gracilariaceae;
OC Gracilariopsis.
OX NCBI_TaxID=2782;
RN [1]
RP SEQUENCE FROM N.A.
RA Lang B.Franz., Goff L.J., Gray M.W.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U59764; AAB17950.1; -;
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1

```
SQ SEQUENCE 13 AA; 1565 MW; 305BD4028745B043 CRC64;
Query Match 36.2%; Score 29; DB 2; Length 13;
Best Local Similarity 42.9%; Pred. No. 8.5e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 9 PPVSWL 15
DB 1 FNYITWI 7

RESULT 3
SOVO SEPOF
ID SOVO SEPOF STANDARD; PRT; 13 AA.
AC P83567;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE SepOvototropin.
OS Sepia officinalis (Common cuttlefish).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Decapodiformes; Sepioidea; Sepiidae; Sepia.
OX NCBI_TaxID=6610;
RN [1]
RP SEQUENCE, FUNCTION, TISSUE SPECIFICITY, MASS SPECTROMETRY, AND
RP AMIDATION.
RC TISSUE-Ovarian follicle;
RX MEDLINE=20483622; PubMed=11027583; DOI=10.1006/bbro.2000.3595;
RA Zatylny C., Gagnon J., Boucaud-Camou E., Henry J.;
RT "The SepOvototropin: a new ovarian peptide regulating oocyte transport
in Sepia officinalis.";
RL Biochem. Biophys. Res. Commun. 276:1013-1018(2000).
CC -!- FUNCTION: Has myotropic activity targeting the genital tract.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Follicle, fully grown oocyte and egg.
CC -!- MASS SPECTROMETRY: MW=1502.8; METHOD=MALDI; RANGE=1-13;
CC NOTE=Ref.1.
KW Amidation; Direct protein sequencing.
FT MOD_RES 13 Tyrosine amide.
SQ SEQUENCE 13 AA; 1503 MW; 483D5C7E34C72727 CRC64;

Query Match 35.0%; Score 28; DB 1; Length 13;
Best Local Similarity 45.5%; Pred. No. 1.2e+03;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 EAVLIQGPY 11
DB 3 DSMLLQVPVY 13

RESULT 4
ALL5 CALVO
ID ALL5 CALVO STANDARD; PRT; 8 AA.
AC P41841;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Callatostatin 5 (Met-callatostatin 1) ([Hyp3]Met-callatostatin).
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RX MEDLINE=932111980; PubMed=8460157;
RA Duve H., Johnsen A.H., Scott A.G., Yu C.G., Yagi K.J., Tobe S.S.,
RA Thorpe A.;
RT "Callatostatins: neuropeptides from the blowfly Calliphora vomitoria
with sequence homology to cockroach allatostatins.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).
RN [2]
RP CHARACTERIZATION, AND HYDROXYLATION.
```

```
RC TISSUE=Head;
RX MEDLINE=94342269; PubMed=8063725;
RA Duve H., Johnsen A.H., Scott A.G., East P., Thorpe A.;
RT "[Hyp3]Met-callatostatin. Identification and biological properties of
a novel neuropeptide from the blowfly Calliphora vomitoria.";
RL J. Biol. Chem. 269:21059-21066(1994).
CC -!- FUNCTION: May act as a neurotransmitter or neuromodulator and play
a role in the integration of information within the brain. May be
involved in the control of visceral muscles due to its ability to
behave as potent inhibitors of peristaltic movements. May also
fulfill a neurohormonal role on muscles of the gut and heart.
CC -!- TISSUE SPECIFICITY: Neurons within brain and abdominal ganglion.
CC -!- SIMILARITY: Belongs to the allatostatin family.
DR PIR, E47393; E47393.
KW Amidation; Direct protein sequencing; Hydroxylation; Neuropeptide.
FT MOD_RES 3 Hydroxyproline (partial).
FT MOD_RES 3 Methionine amide.
SQ SEQUENCE 8 AA; 883 MW; 7D9879CABB47768 CRC64;

Query Match 33.8%; Score 27; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 GPPY 11
DB 1 GPPY 4

RESULT 5
PROX ORYSA
ID PROX ORYSA STANDARD; PRT; 13 AA.
AC P83647;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Probable profilin LP04 (Fragments).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. Indica / IR64; TISSUE=Panicle;
RA Hosseini Salekdeh S.G., Bennett J.;
RT "Proteome analysis of rice panicle.";
RL Submitted (JUL-2003) to Swiss-Prot.
CC -!- FUNCTION: Binds to actin and affects the structure of the
cytoskeleton. At high concentrations, profilin prevents the
polymerization of actin, whereas it enhances it at low
concentrations. By binding to Pip2, it inhibits the formation of
IP3 and DG (By similarity).
CC -!- SUBUNIT: Occurs in many kinds of cells as a complex with monomeric
actin in a 1:1 ratio.
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
protein is: 4.4, its MW is: 14.0 kDa.
CC -!- SIMILARITY: Belongs to the profilin family.
DR InterPro; IPR002097; Profilin.
DR PROSITE; PS00414; PROFILIN; PARTIAL.
KW Actin-binding; Cytoskeleton; Direct protein sequencing;
FT NON_TER 1
FT NON_TER 5
FT NON_TER 13
FT NON_TER 13
SQ SEQUENCE 13 AA; 1362 MW; 0A3022BE0E52C68B CRC64;

Query Match 33.8%; Score 27; DB 1; Length 13;
Best Local Similarity 44.4%; Pred. No. 1.8e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 AVLIQGP 10
DB 5 AYVLIQSEP 13
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Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 AVLILQGPY 11
Db 1 ATYTLPEPPY 10

RESULT 8
QY 07M1H0 PRELIMINARY; PRT; 12 AA.
Db 07M1H0;
AC Q7M1H0;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cycloleoneurin.
OS Leonurus artemisia (Sagebrush motherwort).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiaceae; Lamiaceae; Lamiaceae; Leonurus.
OX NCBI_TaxID=4138;
RN [1]
RP SEQUENCE
RX MEDLINE=91300597; PubMed=2070452;
RA Kinoshita K., Tanaka J., Kuroda K., Koyama K., Natori S.,
RA Kinoshita T.;
RT "Cycloleoneurin, a cyclic peptide from Leonuri fructus.";
RL Chem. Pharm. Bull. 39:712-715(1991).
DR PIR; J00356; J00356.
SQ SEQUENCE 12 AA; 1354 MW; 300727313BC1B768 CRC64;

Query Match 28.7%; Score 23; DB 2; Length 12;
Best Local Similarity 80.0%; Pred. No. 7.9e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 QGPY 11
Db 8 QYPPY 12

RESULT 9
QY 04220 PRELIMINARY; PRT; 13 AA.
Db 04220;
AC Q04220;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE TraA protein (fragment).
OG Name=traA;
OS Plasmid P307.
OC Plasmid P307.
OC Plasmid.
OX NCBI_TaxID=2472;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91261994; PubMed=2096398;
RA Graus-Goeldner A., Graus H., Schlacher T., Hoegenauer G.;
RT "The sequences of genes bordering orit in the enterotoxin plasmid
RT P307: Comparison with the sequences of plasmids F and R1.";
RL Plasmid 24:119-131(1990).
DR EMBL; M62986; AAA2525.1; -.
DR PIR; E37390; E37390.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0000746; P:conjugation; IEA.
DR InterPro; IPR008873; TraA.
DR Pfam; PF05513; TraA; 1.
KW Plasmid.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1259 MW; 864BB8ECD35FC2D5 CRC64;

Query Match 28.7%; Score 23; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 8.6e+03;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

RESULT 6
QY 026075 PRELIMINARY; PRT; 14 AA.
Db 026075;
AC Q26075;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Histone H2A (Fragment).
OS Psammecinus miliaris (Sand sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Echinozoa; Echinacea; Echinacea; Echinacea;
OC Psammecinus.
OX NCBI_TaxID=7660;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85140235; PubMed=2858095;
RA Nordstrom J.L., Hall S.L., Kessler M.M.;
RT "Polyadenylation of sea urchin histone RNA sequences in transfected
RT COS cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:1094-1098(1985).
DR EMBL; M12542; AAA30028.1; -.
FT NON_TER 1 9 histone H2A.
FT CHAIN 1 9
SQ SEQUENCE 14 AA; 1620 MW; 298A3F878A462268 CRC64;

Query Match 31.2%; Score 25; DB 2; Length 14;
Best Local Similarity 57.1%; Pred. No. 4.3e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 LQGPYV 12
Db 5 LSGPPNI 11

RESULT 7
QY 04220 STANDARD; PRT; 15 AA.
Db 04220;
AC P04220;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Superoxide dismutase [Fe-Zn] (EC 1.15.1.1) (Fragment).
GN Names=sod2;
OS Streptomyces griseus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomyces; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1911;
RN [1]
RP SEQUENCE.
RC STRAIN=KCTC 9006; PubMed=8900409;
RX MEDLINE=97056084; PubMed=8900409;
RA Youn H.-D., Youn H., Lee J.-W., Yim Y.-I., Lee J.K., Hah Y.C.,
RA Kang S.-O.;
RT "Unique isozymes of superoxide dismutase in Streptomyces griseus.";
RL Arch. Biochem. Biophys. 334:341-348(1996).
CC -!- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: Binds 1 iron or zinc ion per subunit (By similarity).
CC -!- SUBUNIT: Tetramer.
CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; Sod Fe N; 1.
DR PROSITE; PS00088; SOD MN; PARTIAL.
KW Direct protein sequencing; Iron; Metal-binding; Oxidoreductase; Zinc.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1685 MW; 327993F710861372 CRC64;

Query Match 30.0%; Score 24; DB 1; Length 15;
Best Local Similarity 50.0%; Pred. No. 6.8e+03;
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QY 1 EAVLILQ 8
Db 2 DAILSVQ 9

RESULT 10
CALI_CALGI STANDARD; PRT; 14 AA.
AC P20728;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Calotropin DI (EC 3.4.22.-) (Fragment)
OS Calotropis gigantea (Madar) (Bowstring hemp).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Gentianales; Apocynaceae; Asclepiadoideae; Asclepiadeae;
OC Calotropis.
ON NCBI_TaxID=4066;
RN [1]
RP SEQUENCE.
RA Bhattacharya D., Sengupta A., Sinha N.K.;
RT "Chemical modification and amino terminal sequence of calotropin DI
RT from Calotropis gigantea."
RL Phytochemistry 26:633-636(1987).
CC -!- SIMILARITY: Belongs to peptidase family C1.
DR PIR, PT0026; PT0026.
DR MEROPS, C01.011; -.
DR INTERPRO, IPR000169; Pept_cys_acsite.
DR PROSITE, PS00640; THIOL_PROTEASE ASN; PARTIAL.
DR PROSITE, PS00139; THIOL_PROTEASE_CVS; PARTIAL.
DR PROSITE, PS00639; THIOL_PROTEASE_HIS; PARTIAL.
KW Direct protein sequencing; Hydrolyase; Pyrrolidone carboxylic acid;
KW Thiol protease.
FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1715 MW; D993F0276CDA4662 CRC64;

Query Match 28.7%; Score 23; DB 1; Length 14;
Best Local Similarity 50.0%; Pred. No. 9.3e+03;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 QGPPPVSW 14
Db 1 QRPEYPMW 8

RESULT 11
P81801
ID P81801 PRELIMINARY; PRT; 14 AA.
AC P81801;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Puromycin-hydrolyzing enzyme (EC 3.-.-.-) (Fragment).
OS Streptomyces morookaensis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
ON NCBI_TaxID=1970;
RN [1]
RP SEQUENCE.
RC STRAIN-JCM4673 / KCC S-0673;
RX PubMed=9538199;
RA Nishimura M., Matsuo H., Nakamura A., Sugiyama M.;
RT "Purification and characterization of a puromycin-hydrolyzing enzyme
RT from blastocidin S-producing Streptomyces morookaensis."
RL J. Biochem. 123:247-252(1998).
RN [2]
RP CHARACTERIZATION, AND FUNCTION.
RA Nishimura M., Matsuo H., Sugiyama M.;
RT "Blastocidin S-producing Streptomyces morookaensis possesses an enzyme
RT activity with hydrolyzes puromycin."
RL FEMS Microbiol. Lett. 132:95-100(1995).

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CC -!- FUNCTION: INACTIVATES PUROMYCIN BY CATALYZING THE HYDROLYSIS OF
CC THE AMIDE LINKAGE BETWEEN ITS AMINONUCLEOSIDE AND O-METHYL-L-
CC TYROSINE MOIETIES. THE OPTIMUM PH IS 8.0 AND THE OPTIMAL
CC TEMPERATURE IS 45 DEGREES CELSIUS.
CC -!- FUNCTION: MAY HAVE AMINOPEPTIDASE ACTIVITY.
CC -!- ENZYME REGULATION: STIMULATED BY DTT. STRONGLY INHIBITED BY ZINC
CC ION, FERROUS ION, CUPRIC ION, MERCURY ION, N-BROMOSUCCINIMIDE AND
CC N-ETHYLMALIMIDE. PARTIALLY INHIBITED BY COBALT ION.
CC -!- SUBUNIT: MONOMER.
CC -!- MISCELLANEOUS: HAS AN ISOELECTRIC POINT OF 6.4.
DR GO; GO:0004177; F:aminopeptidase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
KW Amino-peptidase; Hydrolase.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1492 MW; 3F980730E45EF3D8 CRC64;

Query Match 28.7%; Score 23; DB 2; Length 14;
Best Local Similarity 60.0%; Pred. No. 9.3e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 PYVSW 14
Db 5 PYGAW 9

RESULT 12
Q9S8Z0 PRELIMINARY; PRT; 15 AA.
ID Q9S8Z0;
AC Q9S8Z0;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)
DE Light-harvesting antenna of photosystem I 730, LHCI 730.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae;
OC Triticeae; Hordeum.
ON NCBI_TaxID=4513;
RN [1]
RP SEQUENCE.
RX MEDLINE=92267013; PubMed=1587270;
RA Knoetzel J., Svendsen I., Simpson D.J.;
RT "Identification of the photosystem I antenna polypeptides in barley.
RT Isolation of three pigment-binding antenna complexes."
RL Eur. J. Biochem. 206:209-215(1992).
SQ SEQUENCE 15 AA; 1588 MW; 3975624AFD65202D CRC64;

Query Match 28.7%; Score 23; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 1e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 LQGPYV 12
Db 9 LQSPAYL 15

RESULT 13
Q9R3R3 PRELIMINARY; PRT; 13 AA.
ID Q9R3R3;
AC Q9R3R3;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Borrelia burgdorferi plasmid cp32-7, possible partition proteins,
DE complete cds (Borrelia burgdorferi plasmid cp32-6, possible partition
DE proteins, complete cds) (Fragment).
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Plasmid cp32-7, and plasmid cp32-6.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
ON NCBI_TaxID=1139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B31; PLASMID=cp32-7, and cp32-6;

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RX MEDLINE=98361033; PubMed=9695920;
RA Stevenson B., Castjens S., Rosa P.;
RT "Evidence of past recombination events among the genes encoding the
RL Erp antigens of Borrelia burgdorferi.";
RL Microbiology 144:1869-1879(1998).
DR EMBL; AF022483; AAC35454.1; -.
DR EMBL; AF022482; AAC35450.1; -.
KW Plasmid.
FT NON TER
SQ SEQUENCE 13 AA; 1551 MW; 4E441D04BF054373 CRC64;

Query Match 28.1%; Score 22.5; DB 2; Length 13;
Best Local Similarity 44.4%; Pred. NO. 1e+04;
Matches 4; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 7 QGPPYVSWL 15
   |||:|
Db 1 QG-PLIKWI 8

RESULT 14
Q8GL28 PRELIMINARY; PRT; 15 AA.
AC Q8GL28;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE PF-50 protein (Fragment).
GN Name-PF-50;
OS Borrelia burgdorferi (Lyme disease spirochete).
OG Plasmid group cp32-3.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sh-2-82;
RX MEDLINE=22990544; PubMed=14629041;
RA Stevenson B., Miller J.C.;
RT "Intra- and interbacterial genetic exchange of Lyme disease spirochete
RL erp genes generates sequence identity amidst diversity.";
RL J. Mol. Evol. 57:309-324(2003).
DR EMBL; AY142090; AANI7861.1; -.
KW Plasmid.
FT NON TER
SQ SEQUENCE 15 AA; 1777 MW; 4E441D04BF501763 CRC64;

Query Match 28.1%; Score 22.5; DB 2; Length 15;
Best Local Similarity 44.4%; Pred. NO. 1.2e+04;
Matches 4; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 7 QGPPYVSWL 15
   |||:|
Db 3 QG-PLIKWI 10

RESULT 15
ACI THUAL STANDARD; PRT; 8 AA.
AC P18651;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Angiotensin-converting enzyme inhibitor.
OS Thunnus albacares (Yellowfin tuna) (Neohunnus macropterus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8236;
RN [1]
RP SEQUENCE.
RC TISSUE=Muscle;
RX MEDLINE=88326322; PubMed=3415688;
```

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RA Kohama Y., Matsumoto S., Oka H., Teramoto T., Okabe M., Mimura T.;
RT "Isolation of angiotensin-converting enzyme inhibitor from tuna
RT muscle.";
RL Biochem. Biophys. Res. Commun. 155:332-337(1988).
CC 1- FUNCTION: Inhibits angiotensin-converting enzyme.
DR PIR; A31570; A31570.
KW Direct protein sequencing; Metalloprotease inhibitor.
SQ SEQUENCE 8 AA; 953 MW; 6AA863733051F1B7 CRC64;

Query Match 27.5%; Score 22; DB 1; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.8e+06;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 9 PPYVSW 14
   ||::|
Db 1 PTHIKW 6

Search completed: November 14, 2004, 13:16:23
Job time : 101 secs
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OM protein - protein search, using sw model

Run on: November 14, 2004, 13:03:52 ; Search time 18.3333 Seconds
(without alignments)
78.723 Million cell updates/sec

Title: US-09-831-253F-8
Perfect score: 80
Sequence: 1 EAVLLQGPPYVSWL 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_791:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	38.8	13	2 S47361	T-cell antigen rec
2	27	33.8	8	2 E47393	neuropeptide calla
3	25	31.2	15	2 JN0730	hypothetical 1.7K
4	23	28.7	12	2 PH1675	Ig heavy chain V r
5	23	28.7	12	2 JU0356	cycloleucorinin -
6	23	28.7	13	2 PH1676	Ig heavy chain V r
7	23	28.7	13	2 E37390	traA protein - Esc
8	23	28.7	14	2 PH1677	Ig heavy chain V r
9	23	28.7	14	2 PH1705	Ig heavy chain V r
10	23	28.7	14	2 PT0026	calotropin DI - mu
11	23	28.7	15	2 PA0027	protein QAI00006 -
12	23	28.7	15	2 PH1616	Ig H chain V-D-J r
13	23	28.7	15	2 PH1610	Ig H chain V-D-J r
14	22	27.5	8	2 JS0317	leucokinin VII - M
15	22	27.5	8	2 A31570	angiotensin-conver
16	22	27.5	9	2 S26508	collagen alpha 2(V
17	22	27.5	10	2 H28027	protein P11 - curl
18	22	27.5	14	1 LFEQW	trp operon leader
19	22	27.5	14	2 E90858	trp operon leader
20	22	27.5	14	2 B85761	trp operon leader
21	22	27.5	15	2 PQ0192	stylar glycoprotei
22	22	27.5	15	2 PQ0193	stylar glycoprotei
23	22	27.5	15	2 B56046	urinary tract ston
24	22	27.5	15	2 PN0662	dystrophin-associa
25	21.5	26.2	15	2 B45115	peptidylprolyl iso
26	21	26.2	8	2 PQ0012	cholecystokinin -
27	21	26.2	8	2 A43001	cholecystokinin -
28	21	26.2	8	2 JS0318	leucokinin VIII -
29	21	26.2	10	2 A13687	caerulein-like pep

collagen alpha 1(V
glutathione transf
lebetin 1 isoform
dystrophin-associa
stylar glycoprotei
stylar glycoprotei
dystrophin-associa
Ig heavy chain CRD
tryptophyllin, bas
T-call receptor be
phyllacaerulein -
Ig H chain V-D-J r
caerulein - frog (
triacylglycerol li
Ig heavy chain DJ
bradykinin-potent

ALIGNMENTS

RESULT 1

S47361
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47361

R. Lehner, P.J.
submitted to the EMBL Data Library, August 1994

A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A:Reference number: S47355
A:Accession: S47361
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: EMBL:235685; NID:G527459; PIDN:CAA84754.1; PID:G527460
C:Keywords: T-cell receptor

Query Match 38.8%; Score 31; DB 2; Length 13;
Best Local Similarity 71.4%; Pred. No. 63;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 ILQGGPY 11

Db 3 VLQGGPY 9

RESULT 2

E47393
neuropeptide callatostatin 5 - bluebottle fly (Calliphora vomitoria)

C:Species: Calliphora vomitoria
C:Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: E47393
R: Duve, H.; Johnsen, A.H.; Scott, A.G.; Yu, C.G.; Yagi, K.J.; Tobe, S.S.; Thorpe, A.
Proc. Natl. Acad. Sci. U.S.A. 90, 2456-2460, 1993
A:Title: Callatostatin: neuropeptides from the blowfly Calliphora vomitoria with sequ
A:Reference number: A47393; MUID:93211980; PMID:8460157
A:Accession: E47393
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <DUV>
A:Cross-references: UNIPROT:P41841
A:Experimental source: whole flies
A:Note: sequence extracted from NCBI backbone (NCBI:128482)

Query Match 33.8%; Score 27; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 GPPY 11

Db 1 GPPY 4

C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 28.7%; Score 23; DB 2; Length 14;
Best Local Similarity 60.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 YVSWL 15
DB 1 YTSWV 5

RESULT 9

PHI705
Ig heavy chain V region (clone ASC-1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
C;Accession: PHI705
R;McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.
J. Exp. Med. 178, 295-307, 1993
A;Title: Antigen-driven B cell differentiation in vivo.
A;Reference number: PHI675; MUID:93301607; PMID:8315385
A;Accession: PHI705
A;Molecule type: mRNA
A;Residues: 1-14 <MCH>
A;Experimental source: B cell
A;Note: the authors translated the codon GTA for residue 11 as Thr and ACA for residue 1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 28.7%; Score 23; DB 2; Length 14;
Best Local Similarity 60.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 YVSWL 15
DB 1 YTSWV 5

RESULT 10

PT0026
calotropin DI - mudar (fragment)
C;Species: Calotropis gigantea (mudar, madar)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: PT0026
R;Bhattacharya, D.; Sengupta, A.; Sinha, N.K.
Phytochemistry 26, 633-636, 1987
A;Title: Chemical modification and amino terminal sequence of calotropin DI from Calotropis gigantea.
A;Reference number: PT0026
A;Accession: PT0026
A;Molecule type: protein
A;Residues: 1-14 <BHA>
A;Cross-references: UNIPROT:P20728
C;Comment: This enzyme is classified as a plant cysteine protease.
C;Keywords: pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 28.7%; Score 23; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 QGPPYVSW 14
DB 1 QRPEYVW 8

RESULT 11

PA0027
protein QAL00006 - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
C;Accession: PA0027
R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.

submitted to JIPID, July 1994

A;Description: Separation and characterization of Arabidopsis proteins by two-dimension
A;Reference number: PA0001
A;Accession: PA0027
A;Molecule type: protein
A;Residues: 1-15 <RAM>
A;Experimental source: callus

Query Match 28.7%; Score 23; DB 2; Length 15;
Best Local Similarity 45.5%; Pred. No. 1.5e+03;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 VLILQPPYVS 13
DB 1 VLKVVGPXPAS 11

RESULT 12

PHI616
Ig H chain V-D-J region (clone B-less 30) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PHI616
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mic
A;Reference number: PHI580; MUID:93301609; PMID:8315387
A;Accession: PHI616
A;Molecule type: DNA
A;Residues: 1-15 <LEV>
A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin

Query Match 28.7%; Score 23; DB 2; Length 15;
Best Local Similarity 75.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 YVSW 14
DB 11 YLSW 14

RESULT 13

PHI610
Ig H chain V-D-J region (wild-type clone 337) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PHI610
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mic
A;Reference number: PHI580; MUID:93301609; PMID:8315387
A;Accession: PHI610
A;Molecule type: DNA
A;Residues: 1-15 <LEV>
A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin

Query Match 28.7%; Score 23; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.5e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 LQPPY 11
DB 4 LNSPY 9

RESULT 14

JS0317
leucokinin VII - Madeira cockroach
C;Species: Leucophaea maderae (Madeira cockroach)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: JS0317

R;Holman, G.M.; Cook, B.J.; Nachman, R.J.
Comp. Biochem. Physiol. C 88, 31-34, 1987
A;Title: Isolation; primary structure and synthesis of leucokinins VII and VIII: the fin
A;Reference number: JS0317

A;Accession: JS0317
A;Molecule type: protein
A;Residues: 1-8 <HOL>
A;Cross-references: UNIPROT:P19989
C;Comment: Leucokinin, a family of cephalomyotropic peptides, stimulate contractile act
C;Keywords: amidated carboxyl end; cephalomyotropic peptide
F;Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 27.5%; Score 22; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 PPVSW 14
| : |
Db 2 PAFSSW 7

RESULT 15

A31570
angiotensin-converting enzyme inhibitor - yellowfin tuna
C;Species: Thunnus albacares (yellowfin tuna)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C;Accession: A31570
R;Kohama, Y.; Matsumoto, S.; Oka, H.; Teramoto, T.; Okabe, M.; Mimura, T.
Biochem. Biophys. Res. Commun. 155, 332-337, 1988
A;Title: Isolation of angiotensin-converting enzyme inhibitor from tuna muscle.
A;Reference number: A31570; MUID:88326322; PMID:3415688
A;Accession: A31570
A;Molecule type: protein
A;Residues: 1-8 <KOH>
A;Cross-references: UNIPROT:P18691
A;Note: the source is designated as Neothunnus macropterus
C;Superfamily: unassigned animal peptides
C;Keywords: angiotensin-converting enzyme inhibitor

Query Match 27.5%; Score 22; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 9 PPVSW 14
| : |
Db 1 PTHKW 6

Search completed: November 14, 2004, 13:17:23
Job time : 19.3333 secs

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OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:26 ; Search time 11.8085 Seconds
(without alignments)
84.242 Million cell updates/sec

Title: US-09-831-253F-8

Perfect score: 80

Sequence: 1 EAVLIQGPPYVSWL 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 202416

Minimum DB seq length: 0

Maximum DB seq length: 23

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued_Patents_AA.*
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2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
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4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	41.2	14	2	US-08-764-640-39
2	33	41.2	14	3	US-08-973-225-39
3	33	41.2	14	3	US-08-973-225-39
4	33	41.2	14	3	US-08-973-225-39
5	33	41.2	14	3	US-08-973-225-39
6	33	41.2	14	3	US-08-973-225-39
7	33	41.2	14	4	US-09-549-090-39
8	33	41.2	14	4	US-09-549-090-39
9	33	41.2	14	4	US-09-549-090-39
10	32	40.0	11	2	US-08-856-663-12
11	32	40.0	14	2	US-08-764-640-37
12	32	40.0	14	3	US-08-973-225-37
13	32	40.0	14	3	US-09-244-298A-37
14	32	40.0	14	3	US-09-516-704-37
15	32	40.0	14	4	US-09-549-090-37
16	32	40.0	14	4	US-09-832-230A-37
17	32	40.0	18	3	US-08-990-888-40
18	32	40.0	23	2	US-08-985-090-10
19	32	40.0	23	2	US-08-985-090-16
20	32	40.0	23	3	US-09-165-543-10
21	32	40.0	23	3	US-09-165-543-17
22	32	40.0	23	3	US-09-165-543-36
23	31	38.8	9	2	US-08-725-736D-19
24	31	38.8	9	3	US-09-162-368B-19
25	31	38.8	9	3	US-09-161-877B-19
26	31	38.8	15	3	US-09-271-970-6
27	31	38.8	15	4	US-09-760-397-6

28	31	38.8	18	2	US-08-764-640-46	Sequence 46, Appl
29	31	38.8	18	3	US-08-973-225-46	Sequence 46, Appl
30	31	38.8	18	3	US-09-244-298A-46	Sequence 46, Appl
31	31	38.8	18	3	US-09-516-704-46	Sequence 46, Appl
32	31	38.8	18	4	US-09-549-090-46	Sequence 46, Appl
33	31	38.8	18	4	US-09-832-230A-46	Sequence 46, Appl
34	30	37.5	7	1	US-07-807-043B-6	Sequence 6, Appl
35	30	37.5	9	1	US-08-299-849B-6	Sequence 6, Appl
36	30	37.5	9	1	US-08-464-318-6	Sequence 6, Appl
37	30	37.5	9	2	US-08-471-341-6	Sequence 6, Appl
38	30	37.5	9	2	US-08-461-566-6	Sequence 6, Appl
39	30	37.5	9	2	US-08-142-368A-6	Sequence 6, Appl
40	30	37.5	9	3	US-08-967-727-6	Sequence 6, Appl
41	30	37.5	9	3	US-09-064-964-2	Sequence 2, Appl
42	30	37.5	9	3	US-08-037-230D-6	Sequence 2, Appl
43	30	37.5	9	3	US-09-064-174-2	Sequence 2, Appl
44	30	37.5	9	4	US-09-583-850-6	Sequence 6, Appl
45	30	37.5	9	4	US-09-579-197-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-764-640-39
; Sequence 39, Application US/08764640
; Patent No. 5869451
; Patent No. 5869451 5837683
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Cwiria, Steven E.
; APPLICANT: Gates, Christian
; APPLICANT: Schatz, Peter J.
; APPLICANT: Balasubramanian, Palaniappan
; APPLICANT: Wagstrom, Christopher R.
; APPLICANT: Hendren, Richard W.
; APPLICANT: Depinne, Randolph B.
; APPLICANT: Podduturi, Surekha
; APPLICANT: Yin, Qun
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
; TITLE OF INVENTION: RECEPTOR
; NUMBER OF SEQUENCES: 244
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glaxo Wellcome
; STREET: Five Moore Drive, P.O. Box 13398
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/764,640
; FILING DATE: 11-DEC-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Hrubiec, Robert T.
; REGISTRATION NUMBER: 36,392
; REFERENCE/DOCKET NUMBER: PK3281
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-248-1000
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-764-640-39

Query Match 41.2%; Score 33; DB 2; Length 14;
Best Local Similarity 60.0%; Pred. No. 48;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LQGPYPVSWL 15
| | | | |
DB 3 LVGPSLMSWL 12

RESULT 2

US-08-973-225-39
; Sequence 39, Application US/08973225A
; Patent No. 6083913
; GENERAL INFORMATION:

APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwiria, Steven E.
Duffin, David J.
Gates, Christian
Haselden, Sherril S.
Matheakis, Larry C.
Schatz, Peter J.
Wagstrom, Christopher R.
Wrighton, Nicholas C.

TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
THROMBOPOIETIN RECEPTOR

NUMBER OF SEQUENCES: 232

CORRESPONDENCE ADDRESS:

ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
STATE: NC

COUNTRY: USA
ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/973,225A

FILING DATE: 04-Dec-1997

ATTORNEY/AGENT INFORMATION:

NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW
TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-248-1000

INFORMATION FOR SEQ ID NO: 39:

SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 39:

US-08-973-225-39

Query Match 41.2%; Score 33; DB 3; Length 14;
Best Local Similarity 60.0%; Pred. No. 48;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LQGPYPVSWL 15
| | | | |
DB 3 LVGPSLMSWL 12

RESULT 3

US-08-973-225-216
; Sequence 216, Application US/08973225A
; Patent No. 6083913
; GENERAL INFORMATION:

APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwiria, Steven E.
Duffin, David J.
Gates, Christian
Haselden, Sherril S.
Matheakis, Larry C.
Schatz, Peter J.
Wagstrom, Christopher R.
Wrighton, Nicholas C.

TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
THROMBOPOIETIN RECEPTOR

NUMBER OF SEQUENCES: 232

CORRESPONDENCE ADDRESS:

ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
STATE: NC

COUNTRY: USA
ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/973,225A

FILING DATE: 04-Dec-1997

ATTORNEY/AGENT INFORMATION:

NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW
TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-248-1000

INFORMATION FOR SEQ ID NO: 216:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 216:

US-08-973-225-216

Query Match 41.2%; Score 33; DB 3; Length 14;
Best Local Similarity 60.0%; Pred. No. 48;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LQGPYPVSWL 15
| | | | |
DB 3 LVGPSLMSWL 12

RESULT 4

US-09-244-298A-39

; Sequence 39, Application US/09244298A
; Patent No. 612138
; GENERAL INFORMATION:

APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwiria, Steven E.
Gates, Christian
Schatz, Peter J.
Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
Depdince, Randolph B.
Rodduturi, Surekha
Yin, Qun

TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
RECEPTOR
NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:

ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/244,298A
FILING DATE: 11-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: linear
MOLECULE TYPE: peptide
US-09-244-298A-39

Query Match 41.2%; Score 33; DB 3; Length 14;
Best Local Similarity 60.0%; Pred. No. 48;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LOGPPVSWL 15
Db 3 LVGPSLMSWL 12

RESULT 5
US-09-516-704-39
Sequence 39, Application US/09516704
Patent No. 6251864
GENERAL INFORMATION:
APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
Schatz, Peter J.
Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
Deprience, Randolph B.
Podduturi, Surekha
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A RECEPTOR
NUMBER OF SEQUENCES: 244
CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/516,704
FILING DATE: 01-Mar-2000
CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3281
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
MOLECULE TYPE: peptide
US-09-516-704-39

Query Match 41.2%; Score 33; DB 3; Length 14;
Best Local Similarity 60.0%; Pred. No. 48;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LOGPPVSWL 15
Db 3 LVGPSLMSWL 12

RESULT 6
US-09-549-090-39
Sequence 39, Application US/09549090
Patent No. 6465430
GENERAL INFORMATION:
APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
Gates, Christian
Haselden, Sherril S.
Mattheakis, Larry C.
Schatz, Peter J.
Wagstrom, Christopher R.
Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A RECEPTOR
NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/549,090
FILING DATE: 13-Apr-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/973,225
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW
TELEPHONE: 919-248-1000
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear

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; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-549-090-39
Query Match 41.2%; Score 33; DB 4; Length 14;
Best Local Similarity 60.0%; Pred. No. 48;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LQGPVVSWL 15
DB 3 LVGPSLMSWL 12

RESULT 7
US-09-549-090-216
; Sequence 216, Application US/09549090
; Patent No. 6465430
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; BARRETT, RONALD W.
; Cwirla, Steven E.
; Duffin, David J.
; Gates, Christian
; Haseldien, Sherril S.
; Matheakis, Larry C.
; Schatz, Peter J.
; Wagstrom, Christopher R.
; Wrighton, Nicholas C.
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
; THROMBOPOIETIN RECEPTOR
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glaxo Wellcome
; STREET: Five Moore Drive, P.O. Box 13398
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 08/973,225
; FILING DATE: 13-Apr-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/549,090
; FILING DATE: 13-Apr-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: Hrubiec, Robert T.
; REGISTRATION NUMBER: 36,392
; REFERENCE/DOCKET NUMBER: PK3065USW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-248-1000
; INFORMATION FOR SEQ ID NO: 216:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 216:
US-09-549-090-216
Query Match 41.2%; Score 33; DB 4; Length 14;
Best Local Similarity 60.0%; Pred. No. 48;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LQGPVVSWL 15
DB 3 LVGPSLMSWL 12

RESULT 8
US-09-832-230A-39
; Sequence 39, Application US/09832230A
; Patent No. 6506362
; GENERAL INFORMATION:
; APPLICANT: Dower, William J. et al
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
; RECEPTOR
; NUMBER OF SEQUENCES: 244
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glaxo Wellcome
; STREET: Five Moore Drive, P.O. Box 13398
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/832,230A
; FILING DATE: 10-Apr-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Hrubiec, Robert T.
; REGISTRATION NUMBER: 36,392
; REFERENCE/DOCKET NUMBER: PK3281
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-248-1000
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-832-230A-39
Query Match 41.2%; Score 33; DB 4; Length 14;
Best Local Similarity 60.0%; Pred. No. 48;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LQGPVVSWL 15
DB 3 LVGPSLMSWL 12

RESULT 9
US-09-428-082B-67
; Sequence 67, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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OTHER INFORMATION: TPO-MIMETIC PEPTIDE
US-09-428-082B-67

Query Match 41.2%; Score 33; DB 4; Length 14;
Best Local Similarity 60.0%; Pred. No. 48;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LQGPVYVSWL 15
| | | | |
DB 3 LVGPSLMSWL 12

RESULT 10

US-08-856-663-12
Sequence 12, Application US/08856663
Patent No. 5849558

GENERAL INFORMATION:

APPLICANT: MORGAN, RICHARD

APPLICANT: CHANG, ZHIYU

TITLE OF INVENTION: DISCOVERY OF AND

TITLE OF INVENTION: METHOD FOR CLONING AND PRODUCING THE

TITLE OF INVENTION: PSPI RESTRICTION ENDONUCLEASE

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: New England Biolabs, Inc.

STREET: 32 Tozer Road

CITY: Beverly

STATE: MA

COUNTRY: US

ZIP: 01915

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/856,663

FILING DATE: 15-MAY-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Williams, Gregory D

REGISTRATION NUMBER: 30901

REFERENCE/DOCKET NUMBER: NEB-127

TELECOMMUNICATION INFORMATION:

TELEPHONE: 978-927-5054

TELEFAX: 978-927-1705

TELEX:

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-856-663-12

Query Match 40.0%; Score 32; DB 2; Length 11;
Best Local Similarity 75.0%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 LILQGPY 11

| | | | |

DB 2 LILTSPY 9

RESULT 11

US-08-764-640-37

Sequence 37, Application US/08764640

Patent No. 5869451

Patent No. 5869451 5837683

GENERAL INFORMATION:
APPLICANT: Dower, William J.
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwiria, Steven E.
APPLICANT: Gates, Christian
APPLICANT: Schatz, Peter J.
APPLICANT: Balasubramanian, Palaniappan
APPLICANT: Wagstrom, Christopher R.
APPLICANT: Hendren, Richard W.
APPLICANT: Deprience, Randolph B.
APPLICANT: Podduturi, Surekha
APPLICANT: Yin, Qun

TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A

TITLE OF INVENTION: RECEPTOR

NUMBER OF SEQUENCES: 244

CORRESPONDENCE ADDRESS:

ADDRESSEE: Glaxo Wellcome

STREET: Five Moore Drive, P.O. Box 13398

CITY: Research Triangle Park

STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/764,640

FILING DATE: 11-DEC-1996

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Hrubiec, Robert T.

REGISTRATION NUMBER: 36,392

REFERENCE/DOCKET NUMBER: PK3281

TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-248-1000

INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-764-640-37

Query Match 40.0%; Score 32; DB 2; Length 14;
Best Local Similarity 55.6%; Pred. No. 70;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 QGPPYVSWL 15

| | | | |

DB 3 QGPTLTAWL 11

RESULT 12

US-08-973-225-37

Sequence 37, Application US/08973225A

Patent No. 6083913

GENERAL INFORMATION:

APPLICANT: Dower, William J.

Barrett, Ronald W.

Cwiria, Steven E.

Duffin, David J.

Gates, Christian

Haselden, Sherril S.

Mattheakis, Larry C.

Schatz, Peter J.

Wagstrom, Christopher R.

Wrighton, Nicholas C.

TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A

THROMBOPOIETIN RECEPTOR

NUMBER OF SEQUENCES: 232

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Glaxo Wellcome
;; STREET: Five Moore Drive, P.O. Box 13398
;; CITY: Research Triangle Park
;; STATE: NC
;; COUNTRY: USA
;; ZIP: 27709
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/973,225A
;; FILING DATE: 04-Dec-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hrubiec, Robert T.
;; REGISTRATION NUMBER: 36,392
;; REFERENCE/DOCKET NUMBER: PK3065USW
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 919-248-1000
;;
;; INFORMATION FOR SEQ ID NO: 37:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 14 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: <Unknown>
;; TOPOLOGY: linear
;;
;; MOLECULE TYPE: peptide
;; SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-08-973-225-37

Query Match 40.0%; Score 32; DB 3; Length 14;
Best Local Similarity 55.6%; Pred. No. 70;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 QGPPYVSWL 15
||| :||
Db 3 QGPTLTAWL 11

RESULT 13
US-09-244-298A-37
; Sequence 37, Application US/09244298A
; Patent No. 6121238
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Cwiria, Steven E.
; APPLICANT: Gates, Christian
; APPLICANT: Schatz, Peter J.
; APPLICANT: Balasubramanian, Palaniappan
; APPLICANT: Wagstrom, Christopher R.
; APPLICANT: Hendren, Richard W.
; APPLICANT: Deprence, Randolph B.
; APPLICANT: Podduturi, Surekha
; APPLICANT: Yin, Qun
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
; TITLE OF INVENTION: RECEPTOR
; NUMBER OF SEQUENCES: 244
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Glaxo Wellcome
; STREET: Five Moore Drive, P.O. Box 13398
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/244,298A

;; FILING DATE: 11-DEC-1996
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hrubiec, Robert T.
;; REGISTRATION NUMBER: 36,392
;; REFERENCE/DOCKET NUMBER: PK3281
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 919-248-1000
;;
;; INFORMATION FOR SEQ ID NO: 37:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 14 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;;
;; MOLECULE TYPE: peptide
US-09-244-298A-37

Query Match 40.0%; Score 32; DB 3; Length 14;
Best Local Similarity 55.6%; Pred. No. 70;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 QGPPYVSWL 15
||| :||
Db 3 QGPTLTAWL 11

RESULT 14
US-09-516-704-37
; Sequence 37, Application US/09516704
; Patent No. 6251864
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Cwiria, Steven E.
; APPLICANT: Gates, Christian
; APPLICANT: Schatz, Peter J.
; APPLICANT: Balasubramanian, Palaniappan
; APPLICANT: Wagstrom, Christopher R.
; APPLICANT: Hendren, Richard W.
; APPLICANT: Deprence, Randolph B.
; APPLICANT: Podduturi, Surekha
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
; TITLE OF INVENTION: RECEPTOR
; NUMBER OF SEQUENCES: 244
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glaxo Wellcome
; STREET: Five Moore Drive, P.O. Box 13398
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/516,704
; FILING DATE: 01-Mar-2000
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Hrubiec, Robert T.
; REGISTRATION NUMBER: 36,392
; REFERENCE/DOCKET NUMBER: PK3281
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-248-1000
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-09-516-704-37

Query Match 40.0%; Score 32; DB 3; Length 14;
Best Local Similarity 55.6%; Pred. No. 70;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 QGPPYVSWL 15
||| :||
Db 3 QGPTLTAWL 11

RESULT 15

US-09-549-090-37
; Sequence 37, Application US/09549090
; Patent No. 6465430

GENERAL INFORMATION:

APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
Gates, Christian
Haselden, Sherril S.
Mattheakis, Larry C.
Schatz, Peter J.
Wagstrom, Christopher R.
Wrighton, Nicholas C.
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A

NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS:
ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/549,090
FILING DATE: 13-Apr-2000

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/973,225
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Hrubiec, Robert T.

REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW

TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-248-1000

INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:

LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 37:

US-09-549-090-37

Query Match 40.0%; Score 32; DB 4; Length 14;
Best Local Similarity 55.6%; Pred. No. 70;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 QGPPYVSWL 15
||| :||
Db 3 QGPTLTAWL 11

Search completed: November 14, 2004, 12:08:50
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 14, 2004, 12:03:21 ; Search time 35.4255 Seconds
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Title: US-09-831-253F-8

Perfect score: 80

Sequence: 1 EAVLIQPPYVSWL 15

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Gapop 10.0 , Gapext 0.5

Searched: 1568699 seqs, 353819137 residues

Total number of hits satisfying chosen parameters: 294451

Minimum DB seq length: 0

Maximum DB seq length: 23

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09D_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
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- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
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- 18: /cgn2_6/ptodata/1/pubpaa/US10F_PUBCOMB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US10G_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US10H_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
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2	33	41.2	14	14	US-10-083-768-39
3	33	41.2	14	14	US-10-083-768-216
4	33	41.2	14	15	US-10-609-217-67
5	33	41.2	14	15	US-10-632-388-67
6	33	41.2	14	15	US-10-651-723-67
7	33	41.2	14	15	US-10-645-761-67
8	33	41.2	14	15	US-10-666-696-67
9	33	41.2	14	15	US-10-653-048-67
10	33	41.2	18	14	US-10-006-593-33
11	33	41.2	18	14	US-10-307-724-33
12	32	40.0	14	14	US-10-083-768-37
13	32	40.0	21	15	US-10-424-599-256388

14	32	40.0	22	15	US-10-328-916-31	Sequence 31, Appl
15	32	40.0	23	9	US-09-350-206-10	Sequence 10, Appl
16	32	40.0	23	9	US-09-350-206-17	Sequence 17, Appl
17	32	40.0	23	9	US-09-350-206-36	Sequence 36, Appl
18	32	40.0	23	9	US-09-349-755-10	Sequence 10, Appl
19	32	40.0	23	9	US-09-349-755-17	Sequence 17, Appl
20	32	40.0	23	9	US-09-349-755-36	Sequence 36, Appl
21	32	40.0	23	9	US-09-166-334-10	Sequence 10, Appl
22	32	40.0	23	9	US-09-166-334-17	Sequence 17, Appl
23	32	40.0	23	9	US-09-166-334-36	Sequence 36, Appl
24	32	40.0	23	14	US-10-282-958-10	Sequence 10, Appl
25	32	40.0	23	14	US-10-282-958-17	Sequence 17, Appl
26	32	40.0	23	14	US-10-282-958-36	Sequence 36, Appl
27	32	40.0	23	14	US-10-422-262-2	Sequence 2, Appl
28	31.5	39.4	16	14	US-10-281-478-23	Sequence 23, Appl
29	31.5	39.4	16	14	US-10-281-478-95	Sequence 95, Appl
30	31.5	39.4	16	14	US-10-281-478-132	Sequence 132, Appl
31	31	38.8	6	15	US-10-243-613-25	Sequence 25, Appl
32	31	38.8	9	15	US-10-428-335-69	Sequence 69, Appl
33	31	38.8	12	10	US-09-990-832C-71	Sequence 71, Appl
34	31	38.8	15	9	US-09-760-397-6	Sequence 6, Appl
35	31	38.8	15	14	US-10-324-182-6	Sequence 35, Appl
36	31	38.8	18	14	US-10-006-593-35	Sequence 46, Appl
37	31	38.8	18	14	US-10-083-768-46	Sequence 35, Appl
38	31	38.8	18	14	US-10-307-724-35	Sequence 46, Appl
39	31	38.8	19	14	US-10-378-557-46	Sequence 8193, Ap
40	31	38.8	23	14	US-10-106-698-8193	Sequence 13, Appl
41	30	37.5	9	10	US-09-077-439A-13	Sequence 9, Appl
42	30	37.5	9	13	US-10-205-150-9	Sequence 66, Appl
43	30	37.5	9	14	US-10-079-167-66	Sequence 66, Appl
44	30	37.5	9	14	US-10-360-836-66	Sequence 10639, A
45	30	37.5	9	15	US-10-057-475B-10639	

ALIGNMENTS

RESULT 1

US-09-833-245-681
; Sequence 681, Application US/09833245
; Publication No. US20040010134A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 681
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (13)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-833-245-681

Query Match 42.5%; Score 34; DB 11; Length 18;
Best Local Similarity 66.7%; Pred. No. 31e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 7 QGPPYVSWL 15

Db 4 QGCPHPSWL 12

RESULT 2
US-10-083-768-39
; Sequence 39, Application US/10083768
; Publication No. US20030158116A1
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; Barrett, Ronald W.
; Cwirla, Steven E.
; Duffin, David J.
; Gates, Christian
; Haselden, Sherril S.
; Mattheakis, Larry C.
; Schatz, Peter J.
; Wagstrom, Christopher R.
; Wrighton, Nicholas C.
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
; THROMBOPOIETIN RECEPTOR
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glaxo Wellcome
; STREET: Five Moore Drive, P.O. Box 13398
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/083,768
; FILING DATE: 27-Feb-2002
; ATTORNEY/AGENT INFORMATION:
; NAME: Hrubiec, Robert T.
; REGISTRATION NUMBER: 36,392
; REFERENCE/DOCKET NUMBER: PK3065USW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-248-1000
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-10-083-768-39
Query Match 41.2%; Score 33; DB 14; Length 14;
Best Local Similarity 60.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 6 LOGPPYVSWL 15
DB 3 LVGPSLMSWL 12
RESULT 3
US-10-083-768-216
; Sequence 216, Application US/10083768
; Publication No. US20030158116A1
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; Barrett, Ronald W.
; Cwirla, Steven E.
; Duffin, David J.
; Gates, Christian
; Haselden, Sherril S.
; Mattheakis, Larry C.
; Schatz, Peter J.
; Wagstrom, Christopher R.

; Wrighton, Nicholas C.
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
; THROMBOPOIETIN RECEPTOR
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glaxo Wellcome
; STREET: Five Moore Drive, P.O. Box 13398
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/083,768
; FILING DATE: 27-Feb-2002
; ATTORNEY/AGENT INFORMATION:
; NAME: Hrubiec, Robert T.
; REGISTRATION NUMBER: 36,392
; REFERENCE/DOCKET NUMBER: PK3065USW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-248-1000
; INFORMATION FOR SEQ ID NO: 216:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 216:
US-10-083-768-216
Query Match 41.2%; Score 33; DB 14; Length 14;
Best Local Similarity 60.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 6 LOGPPYVSWL 15
DB 3 LVGPSLMSWL 12
RESULT 4
US-10-609-217-67
; Sequence 67, Application US/10609217
; Publication No. US2004004188A1
; GENERAL INFORMATION:
; APPLICANT: PEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/609,217
; CURRENT FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: Patent In version 3.1
; SEQ ID NO: 67
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TPO-MIMETIC PEPTIDE
US-10-609-217-67
Query Match 41.2%; Score 33; DB 15; Length 14;
Best Local Similarity 60.0%; Pred. No. 3.5e+02;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LOGPPVVSWL 15
| | | : | | |
Db 3 LVGPSLSMWL 12

RESULT 5
US-10-632-388-67
; Sequence 67, Application US/10632388
; Publication No. US20040053845A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/632,388
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TPO-MIMETIC PEPTIDE
US-10-632-388-67

Query Match 41.2%; Score 33; DB 15; Length 14;
Best Local Similarity 60.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LOGPPVVSWL 15
| | | : | | |
Db 3 LVGPSLSMWL 12

RESULT 6
US-10-651-723-67
; Sequence 67, Application US/10651723
; Publication No. US20040057953A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/651,723
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TPO-MIMETIC PEPTIDE
US-10-651-723-67

Query Match 41.2%; Score 33; DB 15; Length 14;
Best Local Similarity 60.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LOGPPVVSWL 15
| | | : | | |
Db 3 LVGPSLSMWL 12

RESULT 7
US-10-645-761-67
; Sequence 67, Application US/10645761
; Publication No. US20040071712A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/645,761
; CURRENT FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TPO-MIMETIC PEPTIDE
US-10-645-761-67

Query Match 41.2%; Score 33; DB 15; Length 14;
Best Local Similarity 60.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LOGPPVVSWL 15
| | | : | | |
Db 3 LVGPSLSMWL 12

RESULT 8
US-10-666-696-67
; Sequence 67, Application US/10666696
; Publication No. US20040077022A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; APPLICANT: GUDAS, JEAN MARIE
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527A
; CURRENT APPLICATION NUMBER: US/10/666,696
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/563,286C
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/428,082
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1157
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TPO-mimetic peptide
US-10-666-696-67

Query Match 41.2%; Score 33; DB 15; Length 14;

Best Local Similarity 60.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LOGPPYVSWL 15
| | | : | | |
DB 3 LVGPSLSW 12

RESULT 9
US-10-653-048-67
; Sequence 67, Application US/10653048
; Publication No. US2004008778A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/653,048
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TPO-MIMETIC PEPTIDE
US-10-653-048-67

Query Match 41.2%; Score 33; DB 15; Length 14;
Best Local Similarity 60.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LOGPPYVSWL 15
| | | : | | |
DB 3 LVGPSLSW 12

RESULT 10
US-10-006-593-33
; Sequence 33, Application US/10006593
; Publication No. US20030049683A1
; GENERAL INFORMATION:
; APPLICANT: Bowditch, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
; FILE REFERENCE: 1087-2
; CURRENT APPLICATION NUMBER: US/10/006,593
; CURRENT FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: US 60/251,448
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/288,889
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/294,068
; PRIOR FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 18
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: TPO mimetic with flanking amino acids
US-10-006-593-33

Query Match 41.2%; Score 33; DB 14; Length 18;

Best Local Similarity 41.7%; Pred. No. 4.4e+02;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 LILQPPYVSWL 15
: | : | : | : |
DB 1 MIEGPTLRQWL 12

RESULT 11
US-10-307-724-33
; Sequence 33, Application US/10307724
; Publication No. US20030232972A1
; GENERAL INFORMATION:
; APPLICANT: Bowditch, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
; FILE REFERENCE: 1087-2c1p
; CURRENT APPLICATION NUMBER: US/10/307,724
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US 60/251,448
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: US 60/288,889
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/294,068
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 10/006,593
; PRIOR FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33
; LENGTH: 18
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: TPO mimetic with flanking amino acids
US-10-307-724-33

Query Match 41.2%; Score 33; DB 14; Length 18;
Best Local Similarity 41.7%; Pred. No. 4.4e+02;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 LILQPPYVSWL 15
: | : | : | : |
DB 1 MIEGPTLRQWL 12

RESULT 12
US-10-083-768-37
; Sequence 37, Application US/10083768
; Publication No. US20030158116A1
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; Barrett, Ronald W.
; Cwirila, Steven E.
; Duffin, David J.
; Gates, Christian
; Haselden, Sherril S.
; Mattheakis, Larry C.
; Schatz, Peter J.
; Wagstrom, Christopher R.
; Wrighton, Nicholas C.
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
THROMBOPOIETIN RECEPTOR
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glaxo Wellcome
; STREET: Five Moore Drive, P.O. Box 13398
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:

;
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/083,768
; FILING DATE: 27-Feb-2002
; ATTORNEY/AGENT INFORMATION:
; NAME: Hrubiec, Robert T.
; REGISTRATION NUMBER: 36,392
; REFERENCE/DOCKET NUMBER: PK3065USW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-248-1000
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-10-083-768-37

Query Match 40.0%; Score 32; DB 14; Length 14;
Best Local Similarity 55.6%; Pred. No. 5e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 QGPPVSWL 15
||| .||
Db 3 QGPTLAWL 11

RESULT 13
US-10-424-599-256388
; Sequence 256388, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 256388
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_WRT3847_73542C.1.pep
US-10-424-599-256388

Query Match 40.0%; Score 32; DB 15; Length 21;
Best Local Similarity 50.0%; Pred. No. 7.2e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 5 ILQGPVSW 14
||| .||
Db 4 IIKNMPVLW 13

RESULT 14
US-10-328-916-31
; Sequence 31, Application US/10328916
; Publication No. US20040002114A1
; GENERAL INFORMATION:
; APPLICANT: Gregoire, Francine M.
; APPLICANT: Johnson, Jeffrey D.
; APPLICANT: Blume, John E.
; APPLICANT: Metabolex, Inc.

;
; TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor
; FILE REFERENCE: 016325-007210US
; CURRENT APPLICATION NUMBER: US/10/328,916
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US 60/345,697
; PRIOR FILING DATE: 2002-01-04
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:mouse IC-GPCR
; OTHER INFORMATION: Transmembrane IV domain
US-10-328-916-31

Query Match 40.0%; Score 32; DB 15; Length 22;
Best Local Similarity 46.2%; Pred. No. 7.6e+02;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 3 VLLIQPPVSWL 15
||| .||
Db 10 VTLLTGIPYWL 22

RESULT 15
US-09-350-206-10
; Sequence 10, Application US/09350206
; Patent No. US20020099199A1
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksman
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/350,206
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,780
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-350-206-10

Query Match 40.0%; Score 32; DB 9; Length 23;
Best Local Similarity 50.0%; Pred. No. 7.9e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 5 ILQGPVSW 14
:|:|:
Db 14 LLYGPALSW 23

Search completed: November 14, 2004, 12:27:00
Job time : 36.4255 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:25 ; Search time 43.4043 Seconds
(without alignments)
123.973 Million cell updates/sec

Title: US-09-831-253F-8

Perfect score: 80

Sequence: 1 EAVLILQPPYVSWL 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 718658

Minimum DB seq length: 0

Maximum DB seq length: 23

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_23Sep04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	80	100.0	15	3 AAY92952	Aay92952 Transform
2	80	100.0	15	3 AAY93104	Aay93104 Transform
3	36	45.0	23	3 AAY95812	Aay95812 Modified
4	34.5	43.1	19	7 ADF14790	Adf14790 Diabetes
5	34	42.5	18	4 AAE01738	Aae01738 Human gen
6	34	42.5	18	5 ABG63934	Abg63934 Human alb
7	34	42.5	18	5 ADL77199	Adl77199 Albumin f
8	33	41.2	14	2 AAW09483	Aaw09483 Thrombopo
9	33	41.2	14	2 AAW36634	Aaw36634 Thrombopo
10	33	41.2	14	2 AAW36767	Aaw36767 Thrombopo
11	33	41.2	14	3 AAB17011	Aab17011 TPO-mimet
12	33	41.2	14	4 AAU25853	Aau25853 Human thr
13	33	41.2	14	5 ABB72897	Abb72897 TPO mimet
14	33	41.2	14	7 ADJ73048	Adj73048 TPO mimet
15	33	41.2	14	8 ADJ52683	Adj52683 CHI delet
16	33	41.2	14	8 ADJ51644	Adj51644 CHI delet
17	33	41.2	15	5 ABB05646	Abb05646 Human thy
18	33	41.2	18	5 ABP51685	Abp51685 TPO mimet
19	33	41.2	18	8 ADQ16613	Adq16613 TPO mimet
20	33	41.2	19	2 AAR55260	Aar55260 N-termina
21	32	40.0	9	8 ADK03181	Adk03181 Hepatitis
22	32	40.0	10	8 ADK03184	Adk03184 Hepatitis
23	32	40.0	11	2 AAW83368	Aaw83368 Ppghi met
24	32	40.0	14	2 AAW09481	Aaw09481 Thrombopo
25	32	40.0	14	2 AAW36632	Aaw36632 Thrombopo

26	32	40.0	14	4 AAU25851	Aau25851 Human thr
27	32	40.0	15	5 AAU97014	Aau97014 Human coa
28	32	40.0	17	8 ADM12614	Adm12614 Ii-key/hu
29	32	40.0	17	8 ADO38847	Ado38847 Human Her
30	32	40.0	18	5 ABP48149	Abp48149 GHR bindi
31	32	40.0	23	2 AAW92981	Aaw92981 Human mAC
32	32	40.0	23	2 AAW92987	Aaw92987 Rat mACHR
33	32	40.0	23	2 AAG67842	Aag67842 Rat mACHR
34	32	40.0	23	2 AAG67835	Aag67835 Human mAC
35	32	40.0	23	2 AAG67849	Aag67849 Partial r
36	32	40.0	23	6 ABG76410	Abg76410 Human mus
37	32	40.0	23	6 ABG76424	Abg76424 Rat musca
38	32	40.0	23	6 ABG76417	Abg76417 Rat musca
39	32	40.0	23	8 ADJ55648	Adj55648 Short enz
40	31.5	39.4	14	4 AAM96969	Aam96969 Human pep
41	31.5	39.4	16	7 ADC99952	Adc99952 Murine AX
42	31.5	39.4	16	7 ADC99989	Adc99989 Murine AX
43	31.5	39.4	16	7 ADC99880	Adc99880 Murine AX
44	31	38.8	6	6 ABR55023	Abr55023 MMP-2 sel
45	31	38.8	6	8 ADK14204	Adk14204 Matrix me

ALIGNMENTS

RESULT 1

AA92952

ID AAY92952 standard; peptide; 15 AA.

AC AAY92952;

DT 08-NOV-2000 (first entry)

DE Transforming growth factor inhibitory peptide #8.

XX Hepatotrophic; antagonist; transforming growth factor betaf; TGF-b1;
KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.

XX Homo sapiens.

XX WO200031135-A1.

XX 02-JUN-2000.

XX 23-NOV-1999; 99WO-ES000375.

XX 24-NOV-1998; 98ES-00002465.

XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.

XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
XX Borrás Cuesta F;

XX WPI; 2000-411935/35.

XX Peptides that antagonize binding of transforming growth factor betaf.
XX useful for treatment of liver disease, especially cirrhosis, are partial
XX sequences of the factor or its receptors.

XX Claim 9; Page 82; 86pp; Spanish.

XX The invention relates to synthetic peptides that antagonise the binding
XX of transforming growth (TGF) factor betaf (TGF-b1) to its receptor in
XX vivo which have partial amino acid sequences identical, or similar, with
XX those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
XX examples of the peptides of the invention. The peptides act by
XX competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
XX they are inhibitors of stimulation of collagen synthesis in liver cells
XX and inhibitors of synthesis of proteolytic enzymes able to degrade the
XX extracellular matrix. The peptides, their mimetopes and/or DNA (or
XX expression systems) encoding the peptides are used for treatment of liver
XX disease, specifically cirrhosis

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XX SQ Sequence 15 AA;
Query Match 100.0%; Score 80; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EAVLILQGPYPVSWL 15
Db 1 EAVLILQGPYPVSWL 15
|||||
|||||

RESULT 2
AAY93104
ID AAY93104 standard; peptide; 15 AA.
XX AC AAY93104;
XX DT 08-NOV-2000 (first entry)
XX DE Transforming growth factor inhibitory peptide PI50.
XX KW Hepatotropic; antagonist; transforming growth factor beta1; TGF-beta1;
XX KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
XX KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX OS Homo sapiens.
XX PN WO200031135-A1.
XX PD 02-JUN-2000.
XX PF 23-NOV-1999; 99WO-ES000375.
XX PR 24-NOV-1998; 98ES-00002465.
XX PA (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
XX PI Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
XX PI Borras Cuesta F;
XX DR WPI; 2000-411935/35.
XX PT Peptides that antagonize binding of transforming growth factor beta1,
XX PT useful for treatment of liver disease, especially cirrhosis, are partial
XX PT sequences of the factor or its receptors.
XX PS Disclosure; Page 33; 86pp; Spanish.
XX CC The invention relates to synthetic peptides that antagonise the binding
XX CC of transforming growth (TGF) factor beta1 (TGF-beta1) to its receptor in
XX CC vivo which have partial amino acid sequences identical, or similar, with
XX CC those of TGF-beta1 and/or its receptors. Peptides AAY92945-Y93133 represent
XX CC examples of the peptides of the invention. The peptides act by
XX CC competitive inhibition of the binding of TGF-beta1 to its receptors, e.g.
XX CC they are inhibitors of stimulation of collagen synthesis in liver cells
XX CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
XX CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
XX CC expression systems) encoding the peptides are used for treatment of liver
XX CC disease, specifically cirrhosis
XX SQ Sequence 15 AA;
Query Match 100.0%; Score 80; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EAVLILQGPYPVSWL 15
Db 1 EAVLILQGPYPVSWL 15
|||||
|||||

RESULT 3
AAY95812
ID AAY95812 standard; peptide; 23 AA.
XX AC AAY95812;
XX DT 07-NOV-2000 (first entry)
XX DE Modified human tissue plasminogen activator signal peptide.
XX DE Leptin; human; glycosylation; obesity; diabetes; hyperlipidemia;
XX KW antiobesity; antidiabetic; hyperlipemic; therapy; signal peptide;
XX KW tissue plasminogen activator; mutant; mutein.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200047741-A1.
XX PD 17-AUG-2000.
XX PF 11-FEB-2000; 2000WO-US003652.
XX PR 12-FEB-1999; 99US-00249675.
XX PA (AMGE-) AMGEN INC.
XX PI Martin FH, Elliott SG;
XX DR WPI; 2000-524540/47.
XX KW Glycosylated leptin proteins having a Stokes' radius greater than that of
XX PT a naturally occurring glycosylated human leptin useful for treating
XX PT obesity, diabetes and the effects of high blood lipid content.
XX PS Example 14; Page 99; 156pp; English.
XX CC The present sequence is that of a human tissue plasminogen activator
XX CC signal peptide that is the same as the native signal peptide except that
XX CC the 3 C-terminal amino acid residues are Ser-Trp-Ser. The invention is
XX CC directed to glycosylated leptin proteins (see AAY95799-804) that have a
XX CC Stokes' radius greater than that of naturally occurring human leptin. A
XX CC claimed method for manufacturing a glycosylated leptin involves culturing
XX CC a host cell containing a DNA sequence encoding a signal peptide and a
XX CC glycosylated leptin protein. Preferred signal peptides have a peptidase
XX CC cleavage site optimized for glycosylation efficiency. When
XX CC lepinin-47+69+102 (see AAY95802) was expressed as a fusion with the
XX CC present signal peptide, the degree of glycosylation (on a scale of 1-5)
XX CC was 3.5 in COS host cells and 4 in CHO host cells. Glycosylated leptins,
XX CC or nucleic acids encoding them, are used in the treatment of obesity,
XX CC diabetes and the effects of high blood lipid content (claimed). They have
XX CC longer systemic circulation times in vivo than native leptins
XX SQ Sequence 23 AA;
Query Match 45.0%; Score 36; DB 3; Length 23;
Best Local Similarity 58.3%; Pred No. 1.3e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 VLLILQGPYPVSW 14
Db 11 VLLILCGAVFVSW 22
|||||
|||||

RESULT 4
ADF14790
ID ADF14790 standard; peptide; 19 AA.
XX AC ADF14790;
XX DT 12-FEB-2004 (first entry)
XX DE Diabetes autoantigen-derived peptide - SEQ ID 285.

```


KW plant; deamidation; tissue transglutaminase; TG; celiac disease; CD;
 KW gluten intolerance; autoimmune; rheumatoid arthritis; multiple sclerosis;
 KW systemic lupus erythematosus; Sjogren syndrome; diabetes;
 KW immunosuppressive; antirheumatic; antiarthritic; antidiabetic;
 KW dermatological; antiinflammatory.
 XX Unidentified.
 XX OS
 XX PN EP1332760-A1.
 XX PD 06-AUG-2003.
 XX PP 04-FEB-2002; 2002EP-00075456.
 XX PR 04-FEB-2002; 2002EP-00075456.
 XX PA (ZIEK-) ACAD ZIEKENHUIS LEIDEN.
 XX DR WPI; 2003-647889/62.
 XX PT New gluten peptides or epitopes prone to deamidation by tissue
 PT transglutaminase, useful for treating celiac disease or an autoimmune
 PT disease, rheumatoid arthritis, multiple sclerosis, systemic lupus
 PT erythematosus, or diabetes.
 XX PS Claim 3; SEQ ID NO 285; 143pp; English.
 XX CC The invention relates to a novel peptide or epitope which is prone to
 CC deamidation by tissue transglutaminase (TG) and is a causative factor of
 CC celiac disease (CD, gluten intolerance) or an autoimmune disease such as
 CC rheumatoid arthritis, multiple sclerosis, systemic lupus erythematosus,
 CC Sjogren syndrome or diabetes. The peptide of the invention demonstrates
 CC immunosuppressive, antirheumatic, antiarthritic, antidiabetic,
 CC dermatological and antiinflammatory activities whilst pharmaceutical
 CC compositions comprising the peptides or epitopes may be useful for the
 CC treatment of a celiac disease or an autoimmune disease such as rheumatoid
 CC arthritis, multiple sclerosis, systemic lupus erythematosus, Sjogren
 CC syndrome or diabetes. Gluten-derived peptides may be useful in the
 CC preparation of therapeutic agents capable of eliminating a subset of
 CC cells, particularly gluten-sensitive or auto-antigen sensitive T cells.
 CC The current sequence is that of the diabetes autoantigen-derived peptide
 CC of the invention.
 XX SQ Sequence 19 AA;
 Query Match 43.1%; Score 34.5; DB 7; Length 19;
 Best Local Similarity 53.3%; Pred. No. 1.9e+02;
 Matches 8; Conservative 5; Mismatches 1; Indels 1; Gaps 1;
 QY 2 AVLI-LQGPYPVSWL 15
 :||: |||| :||:
 Db 4 SVLVSLQGPLFLSVL 18
 RESULT 5
 AAE01738
 ID AAE01738 standard; peptide; 18 AA.
 XX AC AAE01738;
 XX DT 18-JUL-2001 (first entry)
 XX DE Human gene 19 encoded secreted protein HYASC80 fragment, SEQ ID NO:151.
 XX KW Human; secreted protein; proliferative disorder; cancer; tumour;
 KW foetal abnormality; developmental abnormality; haematopoietic disorder;
 KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
 KW inflammation; allergy; neurological disorder; Alzheimer's disease;
 KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;
 KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
 KW cardiovascular disorder; angiogenic disorder; kidney disorder;
 KW gastrointestinal disorder; pregnancy-related disorder; gene therapy;
 KW endocrine disorder; infection; wound healing; vulnery; cell culture;

KW chemotaxis; food additive; binding partner identification.
 XX Homo sapiens.
 XX FH Key Location/Qualifiers
 FT Misc-difference 13 /label= Unknown
 FT FT /note= "Encoded by MTM"
 XX PN WO200134767-A2.
 XX PD 17-MAY-2001.
 XX PF 01-NOV-2000; 2000WO-US030036.
 XX PR 05-NOV-1999; 99US-0163576P.
 XX PR 27-JUL-2000; 2000US-0221366P.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX Soppet DR, Komatsoulis G, Shi Y, Olesen HS, Ruben SM;
 DR WPI; 2001-316492/33.
 DR N-PSDB; AAD05559.
 XX Isolated nucleic acid molecule encoding a human secreted protein is used
 PT in preventing, treating or ameliorating a medical condition.
 PT Claim 11; Page 514; 540pp; English.
 XX CC AAD05492-AAD05564 represent cDNAs corresponding to 22 human secreted
 CC protein genes, and AAE01672-AAE01743 represent the proteins they encode.
 CC AAE01744-AAE01763 represent human secreted protein fragments or variants.
 CC The secreted proteins and their genes are useful for preventing, treating
 CC or ameliorating medical conditions, e.g., by protein or gene therapy.
 CC Pathological conditions can be diagnosed by determining the amount of the
 CC new protein in a sample or by determining the presence of mutations in
 CC the new genes. Specific uses are described for each of the 22 genes,
 CC based on the tissues in which they are most highly expressed, and include
 CC developing products for the diagnosis or treatment of proliferative
 CC disorders, cancer, tumours, foetal and developmental abnormalities,
 CC haematopoietic disorders, diseases of the immune system, AIDS, autoimmune
 CC diseases (e.g., rheumatoid arthritis), inflammation, allergies,
 CC neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),
 CC cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,
 CC psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,
 CC angiogenic disorders, kidney disorders, gastrointestinal disorders,
 CC pregnancy-related disorders, endocrine disorders, and infections. The
 CC proteins can also be used to aid wound healing and epithelial cell
 CC proliferation, to prevent skin aging due to sunburn, to maintain organs
 CC before transplantation, for supporting cell culture of primary tissues,
 CC to regenerate tissues, to identify their cognate ligands or binding
 CC partners, and in chemotaxis, and can be used as a food additive or
 CC preservative to modify storage properties. Antibodies specific for a
 CC protein of the invention can be used in alleviating symptoms associated
 CC with the disorders mentioned above, and in diagnostic immunoassays e.g.,
 CC radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The
 CC present sequence represents a human secreted protein fragment of the
 CC invention
 XX SQ Sequence 18 AA;
 Query Match 42.5%; Score 34; DB 4; Length 18;
 Best Local Similarity 66.7%; Pred. No. 2.1e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 7 QGPPYVSWL 15
 |||: |||:
 Db 4 QGCPHPSWL 12
 RESULT 6
 ABG63934

ID ABG63934 standard; protein; 18 AA.
 XX
 AC ABG63934;
 XX
 XX 27-AUG-2002 (first entry)
 DT
 XX Human albumin fusion protein #609.
 DE
 XX
 XX Albumin fusion protein; therapeutic protein X; human albumin; HA;
 KW human serum albumin; HSA; cancer; reproductive disorder;
 KW digestive disorder; immune disorder; endocrine disorder;
 KW haematopoietic disorder; neural disorder; connective disorder;
 KW cytostatic; anti-infectivity; anti-inflammatory; anti-ulcer;
 KW immunomodulator; anti-HIV; antidiabetic; haemostatic; neurotropic;
 KW neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;
 KW osteopathic; antiarthritic.
 KW
 XX Homo sapiens.
 OS
 OS Synthetic.
 OS
 XX WO200177137-A1.
 PN
 XX 18-OCT-2001.
 PD
 XX 12-APR-2001; 2001WO-US011988.
 PF
 XX 12-APR-2000; 2000US-0229358P.
 XX
 PR 25-APR-2000; 2000US-0199384P.
 PR
 XX 21-DEC-2000; 2000US-0256931P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX Rosen CA, Haseltine WA;
 XX
 PI WPI; 2002-010886/01.
 DR
 XX
 XX New fusion protein for treating disease e.g. diabetes comprises an
 PT albumin fused to a therapeutic protein.
 PT
 XX Claim 1; Page 912; 2102pp; English.
 PS
 XX The present invention relates to albumin fusion proteins comprising a
 CC therapeutic protein X and human albumin (HA, also known as human serum
 CC albumin, HSA). The proteins are useful for treating a disease or disorder
 CC that may be modulated by therapeutic protein X. The albumin extends the
 CC shelf-life of protein X, and may increase its biological in vitro/in vivo
 CC activity. The protein is useful for treating and diagnosing disorders
 CC such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's
 CC disease, ulcerative colitis), immune disorders (e.g. acquired
 CC immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes),
 CC haematopoietic disorders, neural disorders (e.g. Alzheimer's,
 CC Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis,
 CC schizophrenia), and connective disorders (e.g. osteoporosis, arthritis).
 CC ABG63326-ABG65518 represent albumin fusion proteins of the invention
 XX
 SQ Sequence 18 AA;
 Query Match 42.5%; Score 34; DB 5; Length 18;
 Best Local Similarity 66.7%; Pred. NO. 2.1e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 7 QGPPYVSWL 15
 ||| : |||
 Db 4 QGCPHPSWL 12
 RESULT 7
 ADL77199
 ID ADL77199 standard; peptide; 18 AA.
 XX
 AC ADL77199;
 XX
 XX 20-MAY-2004 (first entry)
 DT

XX
 DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 681.
 XX
 KW albumin fusion protein; cytostatic; antianaemic; antiarthritic;
 KW antiasthmatic; anti-HIV; immunosuppressive; anti-inflammatory;
 KW antipsoriatic; antibacterial; osteopathic; dermatological; antitumor;
 KW immunomodulator; antiarrhythmic; cardiac; neurotropic; antilipemic;
 KW nephrotropic; uropathic; neuroprotective; antiparkinsonian; tranquilizer;
 KW antidiabetic; anabolic; hypertensive; vulnary; gene therapy; cancer;
 KW reproductive system disorder; therapeutic protein.
 OS Unidentified.
 XX
 PN US2004010134-A1.
 XX
 XX 15-JAN-2004.
 PD
 XX 12-APR-2001; 2001US-00833245.
 PF
 XX 12-APR-2000; 2000US-0229358P.
 PR
 XX 25-APR-2000; 2000US-0199384P.
 PR
 XX 21-DEC-2000; 2000US-0256931P.
 XX
 PA (ROSE/) ROSEN C A.
 XX (HASE/) HASELTINE W A.
 XX
 XX Rosen CA, Haseltine WA;
 XX
 PI WPI; 2004-090519/09.
 DR
 XX New albumin fusion proteins, useful for diagnosing, treating, preventing
 PT or ameliorating diseases or disorders e.g. cancer, anemia, arthritis,
 PT asthma, inflammatory bowel disease or Alzheimer's disease.
 PT
 XX Disclosure; SEQ ID NO 681; 279pp; English.
 PS
 XX The invention relates to a novel albumin fusion protein. The invention
 CC further relates to: a composition comprising the albumin fusion protein
 CC and a pharmaceutical carrier; a kit comprising the composition of the
 CC albumin fusion protein formula; a method of treating a disease or
 CC disorder in a patient comprising the step of administering the albumin
 CC fusion protein; a method of treating a patient with a disease or disorder
 CC that is modulated by Therapeutic protein: X, or its fragment or variant;
 CC a method of extending the shelf life of Therapeutic protein: X, or its
 CC fragment or variant; a nucleic acid molecule comprising a polynucleotide
 CC sequence encoding the albumin fusion protein; a vector comprising the
 CC nucleic acid molecule of the albumin fusion protein; and a host cell
 CC comprising the nucleic acid molecule of the albumin fusion protein. The
 CC albumin fusion protein and its compositions have the following
 CC activities: cytostatic, antianaemic, antiarthritic, antisthmatic, anti-
 CC HIV, immunosuppressive, anti-inflammatory, antipsoriatic, antibacterial,
 CC osteopathic, dermatological, antitumor, immunomodulator, antiarrhythmic,
 CC cardiac, neurotropic, antilipemic, nephrotropic, uropathic,
 CC neuroprotective, antiparkinsonian, tranquilizer, antidiabetic, anabolic,
 CC hypertensive, and vulnary. The albumin fusion protein nucleic acid may
 CC be used in gene therapy to treat disorders. The albumin fusion protein is
 CC useful for diagnosing, treating, preventing or ameliorating diseases or
 CC disorders comprising indication: Y. The diseases or disorders include:
 CC cancer (e.g. leukaemia, colon, bone, breast, liver or lung cancer),
 CC immune or haematopoietic diseases (e.g. anaemia, Hodgkin's disease, acute
 CC lymphocytic anaemia, multiple myeloma, arthritis, asthma, AIDS,
 CC autoimmune disease, inflammatory bowel disease, psoriasis or Lyme
 CC disease), reproductive system disorders (e.g. prostatitis, inguinal
 CC hernia, varicocele, penile carcinoma, ovarian adenocarcinoma or Sertoli-
 CC Leydig tumours), musculoskeletal diseases (e.g. giant cell tumours,
 CC Paget's disease, systemic lupus erythematosus, gout, muscular dystrophy
 CC or cachexia), cardiovascular disease (e.g. rhabdomyomas, heart disease,
 CC arrhythmia, cardiac arrest, heat valve disease, hypernatraemia or
 CC hyponatraemia), mixed foetal diseases (e.g. foetal alcohol syndrome,
 CC Down's syndrome, Patau syndrome, Turner's syndrome, Apter syndrome or Tay
 CC -Sachs disease), excretory diseases (e.g. urinary incontinence, urinary
 CC tract infections or renal disorders), neural or sensory disease (e.g.
 CC Alzheimer's disease, Parkinson's disease, cerebral malaria, meningitis,
 CC

CC cerebellar ataxia, attention deficit disorder, autism or obsessive
 CC compulsive disorder), respiratory disease (e.g. emphysema, lung cancer or
 CC occupational lung disease), endocrine diseases (e.g. diabetes, Addison's
 CC disease or glomerulonephritis), digestive diseases (e.g. portal
 CC hypertension, irritable bowel disease, gastric atrophy or pancreatitis)
 CC or connective tissue or epithelial diseases (e.g. Crohn's disease,
 CC scleroderma, wound healing or epidermolysis bullosa). This sequence
 CC represents a therapeutic protein X relating to the albumin fusion protein
 CC of the invention. The sequence listing data for this specification was
 CC downloaded from the USPTO website.

XX SQ Sequence 18 AA;

Query Match 42.5%; Score 34; DB 8; Length 18;
 Best Local Similarity 66.7%; Pred. No. 2.1e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 QGPPYVSWL 15
 DB 4 QGCPHPSWL 12
 |||:|

RESULT 8
 AAW09483
 ID AAW09483 standard; protein; 14 AA.

XX AC AAW09483;

DT 10-SEP-1997 (first entry)

XX Thrombopoietin receptor binding peptide.

XX Haematology; thrombocytopenia; TPO; TR; proliferation;
 KW bone marrow transfusion; chemotherapy; radiation therapy.

XX Synthetic.

XX WO9640189-A1.

XX 19-DEC-1996.

XX 05-JUN-1996; 96WO-US008998.

XX 07-JUN-1995; 95US-00472371.

XX 07-JUN-1995; 95US-00473604.

XX 07-JUN-1995; 95US-00476168.

XX 07-JUN-1995; 95US-00478128.

XX 07-JUN-1995; 95US-00484090.

XX 07-JUN-1995; 95US-00485301.

XX (GLAX) GLAXO GROUP LTD.

XX Dower WJ, Barrett RW, Cwirila SE, Duffin DJ, Gates CM, Johnson SS;
 PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;

XX WPI; 1997-051883/05.

XX Thrombopoietin receptor-binding/activating peptide(s) and peptide
 PT mimetic(s) - useful in treatment of haematological disorders, esp.
 PT thrombocytopenia resulting from chemotherapy, etc.

XX Disclosure; Page 26; 106pp; English.

XX The present sequence is a peptide which binds to thrombopoietin (TPO)
 CC receptor (TR). The compound can be used for treating patients suffering
 CC from haematological disorders and thrombocytopenia resulting from
 CC chemotherapy, radiation therapy or bone marrow transfusions. The peptide
 CC may also be used to maintain the proliferation and growth of TPO-
 CC dependent cell lines and for use in biological research, for detecting
 CC TPO receptors on living cells

XX SQ Sequence 14 AA;

Query Match 41.2%; Score 33; DB 2; Length 14;
 Best Local Similarity 60.0%; Pred. No. 2.4e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LQGPYVSWL 15
 DB 3 LVGPFLMSWL 12
 |||:|

RESULT 9
 AAW36634
 ID AAW36634 standard; peptide; 14 AA.

XX AC AAW36634;

DT 11-MAR-1998 (first entry)

XX Thrombopoietin receptor binding peptide.

XX Thrombopoietin receptor; binding peptide; treatment; agonist;
 KW haematological disorder; thrombocytopenia; chemotherapy;
 KW radiation therapy; bone marrow transfusion; diagnosis;
 KW signal transduction; receptor activation; cell culture.

XX Synthetic.

XX WO9640750-A1.

XX 19-DEC-1996.

XX 07-JUN-1996; 96WO-US009623.

XX 07-JUN-1995; 95US-00478128.

XX 07-JUN-1995; 95US-00485301.

XX (GLAX) GLAXO GROUP LTD.

XX Dower WJ, Barrett RW, Cwirila SE, Duffin DJ, Gates CM, Johnson SS;
 PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;

XX WPI; 1997-052226/05.

XX Peptides and peptide mimetics which bind to and activate the
 PT thrombopoietin receptor - useful in treatment of haematological
 PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.

XX Disclosure; Page 26; 106pp; English.

XX The present peptide, which binds the thrombopoietin receptor (TR), can be
 CC used to treat disorders which are susceptible to treatment with a
 CC thrombopoietin agonist, preferably haematological disorders and
 CC thrombocytopenia resulting from chemotherapy, radiation therapy or bone
 CC marrow transfusions. It can also be used diagnostically, e.g. to
 CC investigate the mechanism of thrombopoietin signal transduction and
 CC receptor activation, or to maintain the proliferation and growth of
 CC thrombopoietin dependent cell lines

XX SQ Sequence 14 AA;

Query Match 41.2%; Score 33; DB 2; Length 14;
 Best Local Similarity 60.0%; Pred. No. 2.4e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LQGPYVSWL 15
 DB 3 LVGPFLMSWL 12
 |||:|

RESULT 10
 AAW36767
 ID AAW36767 standard; peptide; 14 AA.

XX AC AAW36767;

XX 11-MAR-1998 (first entry)
 XX Thrombopoietin receptor binding peptide.
 DE Thrombopoietin receptor; binding peptide; treatment; agonist;
 KW haematological disorder; thrombocytopaenia; chemotherapy;
 KW radiation therapy; bone marrow transfusion; diagnosis;
 KW signal transduction; receptor activation; cell culture.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Disulfide-bond 1..14
 FT Modified-site 14
 FT /note= "NH2-Cys"
 XX
 XX W09640750-A1.
 XX
 XX 19-DEC-1996.
 XX
 XX 07-JUN-1996; 96WO-US009623.
 XX
 XX 07-JUN-1995; 95US-00478128.
 PR 07-JUN-1995; 95US-00485301.
 XX
 XX (GLAX) GLAXO GROUP LTD.
 XX
 XX Dower WJ, Barret RW, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;
 PI Mattheakis LC, Schatz FU, Wagstrom CR, Wrighton NC;
 XX WPI; 1997-052226/05.
 XX
 XX Peptides and peptide mimetics which bind to and activate the
 PT thrombopoietin receptor - useful in treatment of haematological
 PT disorders, esp. thrombocytopaenia resulting from chemotherapy, etc.
 XX
 XX Example 9; Page 75; 106pp; English.
 XX
 XX The present peptide, which binds the thrombopoietin receptor (TR), can be
 CC used to treat disorders which are susceptible to treatment with a
 CC thrombopoietin agonist, preferably haematological disorders and
 CC thrombocytopaenia resulting from chemotherapy, radiation therapy or bone
 CC marrow transfusions. It can also be used diagnostically, e.g. to
 CC investigate the mechanism of thrombopoietin signal transduction and
 CC receptor activation, or to maintain the proliferation and growth of
 CC thrombopoietin dependent cell lines
 XX
 XX Sequence 14 AA;
 SQ
 Query Match 41.2%; Score 33; DB 2; Length 14;
 Best Local Similarity 60.0%; Pred. No. 2.4e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 6 LQGPVYVSWL 15
 Db 3 LVGPSLMSWL 12
 RESULT 11
 AAB17011
 ID AAB17011 standard; peptide; 14 AA.
 XX
 AC AAB17011;
 XX
 XX 31-OCT-2000 (first entry)
 DT
 XX
 XX TPO-mimetic peptide sequence SEQ ID NO:67.
 DE
 XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
 KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;
 KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW

KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KW vascular endothelial growth factor; matrix metalloproteinase; asthma;
 KW thrombosis; pharmaceutical.
 XX
 OS Synthetic.
 XX
 XX W0200024782-A2.
 PN
 PD 04-MAY-2000.
 XX
 XX 25-OCT-1999; 99WO-US025044.
 PF
 XX 23-OCT-1998; 98US-0105371P.
 PR 22-OCT-1999; 99US-00428082.
 XX
 XX (AMGE-) AMGEN INC.
 PA
 XX Feige U, Liu C, Cheetham J, Boone TC;
 PI WPI; 2000-350702/30.
 XX
 XX Novel composition of matter comprising an Fc domain and pharmacologically
 PT active peptides, useful for treating cancer and autoimmune diseases.
 XX
 XX Claim 19; Page 217; 608pp; English.
 PS
 XX The present invention describes composition of matter (I) comprising an
 CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
 CC (X1)a-P1-(X2)b, where: P1 = an Fc domain; X1 and X2 = are each
 CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-
 CC (L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,
 CC P3, and P4 = are each independently sequences of pharmacologically active
 CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
 CC c, d, e, and f = are each independently 0 or 1, provided that at least 1
 CC of a and b is 1. The composition can have cytostatic, antiasthmatic,
 CC thrombolytic and immunosuppressive activities. DNAs, vectors and host
 CC cells from the present invention can be used for producing pharmaceutical
 CC compositions. The compositions are useful for treating cancer, asthma,
 CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
 CC a Fab domain) can provide a longer half-life or incorporate functions
 CC such as Fc receptor binding, protein A binding, complement fixation, and
 CC possibly placental transfer. AAA69443 to AAA69526 and AAA16955 to
 CC AAB18003 represent nucleotide and amino acid sequences used in the
 CC exemplification of the present invention
 XX
 XX Sequence 14 AA;
 SQ
 Query Match 41.2%; Score 33; DB 3; Length 14;
 Best Local Similarity 60.0%; Pred. No. 2.4e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 6 LQGPVYVSWL 15
 Db 3 LVGPSLMSWL 12
 RESULT 12
 AAU25853
 ID AAU25853 standard; peptide; 14 AA.
 XX
 AC AAU25853;
 XX
 XX 17-DEC-2001 (first entry)
 DT
 XX Human thrombopoietin receptor (TPO-R) activator peptide #39.
 DE
 XX Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;
 KW haemostatic; thrombocytopaenia; chemotherapy; radiation therapy; ELISA;
 KW bone marrow transplantation; haematological disorder; platelet disorder;
 KW enzyme-linked immunosorbent assay; in situ staining; biological fluid;
 KW tissue homogenate; fluorescence-activated cell sorting; Western blotting;
 KW in vitro expansion; megakaryocyte; Headpiece Dimer gene; lacI gene.
 XX

OS Homo sapiens.
 PN USG251864-B1.
 XX
 XX 26-JUN-2001.
 XX
 XX
 XX 01-MAR-2000; 2000US-00516704.
 XX
 XX 07-JUN-1995; 95US-00478128.
 PR 07-JUN-1995; 95US-00485301.
 PR 07-JUN-1996; 96MO-US009623.
 PR 15-AUG-1996; 96US-00699027.
 XX
 XX (GLAX) GLAXO GROUP LTD.
 XX
 XX Dower WJ, Barrett RW, Cwirila SE, Gates CM, Schatz PU,
 PI Balasubramanian P, Wagstrom CR, Hendren RW, Deprince RB, Podduturi S;
 PI Yin Q;
 XX
 XX WPI; 2001-564142/63.
 DR
 XX
 XX Activating thrombopoietin receptors in cells, used to treat
 XX thrombocytopenia and hematological disorders, comprises contacting cells
 PT with peptides and peptide mimetics attached to hydrophilic polymers.
 PT
 XX
 XX Disclosure; Col 20; 128pp; English.
 PS
 XX
 XX Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that
 CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods
 CC of activating thrombopoietin receptors in cells comprise contacting the
 CC cells with effective amounts of peptides and peptide mimetics attached to
 CC hydrophilic polymers. The methods are used to treat thrombocytopenia such
 CC as that due to chemotherapy, radiation therapy or bone-marrow
 CC transplantation and to prevent thrombocytopenia in patients at risk. The
 CC sequences are used to treat and prevent hematological disorders
 CC including thrombocytopenia and platelet disorders. They are used in vitro
 CC as unique tools for understanding the biological role of thrombopoietin
 CC (TPO) and to develop other compounds that bind to and activate the TPO
 CC receptor. The peptides can be used to detect TPO receptors on living
 CC cells and fixed cells, in biological fluids, in tissue homogenates, and
 CC in purified or natural biological materials. They may also be used for in
 CC situ staining, fluorescence-activated cell sorting, Western blotting and
 CC enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can
 CC be used for in vitro expansion of megakaryocytes and their committed
 CC progenitors alone or in conjunction with additional cytokines
 XX
 XX Sequence 14 AA;
 SQ
 Query Match 41.2%; Score 33; DB 4; Length 14;
 Best Local Similarity 60.0%; Pred. No. 2.4e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 6 LQGPYPVSWL 15
 Db 3 LVGFSLSWSL 12
 ||| :|||
 RESULT 13
 ABB72897
 ID ABB72897 standard; peptide; 14 AA.
 XX
 XX ABB72897;
 AC
 XX
 XX 05-APR-2002 (first entry)
 DT
 XX TPO mimetic peptide SEQ ID NO:67.
 DE
 XX
 XX Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;
 KW erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
 KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TNP;
 KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
 KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
 KW cytosstatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;

KW antianaemic; anorectic; antiinfertility; haemostatic; dermatological;
 KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
 KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
 KW sleep disorder; neurological degenerative disease; anaemia;
 KW thrombocytopenia; metastatic tumour; systemic lupus erythematosus;
 KW Fanconi's syndrome.
 XX
 XX Homo sapiens.
 OS
 OS Synthetic.
 XX
 XX WO200183525-A2.
 PN
 XX 08-NOV-2001.
 PD
 XX
 XX 02-MAY-2001; 2001WO-US014310.
 PF
 XX
 XX 03-MAY-2000; 2000US-00563286.
 PR
 XX
 XX (AMGE-) AMGEN INC.
 PA
 XX
 XX Feige U, Liu C, Cheestham JC, Boone TC, Gudas JM;
 PI
 XX WPI; 2002-130313/17.
 DR
 XX
 XX Novel vehicle-peptide molecule or its multimers useful for treating
 PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
 PT diabetic retinopathy, obesity, sleep disorders and infertility.
 PT
 XX
 XX Claim 39; Page 44; 176pp; English.
 PS
 XX
 XX The present invention describes a vehicle-peptide molecule (I) or its
 CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
 CC cytosstatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
 CC antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
 CC neuroprotective activities. (I) can be used as a therapeutic or
 CC prophylactic agent as well as for screening purposes. (I) is useful for
 CC diagnosing diseases characterised by dysfunction of their associated
 CC protein of interest, for identifying normal or abnormal proteins of
 CC interest, as a part of diagnostic kit to detect the presence of their
 CC proteins of interest in a biological sample. Additionally, (I) is useful
 CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
 CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
 CC infertility, and neurological degenerative diseases. (I), comprising EPO-
 CC mimetic compounds are useful for treating disorders characterised by low
 CC red blood cell levels such as anaemia. The TPO-mimetic comprising
 CC compounds are useful for treating conditions that involve an existing
 CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
 CC deficiency, such as thrombocytopenia, aplastic anaemia, metastatic
 CC tumour which result in thrombocytopenia, systemic lupus erythematosus,
 CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
 CC represent amino acid and nucleic acid sequences used in the
 CC exemplification of the present invention
 XX
 XX Sequence 14 AA;
 SQ
 Query Match 41.2%; Score 33; DB 5; Length 14;
 Best Local Similarity 60.0%; Pred. No. 2.4e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 6 LQGPYPVSWL 15
 Db 3 LVGFSLSWSL 12
 ||| :|||
 RESULT 14
 ADJ73048
 ID ADJ73048 standard; peptide; 14 AA.
 XX
 XX ADJ73048;
 AC
 XX
 XX 06-MAY-2004 (first entry)
 DT
 XX TPO mimetic peptide sequence SeqID 502.
 DE

XX mimetic; CDR mimetibody; gene therapy; transgenic; immune;
 KW cardiovascular; infectious; malignant; neurologic disease; anaemia;
 KW immunomodulator; cardiant; antimicrobial; cytostatic; neuroprotective;
 KW TPO.
 XX Synthetic.
 OS
 XX WO2003084477-A2.
 PN
 XX 16-OCT-2003.
 PD
 XX
 XX 24-MAR-2003; 2003WO-US009139.
 PF
 XX
 XX 29-MAR-2002; 2002US-0368791P.
 PR
 XX (CENZ) CENTOCOR INC.
 PA
 XX Heavner GA, Knight DM, Scallion BJ, Ghayeb J;
 PI WPI; 2003-804237/75.
 XX
 XX New CDR mimetibody comprising a portion of a heavy or light chain
 PT variable region comprising human framework or ligand binding region,
 PT useful for preparing a composition for treating e.g., immune,
 PT cardiovascular or neurologic disease.
 XX
 XX Disclosure; SEQ ID NO 502; 97pp; English.
 PS
 XX This invention relates to novel mammalian CDR mimetibodies, specific
 CC portions or variants thereof. Specifically, it refers to an antibody
 CC fragment where a protein has been inserted into, or replaces a portion
 CC of, one or more CDR regions, such that each CDR mimetibody comprises at
 CC least one portion of a heavy chain or light chain variable region, which
 CC itself comprises at least one human framework region and at least one
 CC ligand binding region (LBR). The present invention describes human
 CC mimetibodies, including modified immunoglobulins and cleavage products
 CC that can be useful in gene therapy and the generation of transgenic
 CC plants and animals. Furthermore, the CDR mimetibody is useful for
 CC preparing compositions for modulating, treating or reducing the symptoms
 CC of immune, cardiovascular, infectious, malignant and/or neurologic
 CC diseases, as well as anaemia. Accordingly, they exhibit immunomodulator,
 CC cardiant, antimicrobial, cytostatic and neuroprotective activities. This
 CC peptide sequence is a TPO mimetic peptide sequence used to make a
 CC mimetibody of the invention.
 XX
 XX Sequence 14 AA;
 SQ

Query Match 41.2%; Score 33; DB 7; Length 14;
 Best Local Similarity 60.0%; Pred. No. 2.4e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LOGPPYVSWL 15
 | | | | |
 Db 3 LVGPSLMSWL 12

RESULT 15
 ADJ52683
 ID ADJ52683 standard; peptide; 14 AA.
 XX
 AC ADJ52683;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE CHI deleted mimetibody-related peptide SeqID502.
 XX
 XX CHI deleted mimetibody; immunosuppressive; cardiovascular; cardiant;
 KW hypotensive; neuroprotective; nootropic; antibacterial; virucide;
 KW fungicide; gene therapy; immune disorder; cardiovascular disease;
 KW arrhythmia; hypertension; heart failure; neurodegenerative;
 KW multiple sclerosis; dementia; Alzheimer's disease; anaemia;
 KW cancerous condition; infectious disease; bacterial infection;

KW viral infection; fungal infection.
 XX Unidentified.
 OS Synthetic.
 XX WO2004002417-A2.
 PN
 XX 08-JAN-2004.
 PD
 XX 27-JUN-2003; 2003WO-US020347.
 PF
 XX 28-JUN-2002; 2002US-0392431P.
 PR
 XX (CENZ) CENTOCOR INC.
 PA
 XX Heavner GA, Knight DM, Ghayeb J, Scallion BJ, Nesspor TC;
 PI Kutoloshki KA;
 PI WPI; 2004-082870/08.
 DR
 XX
 XX New CHI-deleted mimetibody polypeptides and nucleic acids, useful for
 PT modulating, treating, alleviating, preventing an immune, cardiovascular,
 PT or neurodegenerative disease or disorder, anemia, cancer, or infectious
 PT diseases.
 XX
 XX Claim 2; SEQ ID NO 502; 129pp; English.
 PS
 XX This invention relates to CHI deleted mimetibodies (and the DNA sequences
 CC which encode them), compositions, methods and uses. The invention may be
 CC useful for the development of compounds with an immunosuppressive,
 CC cardiovascular, cardiant, hypotensive, neuroprotective, nootropic,
 CC antibacterial, virucide or fungicide activity. In addition, the disclosed
 CC sequences may prove useful for gene therapy. The CHI-deleted mimetibody
 CC is useful for diagnosing or treating a disease condition in a cell,
 CC tissue, organ or animal, specifically for modulating, treating,
 CC alleviating, preventing the incidence or reducing the symptoms of an
 CC immune, cardiovascular (for example arrhythmia, hypertension or heart
 CC failure), or neurodegenerative (for example multiple sclerosis, dementia
 CC or Alzheimer's disease) diseases or disorders, anaemia, cancerous
 CC conditions, or infectious diseases (for example bacterial, viral or
 CC fungal infection). The present sequence is that of a peptide which may be
 CC used during the creation of a mimetibody of the invention.
 XX
 XX Sequence 14 AA;
 SQ

Query Match 41.2%; Score 33; DB 8; Length 14;
 Best Local Similarity 60.0%; Pred. No. 2.4e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LOGPPYVSWL 15
 | | | | |
 Db 3 LVGPSLMSWL 12

Search completed: November 14, 2004, 12:02:16
 Job time : 45.4043 secs

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OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:26 ; Search time 40.0532 Seconds
(without alignments)
215.479 Million cell updates/sec

Title: US-09-831-253F-8
Perfect score: 80
Sequence: 1 EAVLIQGPVYSWL 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 17482

Minimum DB seq length: 0
Maximum DB seq length: 23

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	38.8	13	2 Q95925	Q95925 porphyra pu
2	31	38.8	23	2 Q700R6	Q700R6 sus scrofa
3	31	38.8	23	2 CAF32800	CAF32800 sus scrof
4	29	36.2	13	2 Q95808	Q95808 gracilariop
5	29	36.2	16	2 Q9QUW5	Q9QUW5 rattus sp.
6	29	36.2	22	1 MLP RANTE	P56924 rana tempor
7	28	35.0	13	1 SOVO SEPOF	P83567 sepiia offic
8	28	35.0	20	2 Q9UR76	Q9UR76 candida alb
9	27.5	34.4	18	1 D7A1 ACASC	P83402 acanthopagr
10	27	33.8	8	1 ALL5_CALVO	P41841 calliphora
11	27	33.8	13	1 PROX_ORYSA	P83647 oryza sativ
12	27	33.8	21	2 Q9PRQ1	Q9PRQ1 oncorhynch
13	26.5	33.1	17	2 Q9TR22	Q9TR22 bos taurus
14	26	32.5	16	2 Q9SPV1	Q9SPV1 nicotiana t
15	26	32.5	18	2 Q7MLG0	Q7MLG0 triticum ae
16	26	32.5	22	2 Q96JA7	Q96JA7 homo sapien
17	25	31.2	14	2 Q26075	Q26075 psammochinu
18	25	31.2	16	2 Q6NT60	Q6NT60 homo sapien
19	25	31.2	16	2 AAH69320	AAH69320 homo sapi
20	25	31.2	18	2 Q9UCT9	Q9UCT9 homo sapien
21	25	31.2	20	2 Q8NED5	Q8NED5 homo sapien
22	25	31.2	22	2 Q85481	Q85481 rous sarcom
23	25	31.2	23	2 Q9TWJ9	Q9TWJ9 mytilus edu
24	24	30.0	15	1 SODM_STRGR	P80733 streptomyce
25	24	30.0	19	2 Q96TP8	Q96TP8 cryptococcu
26	24	30.0	19	2 Q9ZYW8	Q9ZYW8 ichtneutes b
27	24	30.0	20	1 AROQ_ARYME	P46380 amycolatops
28	24	30.0	21	1 PIL3_ECOLI	P13948 escherichia
29	24	30.0	21	2 Q7S006	Q7S006 neurospora
30	24	30.0	22	2 Q52435	Q52435 burkholderi
31	24	30.0	23	2 Q96TH8	Q96TH8 cryptococcu

Q8xx22 ralstonia s
Q7miH0 leonurus ar
Q04220 plasmid p30
P20728 calotropis
P81801 streptomyce
Q9s820 hordeum vul
Q6ldb6 mus sp. mac
Aag38018 mus muscu
Aap13932 mus sp. m
Q75r67 conger myri
Q75rf1 conger myri
Q75rm2 conger myri
Q75rs8 conger myri
Q75rt8 conger myri

ALIGNMENTS

RESULT 1

Q95925 PRELIMINARY; PRT; 13 AA.
AC Q95925;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cytochrome oxidase subunit 3 (Fragment).
GN Name-cox3;
OS Porphyra purpurea.
OG Mitochondrion.
OC Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra.
OX NCBI_TaxID=2787;
RN [1]
RP SEQUENCE FROM N.A.
RA Lang B.Franz., Goff L.J., Gray M.W.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U59763; AAB17951.1; -.
KW GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1 1
SQ SEQUENCE 13 AA; 1522 MW; 0831666D0E8C65B0 CRC64;

Query Match 38.8%; Score 31; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. NO. 3.9e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 9 PPVSW 14
Db 3 PDVISW 8

RESULT 2

Q700R6 PRELIMINARY; PRT; 23 AA.
AC Q700R6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fas binding protein (Fragment).
GN Name=DAXX;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Barbosa A., Deneure O., Urien C., Milan D., Chardon P., Renard C.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ629179; CAF32800.1; -.
FT NON_TER 1 1
SQ SEQUENCE 23 AA; 2574 MW; 0B078824AA2E0517 CRC64;

Query Match 38.8%; Score 31; DB 2; Length 23;
 Best Local Similarity 50.0%; Pred. No. 7e+02;
 Matches 5; Conservative 1; Mismatches 0; Gaps 0;

QY 6 LQPPPVVSWL 15
 DB 11 LQNPKPPI 20

RESULT 3
 CAF32800 PRELIMINARY; PRT; 23 AA.
 AC CAF32800;
 DT 03-MAR-2004 (TrEMBLrel. 27, Created)
 DT 03-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DE FAS binding protein (fragment).
 GN DAXX.

OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Barbosa A., Demeure O., Urien C., Milan D., Chardon P., Renard C.;
 RT "A physical map of large segments of pig chromosome 7q1.1-ql.4;
 RT comparative analysis with human chromosome 6p21.";
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ629179; CAF32800.1; -;
 FT NON_TER 1 1
 FT NON_TER 23 23
 SQ SEQUENCE 23 AA; 2574 MW; 0B078824AA2E0517 CRC64;

Query Match 38.8%; Score 31; DB 2; Length 23;
 Best Local Similarity 50.0%; Pred. No. 7e+02;
 Matches 5; Conservative 1; Mismatches 0; Gaps 0;

QY 6 LQPPPVVSWL 15
 DB 11 LQNPKPPI 20

RESULT 4
 Q95808 PRELIMINARY; PRT; 13 AA.

AC Q95808;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cytochrome oxidase subunit 3 (fragment).
 GN Namexcox3;
 OS Gracilariopsis lemaneiformis.
 OG Mitochondrion.

OC Eukaryota; Rhodophyta; Florideophyceae; Gracilariaceae;
 OC Gracilariopsis.
 OX NCBI_TaxID=2782;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Lang B., Franz., Goff L.J., Gray M.W.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U59764; AAB17950.1; -;
 DR GO; GO:0005739; C.mitoochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 1 1
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1565 MW; 305BD4028745B043 CRC64;

Query Match 36.2%; Score 29; DB 2; Length 13;
 Best Local Similarity 42.9%; Pred. No. 8.5e+02;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 9 PPVSWL 15
 DB 1 PNYITWI 7

RESULT 5
 Q9QUW5 PRELIMINARY; PRT; 16 AA.

AC Q9QUW5;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE Collagen-like heparin-binding glycoprotein (fragment).
 OS Rattus sp.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10118;
 RN [1]

RP SEQUENCE.
 RX MEDLINE=96278823; PubMed=8662884;
 RA Chermousov M.A., Stahl R.C., Carey D.J.;
 RT "Schwann cells secrete a novel collagen-like adhesive protein that
 RT binds N-syndecan.";
 RL J. Biol. Chem. 271:13844-13853(1996).
 SQ SEQUENCE 16 AA; 1329 MW; 0F03A38D20A9221C CRC64;

Query Match 36.2%; Score 29; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LQPP 10
 DB 8 LQPP 12

RESULT 6

MLP_RANTE STANDARD; PRT; 22 AA.

AC P56324;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Melittin-like peptide (MLP).

OS Rana temporaria (European common frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=8407;
 RN [1]

RP SEQUENCE.

RC TISSUE=Skin secretion;
 RX MEDLINE=97175050; PubMed=9022710;
 RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
 RA Barra D.;
 RT "temporaria, antimicrobial peptides from the European red frog Rana
 RT temporaria.";
 RL Eur. J. Biochem. 242:788-792(1996).

CC -|- SUBCELLULAR LOCATION: Secreted.

CC -|- TISSUE SPECIFICITY: Skin.

KW Amidation; Amphibian defense peptide; Direct protein sequencing.

FT MOD_RES 22 22 Glutamine amide.

SQ SEQUENCE 22 AA; 2313 MW; 0990320F9B0709B3 CRC64;

Query Match 36.2%; Score 29; DB 1; Length 22;
 Best Local Similarity 43.8%; Pred. No. 1.5e+03;
 Matches 7; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

QY 2 AVLILQG--PPVSWL 15
 DB 5 ALKVLGLVPSIVSWV 20

RESULT 7

SOVO_SEPOF

ID SOVO_SEPOF STANDARD; PRT; 13 AA.

AC P83567;

DT 29-MAR-2004 (Rel. 43, Created)

DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE SepOvotropin.
 OS Sepia officinalis (Common cuttlefish).
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
 OC Decapodiformes; Sepioidea; Sepiidae; Sepia.
 OX NCBI_TaxID=6610;
 RN [1]
 RP SEQUENCE, FUNCTION, TISSUE SPECIFICITY, MASS SPECTROMETRY, AND
 RP AMIDATION.
 RC TISSUE=Ovarian follicle;
 RX MEDLINE=20483622; PubMed=11027583; DOI=10.1006/bbrc.2000.3595;
 RA Zatyiny C., Gagnon J., Boucaud-Camou E., Henry J.;
 RT "The SepOvotropin: a new ovarian peptide regulating oocyte transport
 RT in Sepia officinalis.";
 RL Biochem. Biophys. Res. Commun. 276:1013-1018(2000).
 CC -1- FUNCTION: Has myotropic activity targeting the genital tract.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Follicle, fully grown oocyte and egg.
 CC -1- MASS SPECTROMETRY: MW=1502.8; METHOD=MALDI; RANGE=1-13;
 CC NOTE=Ref.1.
 KW Amidation; Direct protein sequencing.
 FT MOD RES 13 Tyrosine amide.
 SQ SEQUENCE 13 AA; 1503 MW; 48305C7E34C72727 CRC64;
 Query Match 35.0%; Score 28; DB 1; Length 13;
 Best Local Similarity 45.5%; Pred. No. 1.2e+03;
 Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 QY 1 EAVILQGPY 11
 DB ::::|::|
 3 DSMLLQVPY 13
 RESULT 8
 Q9UR76 PRELIMINARY; PRT; 20 AA.
 AC Q9UR76;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE N-acetylglucosaminidase A (Fragment).
 OS Candida albicans (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 OX NCBI_TaxID=5476;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=94356217; PubMed=8075797;
 RA Molloy C., Cannon R.D., Sullivan P.A., Shepherd M.G.;
 RT "Purification and characterization of two forms of N-
 RT acetylglucosaminidase from Candida albicans showing widely different
 RT outer chain glycosylation.";
 RL Microbiology 140:1543-1553(1994).
 SQ SEQUENCE 20 AA; 2178 MW; DA602087EDDB4D47 CRC64;
 Query Match 35.0%; Score 28; DB 2; Length 20;
 Best Local Similarity 50.0%; Pred. No. 1.9e+03;
 Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 3 VLILQGPYVSW 14
 DB ::::|::|
 3 VEILPAQSVTW 14
 RESULT 9
 D7A1 ACASC STANDARD; PRT; 18 AA.
 AC P83402;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Aldehyde dehydrogenase family 7 member A1 (EC 1.2.1.3) (Antiquitin 1)

DE (Fragment).
 OS Acanthopagrus schlegelii (Black porgy).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
 OC Sparidae; Acanthopagrus.
 OX NCBI_TaxID=72011;
 RN [1]
 RP SEQUENCE, ACTIVITY, COPACTOR, AND SUBUNIT.
 RC TISSUE=Liver;
 RX MEDLINE=21956475; PubMed=11959129;
 RA Tang W.-K., Cheng C.H.K., Fong W.-P.;
 RT "First purification of the antiquitin protein and demonstration of its
 RT enzymatic activity.";
 RL FEBS Lett. 516:183-186(2002).
 CC -1- CATALYTIC ACTIVITY: An aldehyde + NAD(+) + H(2)O = an acid + NADH.
 CC -1- SUBUNIT: Homotetramer.
 CC -1- MISCELLANEOUS: Optimal pH is 9-10. The Km for acetaldehyde is 2.0
 CC mM and Vmax is 1.3 micromol/min x mg enzyme.
 CC -1- SIMILARITY: Belongs to the aldehyde dehydrogenase family.
 DR GO: 0004029; F:aldehyde dehydrogenase (NAD) activity; IDA.
 DR GO: 0006081; P:aldehyde metabolism; IDA.
 DR InterPro: IPR02086; Aldehyde dehydr.
 DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; PARTIAL.
 DR PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; PARTIAL.
 KW Direct protein sequencing; NAD; Oxidoreductase.
 FT NON TER 18 18
 SQ SEQUENCE 18 AA; 2059 MW; BFF8C3EF1A9B4047 CRC64;
 Query Match 34.4%; Score 27.5; DB 1; Length 18;
 Best Local Similarity 50.0%; Pred. No. 2.1e+03;
 Matches 6; Conservative 2; Mismatches 3; Indels 1; Gaps 1;
 QY 4 LILQGPYVSW 15
 DB ::::|::|
 3 LLINQPKY-SWL 13
 RESULT 10
 AL15 CALVO STANDARD; PRT; 8 AA.
 ID -AL15 CALVO
 AC P41841;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Callotostatin 5 (Met-callotostatin 1) ([Hyp3]Met-callotostatin).
 OS Calliphora vomitoria (Blue blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Calliphoridae; Calliphora.
 OX NCBI_TaxID=27454;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93211980; PubMed=8460157;
 RA Duve H., Johnsen A.H., Scott A.G., Yu C.G., Yagi K.J., Tobe S.S.,
 RA Thorpe A.;
 RT "Callotostatins: neuropeptides from the blowfly Calliphora vomitoria
 RT with sequence homology to cockroach allatostatins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).
 RN [2]
 RP CHARACTERIZATION, AND HYDROXYLATION.
 RC TISSUE=Head;
 RX MEDLINE=94342269; PubMed=8063725;
 RA Duve H., Johnsen A.H., Scott A.G., East P., Thorpe A.;
 RT "[Hyp3]Met-callotostatin. Identification and biological properties of
 RT a novel neuropeptide from the blowfly Calliphora vomitoria.";
 RL J. Biol. Chem. 269:21059-21066(1994).
 CC -1- FUNCTION: May act as a neurotransmitter or neuromodulator and play
 CC a role in the integration of information within the brain. May be
 CC involved in the control of visceral muscles due to its ability to
 CC behave as potent inhibitors of peristaltic movements. May also
 CC fulfill a neurohormonal role on muscles of the gut and heart.
 CC -1- TISSUE SPECIFICITY: Neurons within brain and abdominal ganglion.

CC -1- SIMILARITY: Belongs to the allatostatin family.
 DR PIR; E47393; E47393.
 KW Amidation; Direct protein sequencing; Hydroxylation; Neuropeptide.
 FT MOD_RES 3 3 Hydroxyproline (partial).
 FT MOD_RES 8 8 Methionine amide.
 SQ SEQUENCE 8 AA; 883 MW; 7D9879CABB477768 CRC64;
 Query Match 33.8%; Score 27; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0;
 QY 8 GPPY 11
 Db 1 GPPY 4
 RESULT 11
 PROX ORYSA STANDARD; PRT; 13 AA.
 AC P83677;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Probable profilin LP04 (Fragments).
 OS Oryza sativa (Rice).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 CC Erihartoideae; Oryzoae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=cv. Indica / IR64; TISSUE=Panicle;
 RA Hosseini Salekdeh S.G., Bennett J.;
 RT "Proteome analysis of rice panicle."
 RL Submitted (JUL-2003) to Swiss-Prot.
 CC -1- FUNCTION: Binds to actin and affects the structure of the
 CC cytoskeleton. At high concentrations, profilin prevents the
 CC polymerization of actin, whereas it enhances it at low
 CC concentrations. By binding to FIP2, it inhibits the formation of
 CC IP3 and DG (By similarity).
 CC -1- SUBUNIT: Occurs in many kinds of cells as a complex with monomeric
 CC actin in a 1:1 ratio.
 CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 CC protein is: 4.4, its MW is: 14.0 kDa.
 CC -1- SIMILARITY: Belongs to the profilin family.
 DR InterPro; IPR002097; Profilin.
 DR PROSITE; PS00414; PROFILIN; PARTIAL.
 KW Actin-binding; Cytoskeleton; Direct protein sequencing;
 KM Multigene family.
 FT NON_TER 1 1
 FT NON_CONS 5 6
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1362 MW; 0A3022EE0E52C68B CRC64;
 Query Match 33.8%; Score 27; DB 1; Length 13;
 Best Local Similarity 44.4%; Pred. No. 1.8e+03; Indels 0; Gaps 0;
 Matches 4; Conservative 3; Mismatches 2;
 QY 2 AVLIQGGP 10
 Db 5 AYNVIQGP 13
 RESULT 12
 Q9PRQ1 PRELIMINARY; PRT; 21 AA.
 AC Q9PRQ1;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE 70 kDa cold acclimation-related protein (Fragment).
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=96184500; PubMed=8605981;
 RA Yamashita M., Ojima N., Sakamoto T.;
 RT "Induction of proteins in response to cold acclimation of rainbow
 RT trout cells."
 RL FEBS Lett. 382:261-264 (1996).
 DR PIR; S62893; S62893.
 DR HSSP; 001853; 1E32.
 SQ SEQUENCE 21 AA; 2129 MW; PF68D74564917510 CRC64;
 Query Match 33.8%; Score 27; DB 2; Length 21;
 Best Local Similarity 57.1%; Pred. No. 3e+03; Indels 0; Gaps 0;
 Matches 4; Conservative 2; Mismatches 1;
 QY 4 LILQGGP 10
 Db 2 LILYGGP 8
 RESULT 13
 Q9TR22 PRELIMINARY; PRT; 17 AA.
 ID Q9TR22;
 AC Q9TR22;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE NONAMELOGENIN glycoprotein (Fragment).
 OS Bos taurus (Bovine).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=96126798; PubMed=8564801;
 RA Punzi J.S., DenBesten P.K.;
 RT "Purification of nonamelogenin proteins from bovine secretory
 RT enamel."
 RL Calif. Tissue Int. 57:379-384 (1995).
 SQ SEQUENCE 17 AA; 2032 MW; 9D811CC8228B615D CRC64;
 Query Match 33.1%; Score 26.5; DB 2; Length 17;
 Best Local Similarity 45.5%; Pred. No. 2.9e+03; Indels 3; Gaps 1;
 Matches 5; Conservative 1; Mismatches 2;
 QY 8 GPP---YVSWL 15
 Db 7 GPPPPYSEWM 17
 RESULT 14
 Q9SPV1 PRELIMINARY; PRT; 16 AA.
 ID Q9SPV1;
 AC Q9SPV1;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Nicotiana tabacum (Common tobacco).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 CC Lamiales; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20023723; PubMed=10561067;
 RA Foster E., Hattori J., Labbe H., Ouellet T., Fobert P.R., James L.E.,
 RA Iyer V.N., Miki B.L.;
 RT "A tobacco cryptic constitutive promoter, tCUP, revealed by T-DNA

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RT tagging.";
RL Plant Mol. Biol. 41:45-55(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Foster E., Hattori J., Labbe H., Bedard J., Johnson D., Ouellet T.,
RA Miki B.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF133844; AAD56607.1; -.
KW Hypothetical protein.
FT NON TER 16
SQ SEQUENCE 16 AA; 1725 MW; 6A4C8A093666240D CRC64;

Query Match 32.5%; Score 26; DB 2; Length 16;
Best Local Similarity 45.5%; Pred. No. 3.3e+03;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 EAVLILQPPY 11
Db :||| |||
4 QAVETLYSPFF 14

RESULT 15
Q7M1G0
ID Q7M1G0 PRELIMINARY; PRT; 18 AA.
AC Q7M1G0;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Gluten.
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE.
RX MEDLINE=92111773; PubMed=1309704;
RA Fukudome S., Yoshikawa M.;
RT "Opioid peptides derived from wheat gluten: their isolation and
RT characterization.";
RL FEBS Lett. 296:107-111(1992).
DR PIR; S20322; S20322.
SQ SEQUENCE 18 AA; 2120 MW; 09A80A087DE83926 CRC64;

Query Match 32.5%; Score 26; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 3.8e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 PYVSWL 15
Db ||| |||
9 PYGGWL 14
```

Search completed: November 14, 2004, 12:07:36
Job time : 42.0532 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:25 ; Search time 9.25532 Seconds
(without alignments)
155.938 Million cell updates/sec

Title: US-09-831-253F-8
Perfect score: 80
Sequence: 1 EAVLIQGPPYVSWL 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 4495

Minimum DB seq length: 0
Maximum DB seq length: 23

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	31	38.8	13	2 S47361	T-cell antigen rec
2	31	38.8	16	2 C49048	T-cell receptor be
3	31	38.8	20	2 S65884	translation initia
4	27	33.8	8	2 E47393	neuropeptide calla
5	27	33.8	17	2 S33609	extensin - maize (
6	27	33.8	21	2 S62893	cold-inducible pro
7	26	32.5	18	2 S20322	gluten - wheat
8	25	31.2	15	2 JN0730	hypothetical 1.7K
9	24	30.0	20	2 A47687	3-dehydroquinat d
10	24	30.0	23	2 PH1729	Ig heavy chain V r
11	24	30.0	23	2 I53401	monocyte chemotact
12	23	28.7	12	2 PH1675	Ig heavy chain V r
13	23	28.7	12	2 JU0356	cycloleucurin -
14	23	28.7	13	2 PH1676	Ig heavy chain V r
15	23	28.7	13	2 E37390	traA protein - Esc
16	23	28.7	14	2 PH1677	Ig heavy chain V r
17	23	28.7	14	2 PH1705	Ig heavy chain V r
18	23	28.7	14	2 PT0026	calotropin DI - mu
19	23	28.7	15	2 PA0027	protein QA100006 -
20	23	28.7	15	2 PH1616	Ig H chain V-D-J r
21	23	28.7	15	2 PH1610	Ig H chain V-D-J r
22	23	28.7	16	2 I57530	gene c-fms protein
23	23	28.7	17	2 I51203	myosin heavy chain
24	23	28.7	19	2 A48354	nonstructural prot
25	23	28.7	20	2 A05313	apolipoprotein A-I
26	23	28.7	20	2 P80188	superoxide dismuta
27	23	28.7	21	2 PH1731	Ig heavy chain V r
28	23	28.7	21	2 PH1730	Ig heavy chain V r
29	23	28.7	21	2 PH1690	Ig heavy chain V r

Ig heavy chain V r
Ig heavy chain V r
Ig heavy chain V r
Ig heavy chain V r
Ig heavy chain V r
Ig heavy chain V r
Ig heavy chain V r
Ig heavy chain V r
collagen alpha 1(I
osmotin homolog -
sormatin - sorghum
glutamate-ammonia
Ig heavy chain V r
Ig heavy chain V r
Ig heavy chain V r
Ig heavy chain V r
Ig heavy chain V r

ALIGNMENTS

RESULT 1

S47361 T-cell antigen receptor VJ junction beta chain - human

C;Species: Homo sapiens (man)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999

C;Accession: S47361

R;Lehner, P.J.

submitted to the EMBL Data Library, August 1994

A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T

A;Reference number: S47355

A;Accession: S47361

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-13 <LEH>

A;Cross-references: EMBL:235685; NID:G527459; PIDN:CAA84754.1; PID:G527460

C;Keywords: T-cell receptor

Query Match 38.8%; Score 31; DB 2; Length 13;
Best Local Similarity 71.4%; Pred. NO. 63;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 ILQGGPPY 11

Db 3 VLQGGSPY 9

RESULT 2

C49048

T-cell receptor beta chain V region (CDR3 junction, clone Vbeta20.1) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997

C;Accession: C49048

R;Stoud, M.; Kjeldsen-Kragh, J.; Suleyman, S.; Vinje, O.; Natvig, J.B.; Forre, O.

Eur. J. Immunol. 22, 2413-2418, 1992

A;Title: Limited heterogeneity of T cell receptor variable region gene usage in juvenil

A;Reference number: A49048; MUID:92387250; PMID:1387614

A;Accession: C49048

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-16 <SIO>

A;Experimental source: patient EV, IL-2R+ synovial T-cells

A;Note: sequence extracted from NCBI backbone (NCBIP:113265)

C;Keywords: T-cell receptor

Query Match 38.8%; Score 31; DB 2; Length 16;
Best Local Similarity 83.3%; Pred. NO. 78;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 ILQGGP 10

Db 6 LLQGGP 11

RESULT 3

S65884 translation initiation factor eIF-1 - rabbit (fragments)

C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
 C:Accession: S65884
 R:Kasperaitis, M.A.M.; Voorma, H.O.; Thomas, A.A.M.
 FEBS Lett. 365, 47-50, 1995
 A:Title: The amino acid sequence of eukaryotic translation initiation factor 1 and its
 A:Reference number: S65884; MUID:95293122; PMID:7774713
 A:Accession: S65884
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-9;10-16;17-20 <KAS>

Query Match 38.8%; Score 31; DB 2; Length 20;
 Best Local Similarity 54.5%; Pred. No. 98;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EAVLIQGGPY 11
 |||
 Db 9 EEVIQLQGDFF 19

RESULT 4

E47393 neuropeptide callatostatin 5 - bluebottle fly (Calliphora vomitoria)
 C:Species: Calliphora vomitoria
 C:Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C:Accession: E47393
 R:Duve, H.; Johnsen, A.H.; Scott, A.G.; Yu, C.G.; Yagi, K.J.; Tobe, S.S.; Thorpe, A.
 Proc. Natl. Acad. Sci. U.S.A. 90, 2456-2460, 1993
 A:Title: Callatostatin: neuropeptides from the blowfly Calliphora vomitoria with sequen
 A:Reference number: A47393; MUID:93211980; PMID:8460157
 A:Accession: E47393
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-8 <DUV>
 A:Cross-references: UNIPROT:P41841
 A:Experimental source: whole flies
 A>Note: sequence extracted from NCBI backbone (NCBIP:128482)

Query Match 33.8%; Score 27; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 GPPY 11
 |||
 Db 1 GPPY 4

RESULT 5

S33609 extensin - maize (fragment)
 C:Species: Zea mays (maize)
 C:Date: 19-Mar-1997 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
 C:Accession: S33609
 R:Murphy, J.M.; Hood, E.E.
 Plant Mol. Biol. 21, 885-893, 1993
 A:Title: Molecular basis for extensin size heterogeneity in two maize varieties.
 A:Reference number: S33609; MUID:93222485; PMID:8467081
 A:Accession: S33609
 A:Molecule type: protein
 A:Residues: 1-17 <MUR>
 C:Keywords: glycoprotein; hydroxyproline

Query Match 33.8%; Score 27; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 GPPY 11
 |||

Db 7 GPPY 10

RESULT 6

S62893 cold-inducible protein, 70K - rainbow trout (fragment)
 C:Species: Oncorhynchus mykiss (rainbow trout)
 C:Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 09-Jul-2004
 C:Accession: S62893
 R:Yamashita, M.; Ojima, N.; Sakamoto, T.
 FEBS Lett. 382, 261-264, 1996
 A:Title: Induction of proteins in response to cold acclimation of rainbow trout cells.
 A:Reference number: S62893; MUID:96184500; PMID:8605981
 A:Accession: S62893
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-21 <YAM>
 A:Cross-references: UNIPROT:Q9PRQ1

Query Match 33.8%; Score 27; DB 2; Length 21;
 Best Local Similarity 57.1%; Pred. No. 4.7e+02;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 LILQGGP 10
 ::|||
 Db 2 ILLYGPP 8

RESULT 7

S20322 Gluten - wheat
 C:Species: Triticum aestivum (common wheat)
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
 C:Accession: S20322
 R:Fukudome, S.; Yoshikawa, M.
 FEBS Lett. 296, 107-111, 1992
 A:Title: Opioid peptides derived from wheat gluten: their isolation and characterization
 A:Reference number: S20322; MUID:92111773; PMID:1309704
 A:Accession: S20322
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-18 <FUK>
 A:Cross-references: UNIPROT:Q7MIG0

Query Match 32.5%; Score 26; DB 2; Length 18;
 Best Local Similarity 66.7%; Pred. No. 5.9e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 PYVSWL 15
 |||
 Db 9 PYGWL 14

RESULT 8

JN0730 hypothetical 1.7K protein - phage SP1
 N:Alternate names: hypothetical protein 42.1
 C:Species: phage SP1
 C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999
 C:Accession: JN0730
 R:Chai, S.; Szepan, U.; Lueder, G.; Trautner, T.A.; Alonso, J.C.
 Gene 129, 41-49, 1993
 A:Title: Sequence analysis of the left end of the Bacillus subtilis bacteriophage SP1
 A:Reference number: JN0729; MUID:93328123; PMID:8335259
 A:Accession: JN0730
 A:Molecule type: DNA
 A:Residues: 1-15 <CHA>
 A:Cross-references: EMBL:X65941

Query Match 31.2%; Score 25; DB 2; Length 15;
 Best Local Similarity 40.0%; Pred. No. 7.2e+02;
 Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 LILOGPPYVS 13
:: |||:
Db 1 MLNNGPPFRS 10

RESULT 9

A47687
3-dehydroquininate dehydratase (EC 4.2.1.10) - Amycolatopsis methanolica (fragment)
C;Species: Amycolatopsis methanolica
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A47687
R;Euvierink, G.J.; Hessel, G.I.; Vrijbloed, J.W.; Coggins, J.R.; Dijkhuizen, L.
J. Gen. Microbiol. 138, 2449-2457, 1992
A;Title: Purification and characterization of a dual function 3-dehydroquininate dehydratase
A;Reference number: A47687; MUID:93123995; PMID:1479361
A;Accession: A47687
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-20 <EU>
A;Cross-references: UNIPROT:P46380
A;Experimental source: WV2
A;Note: sequence extracted from NCBI backbone (NCBIP:122129)
C;Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 30.0%; Score 24; DB 2; Length 20;
Best Local Similarity 57.1%; Pred. No. 1.4e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 VLILQGP 9
|: |||
Db 3 VFVLNGP 9

RESULT 10

PH1729
Ig heavy chain V region (clone GCC-9) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
C;Accession: PH1729
R;McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.
J. Exp. Med. 178, 295-307, 1993
A;Title: Antigen-driven B cell differentiation in vivo.
A;Reference number: PH1675; MUID:93301607; PMID:8315385
A;Accession: PH1729
A;Molecule type: mRNA
A;Residues: 1-23 <MCH>
A;Experimental source: B cell
A;Note: the authors translated the codon ACA for residue 13 as Ala
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin

Query Match 30.0%; Score 24; DB 2; Length 23;
Best Local Similarity 60.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 YVSWL 15
|: |||
Db 1 YTSWM 5

RESULT 11

I53401
monocyte chemotactic protein - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000
C;Accession: I53401
R;Steenbergen, E.J.; Verhagen, O.J.; van Leeuwen, E.F.; Behrendt, H.; Merle, P.A.; Weste
Eur. J. Immunol. 24, 900-908, 1994
A;Title: B precursor acute lymphoblastic leukemia third complementarity-determining region
fetal life.
A;Reference number: I53401; MUID:94200227; PMID:8149961
A;Accession: I53401
A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA
A;Residues: 1-23 <RES>
A;Cross-references: GB:S69742; NID:9546303; PIDN:AAD14040.1; PID:94261740
C;Genetics:
A;Gene: IGH-VDJ

Query Match 30.0%; Score 24; DB 2; Length 23;
Best Local Similarity 80.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 PPVVS 13
||| |
Db 5 PPYCS 9

RESULT 12

PH1675
Ig heavy chain V region (clone NP-6-7) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
C;Accession: PH1675
R;McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.
J. Exp. Med. 178, 295-307, 1993
A;Title: Antigen-driven B cell differentiation in vivo.
A;Reference number: PH1675; MUID:93301607; PMID:8315385
A;Accession: PH1675
A;Molecule type: mRNA
A;Residues: 1-12 <MCH>
A;Experimental source: B cell
A;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin

Query Match 28.7%; Score 23; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 YVSWL 15
|: |||
Db 1 YTSWV 5

RESULT 13

JU0356
Cycloleucunin - sagebrush motherwort
C;Species: Leonurus artemisia (sagebrush motherwort)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: JU0356
R;Kinoshita, K.; Tanaka, J.; Kuroda, K.; Koyama, K.; Natori, S.; Kinoshita, T.
Chem. Pharm. Bull. 39, 712-715, 1991
A;Title: Cycloleucunin, a cyclic peptide from Leonuri fructus.
A;Reference number: JU0356; MUID:91300597; PMID:2070452
A;Accession: JU0356
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-12 <KIN>
A;Cross-references: UNIPROT:Q7M1H0

Query Match 28.7%; Score 23; DB 2; Length 12;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 QGPPY 11
|: |||
Db 8 QYPPY 12

RESULT 14

PH1676
Ig heavy chain V region (clone NP-6-5) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
C;Accession: PH1676
R;McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.

J. Exp. Med. 178, 295-307, 1993
A:Title: Antigen-driven B cell differentiation in vivo.
A:Reference number: PH1675; MUID:93301607; PMID:8315385
A:Accession: PH1676
A:Molecule type: mRNA
A:Residues: 1-13 <MCH>
A:Experimental source: B cell
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 28.7%; Score 23; DB 2; Length 13;
Best Local Similarity 60.0%; Pred. NO. 1.3e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 YVSWL 15
| | |
Db 1 YTSWV 5

RESULT 15

E37390
traA protein - Escherichia coli plasmid P307 (fragment)
C:Species: Escherichia coli
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C:Accession: E37390; PQ0480
R:Graus-Goeldner, A.; Graus, H.; Schlacher, T.; Hoegenauer, G.
Plasmid 24, 119-131, 1990
A:Title: The sequences of genes bordering orit in the enterotoxin plasmid P307: comparison
A:Reference number: A37390; MUID:91261994; PMID:2096398
A:Accession: E37390
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-13 <GRA>
A:Cross-references: UNIPROT:Q04220; GB:M62986; NID:G150463; PIDN:AAA25525.1; PID:G150468
C:Genetics:
A:Gene: traA
A:Genome: plasmid
C:Superfamily: fimbrial protein

Query Match 28.7%; Score 23; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. NO. 1.3e+03;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EAVLILQG 8
:|:|:|
Db 2 DAILSVQG 9

Search completed: November 14, 2004, 12:03:14
Job time : 10.2553 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:26 ; Search time 37.383 Seconds
(without alignments)
215.479 Million cell updates/sec

Title: US-09-831-253F-7

Perfect score: 72

Sequence: 1 SNPYSAFQVDITD 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 17482

Minimum DB seq length: 0

Maximum DB seq length: 23

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	40.3	18	2 Q9QV11	Q9qv11 rattus sp.
2	28	38.9	9	2 Q7RA82	Q7ra82 plasmodium
3	27	37.5	20	2 Q9QV82	Q9qv82 mus sp. s
4	26	36.1	13	2 Q79A22	Q79a22 borrelia bu
5	26	36.1	22	2 Q7M0L1	Q7m0l1 clostridium
6	25	34.7	10	2 Q76MM5	Q76mms eurypharynx
7	25	34.7	10	2 BAB87140	Bab87140 euryphary
8	25	34.7	11	2 Q7M154	Q7m154 bacillus th
9	25	34.7	12	2 Q7XB05	Q7xb05 zea mays (m
10	25	34.7	13	2 Q7X761	Q7x761 zea mays (m
11	25	34.7	14	2 P81801	P81801 streptomyc
12	25	34.7	14	2 Q9R518	Q9r518 vibrio algi
13	25	34.7	17	2 Q7XB06	Q7xb06 zea mays (m
14	25	34.7	18	2 Q7XB07	Q7xb07 zea mays (m
15	25	34.7	22	2 Q99LZ5	Q99lz5 mus musculu
16	24	33.3	8	2 Q91U19	Q91u19 influenza a
17	24	33.3	8	2 Q91U21	Q91u21 influenza a
18	24	33.3	12	2 Q9S550	Q9s550 streptococc
19	24	33.3	16	2 Q7RGW0	Q7rgw0 plasmodium
20	24	33.3	16	2 Q7RSP0	Q7rsp0 plasmodium
21	24	33.3	16	2 Q9TOY6	Q9toy6 cryptotolagus
22	24	33.3	20	2 Q9ST52	Q9st52 vicia faba
23	24	33.3	21	2 Q7RKFF7	Q7rkff7 plasmodium
24	24	33.3	21	2 Q8CJEB9	Q8cje9 mus musculu
25	24	33.3	22	2 Q7R7E7	Q7r7e7 plasmodium
26	24	33.3	22	2 Q7RLB6	Q7rlb6 plasmodium
27	24	33.3	22	2 Q9QV59	Q9qv59 cavia (guin
28	23.5	32.6	19	2 Q8SEP2	Q8sep2 genista tyr
29	23.5	32.6	19	2 Q8SKW8	Q8skw8 genista val
30	23.5	32.6	19	2 Q8SKX1	Q8skx1 genista gen
31	23.5	32.6	19	2 Q8SKX3	Q8skx3 genista eph

ALIGNMENTS

RESULT 1

Q9QV11 PRELIMINARY; PRT; 18 AA.
AC Q9QV11
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Sucrase-alpha-dextrinase subunit beta, S-D subunit beta
DE (fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101118;
RN [1]
RP SEQUENCE
RX MEDLINE=920311479; PubMed=1931964;
RA Zhu J.S., Conklin K.A., Scheving L.A., Smith A.J., Gray G.M.;
RT "Structural and functional correlates of sucrase-alpha-dextrinase in
RT intact brush border membranes.";
RL Biochemistry 30:10399-10408(1991).
FT NON_TER 1 1
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 2122 MW; 68FF1ABA87B24E49 CRC64;

Query Match 40.3%; Score 29; DB 2; Length 18;
Best Local Similarity 45.5%; Pred. No. 3.6e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 SNPYSAFQVDI 11
||| |:::
DB 5 SNPISLRVEV 15

RESULT 2

Q7RA82 PRELIMINARY; PRT; 9 AA.
AC Q7RA82;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein (fragment).
GN Name=PY06620;
OS Plasmodium yoelii Yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=12368865;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.M., Pertea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaihi A., Cummings L.M.,

RA Florens L., Yates P.R. III, Raine J.D., Sinden R.E., Harris M.A.,
 RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
 RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
 RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
 RA Carucci D.J.;
 RT "Genome sequence and comparative analysis of the model rodent malaria
 RT parasite *Plasmodium yoelii* yoelii";
 RL Nature 419:512-519(2002).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL; AABL01002263; EAA18865.1; -.
 KW Hypothetical protein. 9
 FT NON_TER 9
 SQ SEQUENCE 9 AA; 1001 MW; 4687A5AB476455B7 CRC64;
 Query Match 38.9%; Score 28; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SNPYS 5
 DB |||||
 3 SNPYS 7
 RESULT 3
 Q9QVB2 PRELIMINARY; PRT; 20 AA.
 ID Q9QVB2
 AC Q9QVB2
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE Serine protease (Fragment).
 OS Mus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10095;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93020730; PubMed=1404084;
 RA Damjanov A., Damjanov I.;
 RT "Isolation of serine protease from granulated metrial gland cells of
 RT mice and rats with lectin from *Dolichos biflorus*.";
 RL J. Reprod. Fertil. 95:679-684(1992).
 SQ SEQUENCE 20 AA; 2290 MW; 0A304F61A22C500D CRC64;
 Query Match 37.5%; Score 27; DB 2; Length 20;
 Best Local Similarity 71.4%; Pred. No. 9.6e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 SNPYSAF 7
 DB |||||
 11 SRPYNAF 17
 RESULT 4
 Q79A22 PRELIMINARY; PRT; 13 AA.
 ID Q79A22
 AC Q79A22
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Moxr protein (Fragment).
 GN Name=moxr;
 OS *Borrelia burgdorferi* (Lyme disease spirochete).
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
 OX NCBI_TaxID=139;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=212;
 RA Old I.G.;
 RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X95668; CAA64970.1; -.

FT NON_TER 13
 SQ SEQUENCE 13 AA; 1484 MW; C7C2DF4CFD83A046 CRC64;
 Query Match 36.1%; Score 26; DB 2; Length 13;
 Best Local Similarity 40.0%; Pred. No. 9.2e+02;
 Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 5 SAFQVDITID 14
 DB |||||
 3 SGFQIDSEVE 12
 RESULT 5
 Q7MOL1 PRELIMINARY; PRT; 22 AA.
 ID Q7MOL1
 AC Q7MOL1
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Exoenzyme C3 (Fragment).
 OS *Clostridium botulinum*.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1491;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=89338716; PubMed=2474453;
 RA Toratani S., Yokosawa N., Yokosawa H., Ishii S.I., Oguma K.;
 RT "Immuno-crossreactivity between botulinum neurotoxin type C1 or D and
 RT exoenzyme C3";
 RL FEBS Lett. 252:83-87(1989).
 DR PIR; S05236; S05236.
 FT NON_TER 1
 FT NON_TER 22
 SQ SEQUENCE 22 AA; 2449 MW; C3A42F8BE7FF41E3 CRC64;
 Query Match 36.1%; Score 26; DB 2; Length 22;
 Best Local Similarity 45.5%; Pred. No. 1.6e+03;
 Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 1 SNPYSAFQVDI 11
 DB |||||
 3 SNTYQEFNTNI 13
 RESULT 6
 Q76MW5 PRELIMINARY; PRT; 10 AA.
 ID Q76MW5
 AC Q76MW5
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE NADH dehydrogenase subunit 2 (Fragment).
 GN Name=ND2;
 OS *Eurypharynx pelecyanoides* (pelican eel).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes;
 OC Eurypharyngidae; Eurypharynx.
 OX NCBI_TaxID=55117;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22967687; PubMed=12949142;
 RA Inoue J.G., Miya M., Tsukamoto K., Nishida M.;
 RT "Evolution of the deep-sea gulper eel mitochondrial genomes: large-
 RT scale gene rearrangements originated within the eels";
 RL Mol. Biol. Evol. 20:1917-1924(2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB046477; BAB87140.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.

```
KW Mitochondrion.
FT NON TER 10
SQ SEQUENCE 10 AA; 1261 MW; 357BFE29C682DB47 CRC64;

Query Match
 34.7%; Score 25; DB 2; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 NPYSAFQV 9
   |||
Db 2 NPYVMFLV 9

RESULT 7
BAB871140
ID BAB871140 PRELIMINARY; PRT; 10 AA.
AC BAB871140;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE NADH dehydrogenase subunit 2 (Fragment).
GN ND2.
OS Eurypharynx pelecanoides (pelican eel).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes;
OC Eurypharyngidae; Eurypharynx.
OX NCBI_TaxID=55117;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A;
RA Inoue J.G., Miya M., Tsukamoto K., Nishida M.;
RT "Evolution of the Deep-Sea Gulper Eel Mitochondrial Genomes: Large-
RT Scale Gene Rearrangements Originated Within the Bels.";
RL Mol. Biol. Evol. 20:1917-1924(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A;
RA Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.;
RT Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB046477; BAB871140.1;
KW Mitochondrion.
FT NON TER 10
SQ SEQUENCE 10 AA; 1261 MW; 357BFE29C682DB47 CRC64;

Query Match
 34.7%; Score 25; DB 2; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 NPYSAFQV 9
   |||
Db 2 NPYVMFLV 9

RESULT 8
Q7M154
ID Q7M154 PRELIMINARY; PRT; 11 AA.
AC Q7M154;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Parasporal crystal protein, wax moth-specific (Fragment).
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE.
RA Chestukhina G.G., Kostina L.I., Zalunin I.A., Khodova O.M.,
RA Stepanov V.M.;
RT "Bacillus thuringiensis ssp. galleriae simultaneously produces two
RT delta-endotoxins differing strongly in primary structure and
RT entomocidal activity.";
RL FEBS Lett. 232:249-251(1988).
```

```
DR PIR; S00616; S00616.
FT NON TER 1
SQ SEQUENCE 11 AA; 1237 MW; C6FF9BD64764444D CRC64;

Query Match
 34.7%; Score 25; DB 2; Length 11;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNPYS 5
   .|||
Db 5 NNPYS 9

RESULT 9
Q7XB05
ID Q7XB05 PRELIMINARY; PRT; 12 AA.
AC Q7XB05;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Phytoene synthase 2 (Fragment).
GN Name-psy2;
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Y-14;
RA Palaisa K.A., Morgante M., Williams M., Rafalski A.;
RT "Contrasting effects of selection on sequence diversity and linkage
RT disequilibrium at two phytoene synthase loci.";
RL Plant Cell 15:1795-1806(2003).
DR EMBL; AY300568; AAP55307.1;
FT NON TER 1
SQ SEQUENCE 12 AA; 1335 MW; 9B1E0AA00869C325 CRC64;

Query Match
 34.7%; Score 25; DB 2; Length 12;
Best Local Similarity 54.5%; Pred. No. 1.3e+03;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 SNPYSAFQVDI 11
   |.:|||
Db 1 SDTVSKFPVDI 11

RESULT 10
Q7X761
ID Q7X761 PRELIMINARY; PRT; 13 AA.
AC Q7X761;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Phytoene synthase 2 (Fragment).
GN Name-psy2;
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=W-17, and W-50;
RA Palaisa K.A., Morgante M., Williams M., Rafalski A.;
RT "Contrasting effects of selection on sequence diversity and linkage
RT disequilibrium at two phytoene synthase loci.";
RL Plant Cell 15:1795-1806(2003).
DR EMBL; AY300592; AAP55331.1; -.
```

```
DR EMBL; AY300599; AAP55338.1; -.
FT NON_TER 1 1
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1449 MW; 9B1E0AA05615C325 CRC64;

Query Match 34.7%; Score 25; DB 2; Length 13;
Best Local Similarity 54.5%; Pred. No. 1.4e+03;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 SNPYSAFQVDI 11
   | | | | |
Db 2 SDTVSKFPVDI 12

RESULT 11
P81801 PRELIMINARY; PRT; 14 AA.
ID P81801;
AC P81801;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Puromycin-hydrolyzing enzyme (SC 3.-.-) (Fragment).
OS Streptomyces morookaensis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1970;
RN [1]
RP SEQUENCE.
RC STRAIN=JCM4673 / KCC S-0673;
RX PubMed=9538199;
RA Nishimura M., Matsumoto H., Nakamura A., Sugiyama M.;
RT "Purification and characterization of a puromycin-hydrolyzing enzyme
from blastocidin S-producing Streptomyces morookaensis.";
RL J. Biochem. 123:247-252(1998).
RN [2]
RP CHARACTERIZATION, AND FUNCTION.
RA Nishimura M., Matsumoto H., Sugiyama M.;
RT "Blastocidin S-producing Streptomyces morookaensis possesses an enzyme
activity with hydrolyzes puromycin.";
RL FEMS Microbiol. Lett. 132:95-100(1995).
CC -1- FUNCTION: INACTIVATES PUROMYCIN BY CATALYZING THE HYDROLYSIS OF
THE AMIDE LINKAGE BETWEEN ITS AMINONUCLEOSIDE AND O-METHYL-L-
TYROSINE MOIETIES. THE OPTIMUM PH IS 8.0 AND THE OPTIMAL
TEMPERATURE IS 45 DEGREES CELSIUS.
CC -1- FUNCTION: MAY HAVE AMINOPEPTIDASE ACTIVITY.
CC -1- ENZYME REGULATION: STIMULATED BY DTT. STRONGLY INHIBITED BY ZINC
ION, FERROUS ION, CUPRIC ION, MERCURY ION, N-BROMOSUCCINIMIDE AND
N-ETHYLMALIMIDE. PARTIALLY INHIBITED BY COBALT ION.
CC -1- SUBUNIT: MONOMER.
CC -1- MISCELLANEOUS: HAS AN ISOELECTRIC POINT OF 6.4.
DR GO; GO:0004177; F:aminopeptidase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
KW Aminoamidase; Hydrolase.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1492 MW; 3F980730E45EF3D8 CRC64;

Query Match 34.7%; Score 25; DB 2; Length 14;
Best Local Similarity 55.6%; Pred. No. 1.5e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 PYSAFQVDI 11
   | | | | |
Db 5 PYGAWQSPI 13

RESULT 12
Q9R518 PRELIMINARY; PRT; 14 AA.
ID Q9R518;
AC Q9R518;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE L-2,4-diaminobutyrate decarboxylase (Fragment).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Eukaryota; Viridiplantae; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;

OS Vibrio alginolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=663;
RN [1]
RP SEQUENCE.
RX MEDLINE=92381494; PubMed=1512577;
RA Yamamoto S., Tsuzaki Y., Tougou K., Shinoda S.;
RT "Purification and characterization of L-2,4-diaminobutyrate
decarboxylase from Acinetobacter calcoaceticus.";
RL J. Gen. Microbiol. 138:1461-1465(1992).
RQ PIR; B44854; B44854.
SQ SEQUENCE 14 AA; 1643 MW; 9F1B13DD35168ABA CRC64;

Query Match 34.7%; Score 25; DB 2; Length 14;
Best Local Similarity 55.6%; Pred. No. 1.5e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 SAFQVDITI 13
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Db 2 TAFEVDSNI 10

RESULT 13
Q7XB06 PRELIMINARY; PRT; 17 AA.
ID Q7XB06;
AC Q7XB06;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Phytoene synthase 2 (Fragment).
GN Name=psy2;
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PI587132;
RX MEDLINE=22779048; PubMed=12897253;
RA Palaisa K.A., Morgante M., Williams M., Rafalski A.;
RT "Contrasting effects of selection on sequence diversity and linkage
disequilibrium at two phytoene synthase loci.";
RL Plant Cell 15:1795-1806(2003).
DR EMBL; AY300558; AAP55297.1; -.
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1869 MW; 8EB5FAA056459674 CRC64;

Query Match 34.7%; Score 25; DB 2; Length 17;
Best Local Similarity 54.5%; Pred. No. 1.9e+03;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 SNPYSAFQVDI 11
   | | | | |
Db 6 SDTVSKFPVDI 16

RESULT 14
Q7XB07 PRELIMINARY; PRT; 18 AA.
ID Q7XB07;
AC Q7XB07;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Phytoene synthase 2 (Fragment).
GN Name=psy2;
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
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RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=PI221785;
RX  MEDLINE=22779048; PubMed=12897253;
RA  Palaisa K.A., Morgante M., Williams M., Rafalski A.;
RT  "Contrasting effects of selection on sequence diversity and linkage
RL  disequilibrium at two phytoene synthase loci.";
DR  Plant Cell 15:1795-1806(2003).
FT  EMBL; AY300550; AAP55289.1; -.
FT  NON_TER 1 18
FT  NON_TER 18 18
SQ  SEQUENCE 18 AA; 2000 MW; 8ECB4B9056459674 CRC64;

Query Match      34.7%; Score 25; DB 2; Length 18;
Best Local Similarity 54.5%; Pred. No. 2e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  1 SNPYSAFQVDI 11
DB  |:-|||
    7 SDTVSKFPVDI 17

RESULT 15
Q99LZ5 PRELIMINARY; PRT; 22 AA.
AC Q99LZ5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE AW125753 protein.
GN Name=Ptpn22; Synonyms=AW125753;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=mix FVB/N;
RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haiech F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=mix FVB/N;
RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002154; AA02154.1; -.
DR MGD; MGI:104574; Ptpn22.
SQ SEQUENCE 22 AA; 2559 MW; 34843A007475028A CRC64;

Query Match      34.7%; Score 25; DB 2; Length 22;
Best Local Similarity 44.4%; Pred. No. 2.5e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
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QY 6 AFQVDITID 14
|:-|||
DB 12 AYSVDASLD 20

Search completed: November 14, 2004, 12:07:34
Job time : 37.383 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2004, 13:04:13 ; Search time 23.3333 Seconds
(without alignments)
42.633 Million cell updates/sec

Title: US-09-831-253F-8

Perfect score: 80

Sequence: 1 EAVLILQGPVYSWL 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 157298

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	41.2	14	2	US-08-764-640-39
2	33	41.2	14	3	US-08-973-225-39
3	33	41.2	14	3	US-08-973-225-39
4	33	41.2	14	3	US-08-973-225-39
5	33	41.2	14	3	US-09-244-298A-39
6	33	41.2	14	3	US-09-516-704-39
7	33	41.2	14	4	US-09-549-090-39
8	33	41.2	14	4	US-09-549-090-216
9	33	41.2	14	4	US-09-832-230A-39
10	32	40.0	11	2	US-09-428-082B-67
11	32	40.0	14	2	US-08-856-663-12
12	32	40.0	14	3	US-08-764-640-37
13	32	40.0	14	3	US-08-973-225-37
14	32	40.0	14	3	US-09-244-298A-37
15	32	40.0	14	4	US-09-516-704-37
16	32	40.0	14	4	US-09-549-090-37
17	31	38.8	9	2	US-09-832-230A-37
18	31	38.8	9	3	US-08-725-726D-19
19	31	38.8	9	3	US-09-162-368B-19
20	31	38.8	15	3	US-09-271-970-6
21	31	38.8	15	4	US-09-760-397-6
22	30	37.5	7	1	US-07-807-043B-6
23	30	37.5	9	1	US-08-239-849B-6
24	30	37.5	9	1	US-08-464-318-6
25	30	37.5	9	2	US-08-471-341-6
26	30	37.5	9	2	US-08-461-566-6
27	30	37.5	9	2	US-08-142-368A-6

28	30	37.5	9	3	US-08-967-727-6	Sequence 6, Appli
29	30	37.5	9	3	US-09-064-964-2	Sequence 2, Appli
30	30	37.5	9	3	US-08-037-230D-6	Sequence 6, Appli
31	30	37.5	9	3	US-09-064-174-2	Sequence 2, Appli
32	30	37.5	9	4	US-09-583-850-6	Sequence 6, Appli
33	30	37.5	9	4	US-09-579-197-6	Sequence 6, Appli
34	30	37.5	9	4	US-09-404-026-6	Sequence 6, Appli
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36	30	37.5	9	4	US-09-454-204A-66	Sequence 66, Appli
37	30	37.5	9	4	US-09-168-832-2	Sequence 2, Appli
38	30	37.5	9	4	US-08-977-787-7	Sequence 7, Appli
39	30	37.5	13	4	US-08-977-787-8	Sequence 7, Appli
40	29	36.2	11	4	US-09-359-268A-12	Sequence 12, Appli
41	29	36.2	14	4	US-09-149-476-722	Sequence 722, App
42	29	36.2	15	2	US-08-764-640-213	Sequence 213, App
43	29	36.2	15	3	US-09-244-298A-213	Sequence 213, App
44	29	36.2	15	3	US-09-516-704-213	Sequence 213, App
45	29	36.2	15	4	US-09-268-480-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-764-640-39
; Sequence 39, Application US/08764640
; Patent No. 5869451
; Patent No. 5869451 5837683
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Cwirla, Steven E.
; APPLICANT: Gates, Christian
; APPLICANT: Schatz, Peter J.
; APPLICANT: Balasubramanian, Palaniappan
; APPLICANT: Wagstrom, Christopher R.
; APPLICANT: Hendren, Richard W.
; APPLICANT: Deprence, Randolph B.
; APPLICANT: Podduturi, Surekha
; APPLICANT: Yin, Qun
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
; TITLE OF INVENTION: RECEPTOR
; NUMBER OF SEQUENCES: 244
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glaxo Wellcome
; STREET: Five Moore Drive, P.O. Box 13398
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM: Floppy disk
; MEDIUM TYPE: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/764,640
; FILING DATE: 11-DEC-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Hrubiec, Robert T.
; REGISTRATION NUMBER: 36,392
; REFERENCE/DOCKET NUMBER: PK3281
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-248-1000
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-764-640-39

Query Match 41.2%; Score 33; DB 2; Length 14;
Best Local Similarity 60.0%; Pred. No. 48;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LQGPYPVSWL 15
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DB 3 LVGPSLMSWL 12

RESULT 2

US-08-973-225-39
; Sequence 39, Application US/08973225A
; Patent No. 6083913

GENERAL INFORMATION:

APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
Gates, Christian
Haselden, Sherril S.
Matheakis, Larry C.
Schatz, Peter J.
Wagstrom, Christopher R.
Wrighton, Nicholas C.

TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
THROMBOPOIETIN RECEPTOR

NUMBER OF SEQUENCES: 232

CORRESPONDENCE ADDRESS:

ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
STATE: NC

COUNTRY: USA
ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/973,225A

FILING DATE: 04-Dec-1997

ATTORNEY/AGENT INFORMATION:

NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW
TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-248-1000

INFORMATION FOR SEQ ID NO: 39:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 39:

US-08-973-225-39

Query Match 41.2%; Score 33; DB 3; Length 14;
Best Local Similarity 60.0%; Pred. No. 48;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LQGPYPVSWL 15
| | | : | | |
DB 3 LVGPSLMSWL 12

RESULT 3

US-08-973-225-216

; Sequence 216, Application US/08973225A

; Patent No. 6083913

; GENERAL INFORMATION:

APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Duffin, David J.
Gates, Christian
Haselden, Sherril S.
Matheakis, Larry C.
Schatz, Peter J.
Wagstrom, Christopher R.
Wrighton, Nicholas C.

TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
THROMBOPOIETIN RECEPTOR

NUMBER OF SEQUENCES: 232

CORRESPONDENCE ADDRESS:

ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/973,225A

FILING DATE: 04-Dec-1997

ATTORNEY/AGENT INFORMATION:

NAME: Hrubiec, Robert T.
REGISTRATION NUMBER: 36,392
REFERENCE/DOCKET NUMBER: PK3065USW

TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-248-1000

INFORMATION FOR SEQ ID NO: 216:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 216:

US-08-973-225-216

Query Match 41.2%; Score 33; DB 3; Length 14;
Best Local Similarity 60.0%; Pred. No. 48;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LQGPYPVSWL 15
| | | : | | |
DB 3 LVGPSLMSWL 12

RESULT 4

US-09-244-298A-39

; Sequence 39, Application US/09244298A

; Patent No. 6121238

; GENERAL INFORMATION:

APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirla, Steven E.
Gates, Christian
Schatz, Peter J.
Balasubramanian, Palaniappan
Wagstrom, Christopher R.
Hendren, Richard W.
Deprince, Randolph B.
Poddaturi, Surekha
Yin, Qun

TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A

RECEPTOR

NUMBER OF SEQUENCES: 244

CORRESPONDENCE ADDRESS:

CLASSIFICATION: <Unknown>

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; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-549-090-39

Query Match      41.2%; Score 33; DB 4; Length 14;
Best Local Similarity 60.0%; Pred. No. 48;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      6 LQPPYVSWL 15
Db      3 LVGPSLSMWL 12

RESULT 7
US-09-549-090-216
; Sequence 216, Application US/09549090
; Patent No. 6465430
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; Barrett, Ronald W.
; Cwiria, Steven E.
; Duffin, David J.
; Gates, Christian
; Haselgen, Sherril S.
; Matheakis, Larry C.
; Schatz, Peter J.
; Wagstrom, Christopher R.
; Wrighton, Nicholas C.
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
; THROMBOPOIETIN RECEPTOR
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glaxo Wellcome
; STREET: Five Moore Drive, P.O. Box 13398
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/549,090
; FILING DATE: 13-Apr-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/973,225
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Hrubiec, Robert T.
; REGISTRATION NUMBER: 36,392
; REFERENCE/DOCKET NUMBER: PK3065USW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-248-1000
; INFORMATION FOR SEQ ID NO: 216:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 216:
US-09-549-090-216

Query Match      41.2%; Score 33; DB 4; Length 14;
Best Local Similarity 60.0%; Pred. No. 48;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      6 LQPPYVSWL 15
Db      3 LVGPSLSMWL 12

RESULT 8
US-09-832-230A-39
; Sequence 39, Application US/09832230A
; Patent No. 6506362
; GENERAL INFORMATION:
; APPLICANT: Dower, William J. et al
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
; RECEPTOR
; NUMBER OF SEQUENCES: 244
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glaxo Wellcome
; STREET: Five Moore Drive, P.O. Box 13398
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/832,230A
; FILING DATE: 10-Apr-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Hrubiec, Robert T.
; REGISTRATION NUMBER: 36,392
; REFERENCE/DOCKET NUMBER: PK3281
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-248-1000
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-832-230A-39

Query Match      41.2%; Score 33; DB 4; Length 14;
Best Local Similarity 60.0%; Pred. No. 48;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      6 LQPPYVSWL 15
Db      3 LVGPSLSMWL 12

RESULT 9
US-09-428-082B-67
; Sequence 67, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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OTHER INFORMATION: TPO-MIMETIC PEPTIDE
US-09-428-082B-67

Query Match 41.2%; Score 33; DB 4; Length 14;
Best Local Similarity 60.0%; Pred. No. 48;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 6 LQPPYVSWL 15
| | | : | | |
Db 3 LVGPSLMSWL 12

RESULT 10
US-08-856-663-12
; Sequence 12, Application US/08856663
; Patent No. 5849558
; GENERAL INFORMATION:
; APPLICANT: MORGAN, RICHARD
; APPLICANT: CHANG, ZHIYU
; TITLE OF INVENTION: DISCOVERY OF AND
; TITLE OF INVENTION: METHOD FOR CLONING AND PRODUCING THE
; TITLE OF INVENTION: PSPGI RESTRICTION ENDONUCLEASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: New England Biolabs, Inc.
; STREET: 32 Tozer Road
; CITY: Beverly
; STATE: MA
; COUNTRY: US
; ZIP: 01915
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/856,663
; FILING DATE: 15-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Gregory D
; REGISTRATION NUMBER: 30901
; REFERENCE/DOCKET NUMBER: NEB-127
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 978-927-5054
; TELEFAX: 978-927-1705
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-856-663-12

Query Match 40.0%; Score 32; DB 2; Length 11;
Best Local Similarity 75.0%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 LILQPPY 11
| | | | |
Db 2 LILTPPY 9

RESULT 11
US-08-764-640-37
; Sequence 37, Application US/08764640
; Patent No. 5869451
; Patent No. 5869451 5837683

GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Cwirla, Steven E.
; APPLICANT: Gates, Christian
; APPLICANT: Schatz, Peter J.
; APPLICANT: Balasubramanian, Palaniappan
; APPLICANT: Wagstrom, Christopher R.
; APPLICANT: Hendren, Richard W.
; APPLICANT: Deprince, Randolph B.
; APPLICANT: Poduturi, Surekha
; APPLICANT: Yin, Qun
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
; TITLE OF INVENTION: RECEPTOR
; NUMBER OF SEQUENCES: 244
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glaxo Wellcome
; STREET: Five Moore Drive, P.O. Box 13398
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/764,640
; FILING DATE: 11-DEC-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Hrubiec, Robert T.
; REGISTRATION NUMBER: 36,392
; REFERENCE/DOCKET NUMBER: PK3281
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-248-1000
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-764-640-37

Query Match 40.0%; Score 32; DB 2; Length 14;
Best Local Similarity 55.6%; Pred. No. 70;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 QGPPYVSWL 15
| | | | |
Db 3 QGPTLTAWL 11

RESULT 12
US-08-973-225-37
; Sequence 37, Application US/08973225A
; Patent No. 6083913
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Cwirla, Steven E.
; APPLICANT: Duffin, David J.
; APPLICANT: Gates, Christian
; APPLICANT: Haselden, Sherril S.
; APPLICANT: Mattheakis, Larry C.
; APPLICANT: Schatz, Peter J.
; APPLICANT: Wagstrom, Christopher R.
; APPLICANT: Wrighton, Nicholas C.
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
; TITLE OF INVENTION: THROMBOPOIETIN RECEPTOR
; NUMBER OF SEQUENCES: 232

;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Glaxo Wellcome
;/ STREET: Five Moore Drive, P.O. Box 13398
;/ CITY: Research Triangle Park
;/ STATE: NC
;/ COUNTRY: USA
;/ ZIP: 27709
;/
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/973,225A
;/ FILING DATE: 04-Dec-1997
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Hrubiec, Robert T.
;/ REGISTRATION NUMBER: 36,392
;/ REFERENCE/DOCKET NUMBER: PK3065USW
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 919-248-1000
;/ INFORMATION FOR SEQ ID NO: 37:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 14 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS: <Unknown>
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide
;/ SEQUENCE DESCRIPTION: SEQ ID NO: 37:
;/
;/ US-08-973-225-37
;/
;/ Query Match 40.0%; Score 32; DB 3; Length 14;
;/ Best Local Similarity 55.8%; Pred. No. 70;
;/ Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
;/
;/ QY 7 QGPPYVSWL 15
;/ ||| :||
;/ Db 3 QGPTLTAWL 11
;/
;/ RESULT 13
;/ US-09-244-298A-37
;/ Sequence 37, Application US/09244298A
;/ Patent No. 6121238
;/ GENERAL INFORMATION:
;/ APPLICANT: Dower, William J.
;/ APPLICANT: Barrett, Ronald W.
;/ APPLICANT: Cwirla, Steven E.
;/ APPLICANT: Gates, Christian
;/ APPLICANT: Schatz, Peter J.
;/ APPLICANT: Balasubramanian, Palaniappan
;/ APPLICANT: Wagstrom, Christopher R.
;/ APPLICANT: Hendren, Richard W.
;/ APPLICANT: Deprence, Randolph B.
;/ APPLICANT: Yin, Qun
;/ TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
;/ TITLE OF INVENTION: RECEPTOR
;/ NUMBER OF SEQUENCES: 244
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Glaxo Wellcome
;/ STREET: Five Moore Drive, P.O. Box 13398
;/ CITY: Research Triangle Park
;/ STATE: NC
;/ COUNTRY: USA
;/ ZIP: 27709
;/
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/09/244,298A
;/

;/ FILING DATE: 11-DEC-1996
;/ CLASSIFICATION: 514
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Hrubiec, Robert T.
;/ REGISTRATION NUMBER: 36,392
;/ REFERENCE/DOCKET NUMBER: PK3281
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 919-248-1000
;/ INFORMATION FOR SEQ ID NO: 37:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 14 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS:
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide
;/ US-09-244-298A-37
;/
;/ Query Match 40.0%; Score 32; DB 3; Length 14;
;/ Best Local Similarity 55.6%; Pred. No. 70;
;/ Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
;/
;/ QY 7 QGPPYVSWL 15
;/ ||| :||
;/ Db 3 QGPTLTAWL 11
;/
;/ RESULT 14
;/ US-09-516-704-37
;/ Sequence 37, Application US/09516704
;/ Patent No. 6251864
;/ GENERAL INFORMATION:
;/ APPLICANT: Dower, William J.
;/ APPLICANT: Barrett, Ronald W.
;/ APPLICANT: Cwirla, Steven E.
;/ APPLICANT: Gates, Christian
;/ APPLICANT: Schatz, Peter J.
;/ APPLICANT: Balasubramanian, Palaniappan
;/ APPLICANT: Wagstrom, Christopher R.
;/ APPLICANT: Hendren, Richard W.
;/ APPLICANT: Deprence, Randolph B.
;/ APPLICANT: Podduturi, Surekha
;/ TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
;/ TITLE OF INVENTION: RECEPTOR
;/ NUMBER OF SEQUENCES: 244
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Glaxo Wellcome
;/ STREET: Five Moore Drive, P.O. Box 13398
;/ CITY: Research Triangle Park
;/ STATE: NC
;/ COUNTRY: USA
;/ ZIP: 27709
;/
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/09/516,704
;/ FILING DATE: 01-Mar-2000
;/ CLASSIFICATION: <Unknown>
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Hrubiec, Robert T.
;/ REGISTRATION NUMBER: 36,392
;/ REFERENCE/DOCKET NUMBER: PK3281
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 919-248-1000
;/ INFORMATION FOR SEQ ID NO: 37:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 14 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS: <Unknown>
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide
;/

SEQUENCE DESCRIPTION: SEQ ID NO: 37;
US-09-516-704-37

Query Match 40.0%; Score 32; DB 3; Length 14;
Best Local Similarity 55.6%; Pred. No. 70;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 QGPPYVSWL 15
|||:|
Db 3 QGPTLTAWL 11

RESULT 15

US-09-549-090-37
; Sequence 37, Application US/09549090
; Patent No. 6465430

GENERAL INFORMATION:

APPLICANT: Dower, William J.
Barrett, Ronald W.
Cwirka, Steven E.
Duffin, David J.
Gates, Christian
Haselden, Sherril S.
Mattheakis, Larry C.
Schatz, Peter J.
Wagstrom, Christopher R.
Wrighton, Nicholas C.

TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
THROMBOPOIETIN RECEPTOR

NUMBER OF SEQUENCES: 232

CORRESPONDENCE ADDRESS:

ADDRESSEE: Glaxo Wellcome
STREET: Five Moore Drive, P.O. Box 13398
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/549,090

FILING DATE: 13-Apr-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/973,225

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Hrubiec, Robert T.

REGISTRATION NUMBER: 36,392

REFERENCE/DOCKET NUMBER: PK3065USW

TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-248-1000

INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 37:

US-09-549-090-37

Query Match 40.0%; Score 32; DB 4; Length 14;
Best Local Similarity 55.6%; Pred. No. 70;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 QGPPYVSWL 15
|||:|
Db 3 QGPTLTAWL 11

Search completed: November 14, 2004, 13:18:38
Job time : 23.3333 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2004, 13:32:33 ; Search time 22.5 Seconds
(without alignments)
59.868 Million cell updates/sec

Title: US-09-831-253F-7
Perfect score: 72
Sequence: 1 SNPSAFQVDITID 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues ;

Total number of hits satisfying chosen parameters: 2096

Minimum DB seq length: 0
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	34.7	11	2 S00616	parasporal crystal
2	25	34.7	11	2 B44854	L-2,4-diaminobutyr
3	23	31.9	13	2 A54326	glandular kallikre
4	22	30.6	12	2 A61360	vespakinin M - hor
5	22	30.6	14	2 PS0371	hypothetical prote
6	21	29.2	11	2 A40795	glycoprotein H-a -
7	21	29.2	12	2 S36899	ribosomal protein
8	21	29.2	13	2 PC2369	unidentified 85K p
9	20	27.8	9	2 S10784	enamelin i - bovin
10	20	27.8	11	2 PT0229	Ig heavy chain CDR
11	20	27.8	14	2 A59018	MUC1 enhancer bind
12	19	26.4	9	2 S36898	ribosomal protein
13	19	26.4	13	2 G22565	R-phycocerythrin ga
14	19	26.4	14	2 PT0077	proteochondritin c
15	19	26.4	14	2 A28018	very late antigen-
16	18	25.0	8	2 D47393	neuropeptide calla
17	18	25.0	11	2 PT0250	Ig heavy chain CDR
18	18	25.0	12	2 S70344	amine oxidase (cop
19	18	25.0	13	2 D20907	Ig kappa-1 chain J
20	18	25.0	14	2 S29209	avenin alpha-2 - o
21	18	25.0	14	2 B56884	Pax-QNR, long form
22	17	23.6	8	2 I49404	prealbumin - weste
23	17	23.6	9	2 PQ0914	MHC class I histoc
24	17	23.6	10	2 PA0050	protein QA100052 -
25	17	23.6	10	2 C39111	Ig heavy chain C r
26	17	23.6	10	2 B33710	ornithine decarbox
27	17	23.6	11	2 PS0275	NADH2 dehydrogenas
28	17	23.6	11	2 A34243	H-hyosophorin - Ja
29	17	23.6	12	2 PH0771	T-cell receptor be

30	17	23.6	12	2 PH1462	T-cell receptor be
31	17	23.6	12	2 PH1457	T-cell receptor be
32	17	23.6	13	2 S47361	T-cell antigen rec
33	17	23.6	13	2 S65612	tubulin alpha-chai
34	17	23.6	14	2 PH1615	Ig H chain V-D-J r
35	17	23.6	14	2 S07768	soluble hydrogenas
36	17	23.6	14	2 A61362	bradykinin-like pe
37	16	22.2	8	2 S71919	alcohol dehydrogen
38	16	22.2	10	2 PH0916	T-cell receptor be
39	16	22.2	11	2 A26930	ermg leader peptid
40	16	22.2	11	2 A61365	phyllokinin - Rohd
41	16	22.2	12	2 S26546	T-cell receptor be
42	16	22.2	12	2 PT0257	Ig heavy chain CDR
43	16	22.2	12	2 A61359	vespakinin x - hor
44	16	22.2	13	2 A61288	spore proteinase g
45	16	22.2	13	2 A33660	osteoclast functio

ALIGNMENTS

RESULT 1

S00616
parasporal crystal protein, wax moth-specific - Bacillus thuringiensis (strain galleriae
N/Alternate names: delta-endotoxin; parasporal crystal protein positive chain
C:Species: Bacillus thuringiensis
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C:Accession: S00616
R:Chestukhina, G.G.; Kostina, L.I.; Zalunin, I.A.; Khodova, O.M.; Stepanov, V.M.
FEBS Lett. 232, 249-251, 1988
A:Title: Bacillus thuringiensis ssp. galleriae simultaneously produces two delta-endotoxi
A:Reference number: S00615
A:Accession: S00616
A:Molecule type: protein
A:Residues: 1-11 <CHE>
A:Cross-references: UNIPROT:Q7M154
C:Comment: This toxin is effective against the larvae of Galleria melonella (greater wax
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 34.7%; Score 25; DB 2; Length 11;
Best Local Similarity 80.0%; Pred. No. 2e+02; Mismatches 1; Indels 0; Gaps 0;
Matches 4; Conservative 1;

QY 1 SNPYS 5
Db 5 NNPYS 9

RESULT 2

B44854
L-2,4-diaminobutyrate decarboxylase (EC 4.1.1.1.-) - Vibrio alginolyticus (fragment)
C:Species: Vibrio alginolyticus
C:Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: B44854; B41817
R:Yamamoto, S.; Tsuzaki, Y.; Tougou, K.; Shinoda, S.
J. Gen. Microbiol. 138, 1461-1465, 1992
A:Title: Purification and characterization of L-2,4-diaminobutyrate decarboxylase from A
A:Reference number: A44854; MUID:92381494; PMID:1512577
A:Accession: B44854
A:Molecule type: protein
A:Residues: 1-14 <YAM>
A:Cross-references: UNIPROT:Q9R5I8
A:Note: sequence extracted from NCBI backbone (NCBIP:112332)
C:Keywords: carbon-carbon lyase; carboxy-lyase

Query Match 34.7%; Score 25; DB 2; Length 14;
Best Local Similarity 55.6%; Pred. No. 2.6e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 5; Conservative 2;

QY 5 SAFQVDITII 13
Db 2 TAFEVDSNI 10

```

RESULT 3
A54326
glandular kallikrein-1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 29-Aug-1994 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995
C:Accession: A54326
R:Riegman, P.H.; Vlietstra, R.J.; van der Korput, H.A.; Romijn, J.C.; Trapman, J.
Mol. Cell. Endocrinol. 76, 181-190, 1991
A:Title: Identification and androgen-regulated expression of two major human glandular k
A:Reference number: A54326; MUID:92324494; PMID:1726490
A:Accession: A54326
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-13 <RIE>
A:Experimental source: prostate
A>Note: sequence extracted from NCBI backbone (NCBIP:108060)

Query Match 31.9%; Score 23; DB 2; Length 13;
Best Local Similarity 80.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNPS 5
DB 2 SHPS 6

RESULT 4
A61360
vespakinin M - hornet (Vespa mandarinia)
C:Species: Vespa mandarinia
C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
C:Accession: A61360
R:Kishimura, H.; Yasuhara, T.; Yoshida, H.; Nakajima, T.
Chem. Pharm. Bull. 24, 2896-2897, 1976
A:Title: Vespakinin-M, a novel bradykinin analogue containing hydroxyproline, in the ven
A:Reference number: A61360; MUID:77114342; PMID:1017116
A:Accession: A61360
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-12 <KIS>
A:Cross-references: UNIPROT:Q7M3T3
C:Superfamily: unassigned animal peptides
C:Keywords: hydroxyproline; venom
F,4/Modified site: 4-hydroxyproline (Pro) #status experimental

Query Match 30.6%; Score 22; DB 2; Length 12;
Best Local Similarity 42.9%; Pred. No. 7.7e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 YSAFQVD 10
DB 6 FSPFRID 12

RESULT 5
PS0371
hypothetical protein (psaC region) - Synecchococcus sp. (fragment)
C:Species: Synecchococcus sp.
C:Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 08-Oct-1999
C:Accession: PS0371
R:Rhie, E.; Stirewalt, V.L.; Gasparich, G.E.; Bryant, D.A.
Gene 112, 123-128, 1992
A:Title: The psaC genes of Synecchococcus sp. PCC7002 and Cyanophora paradoxa: cloning an
A:Reference number: JS0694; MUID:92201692; PMID:1551590
A:Accession: PS0371
A:Molecule type: DNA
A:Residues: 1-14 <RHI>
A:Cross-references: GB:M86238; NID:g154574; PIDN:AAA27351.1; PID:g552030

Query Match 30.6%; Score 22; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 9.2e+02;

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Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 7 FOVDIT 12
DB 4 FKLDVT 9

RESULT 6
A40795
glycoprotein H-a - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Apr-1992 #sequence_revision 10-Apr-1992 #text_change 31-Dec-1993
C:Accession: A40795
R:Christie, D.L.; Batchelor, D.C.; Palmer, D.J.
J. Biol. Chem. 266, 15679-15683, 1991
A:Title: Identification of kex2-related proteases in chromaffin granules by partial amin
A:Reference number: A40795; MUID:91340701; PMID:1874725
A:Accession: A40795
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-11 <CHR>
C:Keywords: glycoprotein

Query Match 29.2%; Score 21; DB 2; Length 11;
Best Local Similarity 30.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 YSAFQVDITI 13
DB 2 YDINEIDINV 11

RESULT 7
S36899
ribosomal protein S6 - Mycobacterium bovis (fragment)
C:Species: Mycobacterium bovis
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Jan-1995
C:Accession: S36899
R:Ohara, N.; Kimura, M.; Higashi, Y.; Yamada, T.
FEBS Lett. 331, 9-14, 1993
A:Title: Isolation and amino acid sequence of the 30S ribosomal protein S19 from Mycobact
A:Reference number: S36887; MUID:94009653; PMID:8405418
A:Accession: S36899
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-12 <OHA>
C:Keywords: protein biosynthesis; ribosome

Query Match 29.2%; Score 21; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 PYSAFQVD 10
DB 3 PYEIMWVD 10

RESULT 8
PC2369
unidentified 85K protein [imported] - Bacillus cereus (strain ts-4) (fragment)
C:Species: Bacillus cereus
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: PC2369
R:Matsumoto, K.; Miyamoto, T.; Yamaguchi, K.; Sayed, M.A.; Kajiwara, T.; Hatano, S.
BioSci. Biotechnol. Biochem. 59, 231-235, 1995
A:Title: Identification of DNA-binding proteins changed after induction of sporulation in
A:Reference number: PC2369; MUID:95218265; PMID:7766022
A:Accession: PC2369
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-13 <MAS>
A:Cross-references: UNIPROT:Q7M0L4

```


Query Match 29.2%; Score 21; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAF 7
DB 8 NPWAKF 13

RESULT 9
S10784
enamelin i - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
C:Accession: S10784
R:Strawich, E.; Glimcher, M.J.
Eur. J. Biochem. 191, 47-56, 1990
A:Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is also
A:Reference number: S10780; PMID:90336641; PMID:2379503
A:Accession: S10784
A:Molecule type: protein
A:Residues: 1-9 <STR>
A:Cross-references: UNIPROT:O7M2M7
C:Keywords: enamel; phosphoprotein

Query Match 27.8%; Score 20; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 PYSAF 7
DB 2 PYDGF 6

RESULT 10
PT0229
Ig heavy chain CDR3 region (clone 1-115) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0229
R:Yanada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: PT0222; PMID:91108337; PMID:1899102
A:Accession: PT0229
A:Molecule type: DNA
A:Residues: 1-11 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 27.8%; Score 20; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NPY 4
DB 2 NPY 4

RESULT 11
A59018
MUC1 enhancer binding protein 70K chain MUC1EBP-70 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 08-May-1998
C:Accession: A59018
R:Abel, M.; Smith, C.J.; Larson, C.J.
submitted to the Protein Sequence Database, May 1998
A:Description: Involvement of "Ku-like" proteins in the transcription of MUC1/DF3, a bre
A:Reference number: A59018
A:Accession: A59018
A:Molecule type: protein
A:Residues: 1-14 <ABE>
A:Experimental source: breast cancer cell line MCF-7

Query Match 27.8%; Score 20; DB 2; Length 14;
Best Local Similarity 33.3%; Pred. No. 2.1e+03;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 SNPYSAFQV 9
DB 2 SQIYGSVQI 10

RESULT 12
S36898
ribosomal protein S8 - Mycobacterium bovis (fragment)
C:Species: Mycobacterium bovis
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Jan-1995
C:Accession: S36898
R:Ohara, N.; Kimura, M.; Higashi, Y.; Yamada, T.
FEBS Lett. 331, 9-14, 1993
A:Title: Isolation and amino acid sequence of the 30S ribosomal protein S19 from Mycobact
A:Reference number: S36887; PMID:94009653; PMID:8405418
A:Accession: S36898
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <OHA>
C:Keywords: protein biosynthesis; ribosome

Query Match 26.4%; Score 19; DB 2; Length 9;
Best Local Similarity 42.9%; Pred. No. 2.8e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNPYSAF 7
DB 3 TDPIAAF 9

RESULT 13
G22565
R-phycoerythrin gamma-B chain - red alga (Gastrocloonium coulteri) (fragment)
C:Species: Gastrocloonium coulteri
C:Date: 07-Mar-1998 #sequence_revision 07-Mar-1998 #text_change 09-Jul-2004
C:Accession: G22565
R:Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A:Reference number: A22565; PMID:85182601; PMID:3886644
A:Accession: G22565
A:Molecule type: protein
A:Residues: 1-13 <KLO>
A:Cross-references: UNIPROT:Q7M268

Query Match 26.4%; Score 19; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 1e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 PYSAFQ 8
DB 7 PQAAFE 12

RESULT 14
PT0077
proteochondroitin core protein - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 04-Sep-1998
C:Accession: PT0077
R:Marcum, J.A.; Thompson, M.A.
Biochem. Biophys. Res. Commun. 175, 706-712, 1991
A:Title: The amino-terminal region of a proteochondroitin core protein, secreted by aort
om human bone.
A:Reference number: PT0077; PMID:91207372; PMID:2018513
A:Accession: PT0077

A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-14 <MAR>
C;Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan

Query Match 26.4%; Score 19; DB 2; Length 14;
Best Local Similarity 60.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 DITID 14
| | |
Db 10 DFTLD 14

RESULT 15
A28018
very late antigen-1 alpha chain - human (fragment)
N;Alternate names: VIA-1 alpha chain
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 12-May-1994
C;Accession: A28018
R;Takada, Y.; Strominger, J.L.; Hemler, M.E.
Proc. Natl. Acad. Sci. U.S.A. 84, 3239-3243, 1987
A;Title: The very late antigen family of heterodimers is part of a superfamily of molecu
A;Reference number: A94151; MUID:87204112; PMID:3033641
A;Accession: A28018
A;Molecule type: protein
A;Residues: 1-14 <TRK>
C;Keywords: duplication; heterodimer; membrane protein

Query Match 26.4%; Score 19; DB 2; Length 14;
Best Local Similarity 60.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 FQVDI 11
| | |
Db 1 FNVDV 5

Search completed: November 14, 2004, 13:45:47
Job time : 22.5 secs

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OM protein - protein search, using sw model

Run on: November 14, 2004, 13:18:48 ; Search time 110.5 Seconds
(without alignments)
45.450 Million cell updates/sec

Title: US-09-831-253F-7

Perfect score: 72

Sequence: 1 SNPSAFQVDITID 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 359729299 residues

Total number of hits satisfying chosen parameters: 543373

Minimum DB seq length: 0
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Query Match	Length	DB ID	Description
1	72	100.0	14	3	AAY92951 Transform
2	72	100.0	14	3	AAY93099 Transform
3	28	38.9	10	5	ABP47086 Human Bly
4	28	38.9	10	7	ADG97913 scFV VHCD
5	28	38.9	13	3	AAB10012 H. pylori
6	28	38.9	13	4	AAB86092 H. pylori
7	28	38.9	13	4	AAB86060 H. pylori
8	27	37.5	11	7	ADH48572 ATP-depen
9	27	37.5	11	5	ABP46828 Human Bly
10	27	37.5	11	7	ADG97655 scFV VHCD
11	27	37.5	12	7	ADG44449 Endotheli
12	27	37.5	14	2	AAR67117 Anti-infl
13	27	37.5	14	3	AAY99306 HLA class
14	27	37.5	14	3	AAY99201 HLA class
15	27	37.5	14	3	AAY99305 HLA class
16	26.5	36.8	10	6	ABP60532 APRIL bin
17	26	36.1	7	2	AAR83019 Calcium-i
18	26	36.1	7	2	AAW01480 Calcium-i
19	26	36.1	7	2	AAW13164 Ca-indepe
20	26	36.1	7	2	AAW17850 Cytosolic
21	26	36.1	7	2	AAW81826 Phospholi
22	26	36.1	7	5	ABB82216 Calcium i
23	26	36.1	7	8	ADN08708 Cotton wi
24	26	36.1	9	2	AAY55426 HLA bindi
25	26	36.1	9	2	AAY55528 HLA bindi

26	26	36.1	13	4	AAB88035	AAB88035	CD66, pept
27	26	36.1	14	2	AAR21773	AAR21773	MHC bindi
28	26	36.1	14	3	AAY99258	AAY99258	HLA class
29	26	36.1	14	3	AAY99308	AAY99308	HLA class
30	25	34.7	7	8	ADH68251	ADH68251	Human G-p
31	25	34.7	8	2	AAR35820	AAR35820	Hepatitis
32	25	34.7	8	2	AAR35821	AAR35821	Hepatitis
33	25	34.7	9	2	AAW49445	AAW49445	Human leu
34	25	34.7	9	4	AAB86080	AAB86080	H. pylori
35	25	34.7	9	4	AAB86048	AAB86048	H. pylori
36	25	34.7	9	6	ABR18651	ABR18651	Human can
37	25	34.7	9	6	ABR17659	ABR17659	Human can
38	25	34.7	9	6	ABR07147	ABR07147	Human can
39	25	34.7	9	6	ABR07334	ABR07334	Human can
40	25	34.7	9	6	ABR18452	ABR18452	Human can
41	25	34.7	9	7	ADD94198	ADD94198	Mouse HUI
42	25	34.7	10	4	AAG96234	AAG96234	Human com
43	25	34.7	10	6	ABR17761	ABR17761	Human can
44	25	34.7	10	6	ABR18701	ABR18701	Human can
45	25	34.7	10	6	ABR17498	ABR17498	Human can

ALIGNMENTS

RESULT 1

AA92951
ID AAY92951 standard; peptide; 14 AA.

XX AAY92951;

XX 08-NOV-2000 (first entry)

XX Transforming growth factor inhibitory peptide #7.

XX Hepatotropic; antagonist; transforming growth factor beta1; TGF-beta1;
XX competitive inhibition; collagen synthesis stimulation inhibitor; liver;
XX extracellular matrix degradation inhibitor; mimotope; cirrhosis.

XX Homo sapiens.

XX WO2000031135-A1.

XX 02-JUN-2000.

XX 23-NOV-1999; 99WO-ES000375.

XX 24-NOV-1998; 98ES-00002465.

XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.

XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
XX Borrás Cuesta F;

XX WPI; 2000-411935/35.

XX Peptides that antagonize binding of transforming growth factor beta1,
XX useful for treatment of liver disease, especially cirrhosis, are partial
XX sequences of the factor or its receptors.

XX Claim 8; Page 82; 86pp; Spanish.

XX The invention relates to synthetic peptides that antagonise the binding
XX of transforming growth (TGF) factor beta1 (TGF-beta1) to its receptor in
XX vivo which have partial amino acid sequences identical, or similar, with
XX those of TGF-beta1 and/or its receptors. Peptides AAY92945-93133 represent
XX examples of the peptides of the invention. The peptides act by
XX competitive inhibition of the binding of TGF-beta1 to its receptors, e.g.
XX they are inhibitors of stimulation of collagen synthesis in liver cells
XX and inhibitors of synthesis of proteolytic enzymes able to degrade the
XX extracellular matrix. The peptides, their mimetopes and/or DNA (or
XX expression systems) encoding the peptides are used for treatment of liver
XX disease, specifically cirrhosis

XX	SQ	Sequence 14 AA;
XX	Query Match	100.0%; Score 72; DB 3; Length 14;
XX	Best Local Similarity	100.0%; Pred. No. 1.2e-06;
XX	Matches 14; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 SNPSAFQVDITID 14	
DB	1 SNPSAFQVDITID 14	
RESULT 2		
AAAY93099		
ID	AAAY93099 standard; peptide; 14 AA.	
XX	AC	ABP47086;
XX	DT	19-AUG-2002 (first entry)
DE	Human BlyS binding scFv VH CDR3 SEQ ID 3097.	
KW	BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;	
KW	tumour necrosis factor; B cell proliferation; B cell differentiation;	
KW	immunosuppressive; immunostimulant; immunomodulatory; antineumatic;	
KW	antiAIDS; vaccine; immune; autoimmune disorder; immunodeficiency;	
KW	systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;	
KW	common variable immunodeficiency; acquired immunodeficiency syndrome.	
OS	Homo sapiens.	
XX	WO200202641-AI.	
PN	10-JAN-2002.	
PF	15-JUN-2001; 2001WO-US019110.	
PR	16-JUN-2000; 2000US-0212210P.	
PR	17-OCT-2000; 2000US-0240816P.	
PR	16-MAR-2001; 2001US-0276248P.	
PR	21-MAR-2001; 2001US-0277379P.	
PR	25-MAY-2001; 2001US-0293499P.	
XX	(HUMA-) HUMAN GENOME SCI INC.	
PA	(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.	
PI	Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;	
XX	WPI; 2002-114799/15.	
PT	Antibodies against B Lymphocyte Stimulating polypeptides, useful for the	
XX	diagnosis and treatment of cancers and immune disorders.	
PS	Claim 2; Page 3114; 3148pp; English.	
CC	This invention describes novel antibodies that immunospecifically bind to	
CC	B Lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the	
CC	tumour necrosis factor (TNF) super family and induces B cell	
CC	proliferation and differentiation. The antibodies of the invention have	
CC	cytostatic, immunosuppressive, immunostimulant, immunomodulatory,	
CC	antirheumatic and antiAIDS activity and can be used in vaccines to	
CC	inhibit the expression and activity of BlyS. The antibodies bind to BlyS	
CC	and so may be used to detect and quantitate the presence of BlyS in	
CC	biological samples and may be used in this way to diagnose disease	
CC	associated with aberrant expression of BlyS. They may also be	
CC	administered to treat diseases associated with aberrant BlyS expression	
CC	and activity such as cancer, immune, and autoimmune disorders and	
CC	diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,	
CC	immunodeficiency (e.g. common variable immunodeficiency (CVID) and	
CC	acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent	
CC	the antibodies and fragments of the antibodies described in the method of	
CC	the invention	
XX	.Sequence 10 AA;	
SQ	Query Match	38.9%; Score 28; DB 5; Length 10;
SQ	Best Local Similarity	50.0%; Pred. No. 1.8e+02;
SQ	Matches 4; Conservative	2; Mismatches 2; Indels 0; Gaps 0;
QY	2 NPYSAFQV 9	
DB	3 SPYDAFDI 10	
RESULT 4		
ADG97913		

ID ADG97913 standard; peptide; 10 AA.
AC ADG97913;
XX
DT
XX
DE 11-MAR-2004 (first entry)
XX
DE scFV VHCDR3 peptide that immunospecifically binds BlyS SeqID 3097.
XX
KW antibody; B lymphocyte stimulator; BlyS; tumour necrosis factor;
XX B cell proliferation; differentiation; scFv; myasthenia gravis;
KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KW carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
KW antiinflammatory; antiasthmatic; antiallergic; cytostatic.
XX
OS Unidentified.
XX
XX WO2003055979-A2.
XX
XX 10-JUL-2003.
XX
XX 14-NOV-2002; 2002WO-US036496.
XX
XX 16-NOV-2001; 2001US-0331469P.
XX
XX 19-DEC-2001; 2001US-0340817P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
XX
XX WPI; 2003-505530/47.
XX
XX Novel antibody that immunospecifically binds to a B lymphocyte stimulator
XX (BlyS), useful for detecting and treating diseases or disorders e.g.
XX rheumatoid arthritis, asthma and leukemia.
XX
XX Example 1; SEQ ID NO 3097; 394pp; English.
XX
XX This invention relates to novel antibodies that immunospecifically bind
XX to B lymphocyte stimulator (BlyS). The BlyS gene has been mapped to
XX chromosome 13q34 and encodes a protein that is a member of the tumour
XX necrosis factor superfamily and induces both in vivo and in vitro B cell
XX proliferation and differentiation. Specifically, it refers to single
XX chain antibody molecules (scFvs) derived, preferably, from the variable
XX heavy CDR3 region that immunospecifically bind to a polypeptide, or
XX fragment thereof, of either human, murine, rat or monkey BLYS. The
XX present invention refers to the use of such antibodies in various methods
XX for the detection, diagnosis and prognosis of diseases related to the
XX aberrant expression or inappropriate function of BlyS or its receptor. As
XX such, these compositions are useful for identifying immune disorders
XX including myasthenia gravis and multiple sclerosis, inflammatory
XX disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
XX as AIDS and proliferative disorders including leukaemia, carcinoma and
XX lymphoma. Accordingly, they can be described as exhibiting various
XX activities such as antirheumatic, antiarthritic, neuroprotective,
XX antiinflammatory, antiasthmatic, antiallergic and cytostatic. This
XX peptide sequence is a single chain antibody variable heavy CDR3 peptide
XX that immunospecifically binds BlyS of the invention.
XX
XX Sequence 10 AA;
XX
XX Query Match 38.9%; Score 28; DB 7; Length 10;
XX Best Local Similarity 50.0%; Pred. No. 1.8e+02;
XX Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 2 NPYSAFQV 9
XX :||| :
XX 3 SPYDAFDI 10
XX
XX DB
XX
XX RESULT 5
XX AAB10012
XX ID AAB10012 standard; protein; 13 AA.
XX
XX AC

AC AAB10012;
XX
XX 01-NOV-2000 (first entry)
XX
XX H. pylori beta-urease-binding antibody heavy chain CDR3 protein #2.
XX
XX Acid-resistant microorganism; detection; faecal; intestine; infection;
XX monoclonal antibody; heavy chain; complementarity determining region;
XX CDR; beta-urease.
XX
XX Unidentified.
XX
XX WO200026671-A1.
XX
XX 11-MAY-2000.
XX
XX 29-OCT-1999; 99WO-EP008212.
XX
XX 29-OCT-1998; 98EP-00120517.
XX
XX 06-NOV-1998; 98EP-00120697.
XX
XX (CONN-) CONNEX GMBH.
XX
XX Reiter C, Cullmann G, Friedrichs U, Heppner P, Lakner M;
XX Ringels A;
XX
XX WPI; 2000-365747/31.
XX
XX N-PSDB; AAA40168.
XX
XX Detecting infection by acid-fast microbes for diagnosis of Helicobacter
XX pylori, comprises reacting a fecal sample with two binding reagents for
XX antigens that survive intestinal passage.
XX
XX Claim 26; Page 22; 84pp; German.
XX
XX This invention describes a novel method for the detection of a mammalian
XX infection by an acid-resistant microorganism (A) by treating a faecal
XX sample with at least two different monoclonal antibodies (MAB) for their
XX fragments or derivatives) or aptamers (collectively (I)) and detecting
XX formation of a complex (C) between (I) and the corresponding antigen of
XX (A). The first and second (I) bind to epitopes of different antigens
XX (Ag). These epitopes are present, after passage through the intestines,
XX in at least some mammals, and have either: (i) their native structure; or
XX (ii) a structure against which an antibody is produced by an animal
XX infected or immunized with (A), or its extract, lysate, derived protein
XX or fragment, or with a synthetic peptide. Practically all mammals display
XX at least one of the specified epitopes. The method is used to detect
XX infection by acid-fast bacteria, particularly of the genera Helicobacter,
XX Mycobacterium and Campylobacter, specifically H. pylori, H. hepaticus, M.
XX tuberculosis, C. jejuni and C. pylori. (I) may also be used
XX therapeutically. The method is direct and non-invasive, and provides an
XX inexpensive and easily standardizable diagnosis, despite possible
XX degradation of antigens during passage through the intestines. This
XX sequence represents a fragment of a H. pylori beta-urease-binding
XX antibody heavy chain complementarity determining region CDR3 which is
XX used to illustrate the method of the invention
XX
XX Sequence 13 AA;
XX
XX Query Match 38.9%; Score 28; DB 3; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 SNPYS 5
XX :||| :
XX 6 SNPYS 10
XX
XX DB
XX
XX RESULT 6
XX AAB86092
XX ID AAB86092 standard; peptide; 13 AA.
XX
XX AC AAB86092;

XX 17-JUL-2001 (first entry)
 XX H. pylori beta-urease derived antibody light chain CDR3 #1.
 XX Catalase; beta-urease; antibody; antigen; detection; infection; epitope;
 KW acid-resistant microorganism; complementarity determining region; CDR;
 KW feces; heavy chain; light chain.
 XX Unidentified.
 XX WO200127612-A2.
 XX 19-APR-2001.
 XX 12-OCT-2000; 2000WO-EP010057.
 XX 12-OCT-1999; 99EP-00120351.
 PR 16-MAR-2000; 2000EP-00105592.
 PR 31-MAR-2000; 2000EP-00107028.
 PR 10-MAY-2000; 2000EP-00110110.
 XX (CONN-) CONNEX GES OPTIMIERUNG VON FORSCHUNG & E.
 PA Reiter C, Cullmann G, Lakner M, Truee A, Dehnert S, Schwartz G;
 PI WPI; 2001-282086/29.
 DR N-PSDB; AAF88119.
 XX Detecting infections by acid-resistant microorganisms, particularly for
 PT diagnosing Helicobacter pylori, comprises immunochromatographic detection
 PT of antigen in feces.
 XX Claim 27; Page 27; 90pp; German.
 XX This invention describes a novel method for detecting infection by an
 CC acid-resistant microorganism (A), in a mammal, using
 CC immunochromatography. The method is used to diagnose infection by an acid
 CC -resistant microorganism (A), in a mammal, such as Helicobacter,
 CC Campylobacter or Mycobacterium, particularly H. pylori (most preferred),
 CC H. hepatica, C. jejuni and M. tuberculosis. The method is rapid, simple,
 CC inexpensive and non-invasive, and may indicate the stage of infection. A
 CC test strip used in the method may include a filter to eliminate particles
 CC present in the sample and only a single receptor provides a reasonably
 CC secure diagnosis, with specificity and selectivity improved by detecting
 CC several epitopes (of catalase) or different antigens (catalase and beta-
 CC urease). The method can be automated. This sequence represents a
 CC complementarity determining region (CDR) from an antibody raised against
 CC the H. pylori catalase or beta-urease antigen which is used to illustrate
 CC the method of the invention
 XX Sequence 13 AA;
 SQ Query Match 38.9%; Score 28; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.5e-02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SNPS 5
 Db |||||
 6 SNPS 10
 RESULT 7
 AAB86060
 ID AAB86060 standard; peptide; 13 AA.
 XX AAB86060;
 XX 17-JUL-2001 (first entry)
 DT H. pylori beta-urease derived antibody light chain CDR3 #1.
 DE Heavy chain; light chain; catalase; beta-urease; detection; CDR; antigen;
 KW

KW infection; acid-resistant microorganism; fecal; antibody; diagnosis;
 KW antibacterial; complementarity determining region.
 XX Unidentified.
 XX WO200127613-A2.
 XX 19-APR-2001.
 XX 12-OCT-2000; 2000WO-EP010058.
 XX 12-OCT-1999; 99EP-00120351.
 PR 16-MAR-2000; 2000EP-00105592.
 PR 31-MAR-2000; 2000EP-00107028.
 PR 10-MAY-2000; 2000EP-00110110.
 XX (CONN-) CONNEX GES OPTIMIERUNG VON FORSCHUNG & E.
 PA Reiter C, Cullmann G, Heppner P, Ringels A, Mueller H, Haindl E;
 PI WPI; 2001-282087/29.
 DR N-PSDB; AAF88062.
 XX Detecting infections by acid-resistant microorganisms, particularly for
 PT diagnosing Helicobacter pylori, comprises an immunoassay on a fecal
 PT sample.
 XX Claim 23; Page 17; 89pp; German.
 XX This invention describes a novel method for detecting, in a mammal,
 CC infection by an acid-resistant microorganism (A) which comprises reacting
 CC a fecal sample with: (i) a receptor (R) such that a complex is formed
 CC with an antigen (Ag) of (A); or (ii) two different R so that a three-part
 CC complex is formed with Ag, and the formation of a complex detected. R are
 CC specific for an Ag which, after passage through the intestines, at least
 CC in some mammals, retains a native (or corresponding) structure against
 CC which the mammal produces antibodies (when immunized or infected with
 CC (A), or its extracts, lysates or derived proteins (or fragments) or
 CC synthetic peptides). The products of the invention have antibacterial
 CC activity. The method is used to diagnose infection by Helicobacter,
 CC Campylobacter or Mycobacterium, particularly H. pylori (most preferred),
 CC H. hepatica, C. jejuni and M. tuberculosis, and also to monitor the
 CC progress of treatment. Receptors, particularly antibodies, directed
 CC against Ag can be used therapeutically for treatment of infections. The
 CC method requires only one R to provide a reasonably secure diagnosis
 CC (although use of two R improves sensitivity), so is relatively
 CC inexpensive and more easily standardized. Also it is direct, non-
 CC invasive, suitable for automation and may indicate the stage of an
 CC infection. This sequence represents a complementarity determining region
 CC (CDR) from an antibody generated against a Helicobacter pylori antigen
 CC (catalase or beta-urease) which is used to illustrate the method of the
 CC invention
 XX Sequence 13 AA;
 SQ Query Match 38.9%; Score 28; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.5e-02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SNPS 5
 Db |||||
 6 SNPS 10
 RESULT 8
 ADH48572
 ID ADH48572 standard; peptide; 10 AA.
 XX ADH48572;
 XX 25-MAR-2004 (first entry)
 DT ATP-dependant Clp proteinase (clpL) epitopic peptide #SEQ ID 12.
 XX

XX Antimicrobial; immunostimulant; gene therapy;
 KW ATP-dependent Clp protease; proline dipeptidase; chorismate mutase;
 KW aminotransferase; serine hydroxymethyltransferase;
 KW O-acetylserine sulphydrolase B; translocase; tRNA methyltransferase;
 KW 3-dehydroquinate synthase.
 XX Staphylococcus aureus.
 OS WO2003025005-A2.
 PN 27-MAR-2003.
 PD 20-SEP-2002; 2002WO-CA001426.
 XX 21-SEP-2001; 2001US-0324135P.
 PR 21-SEP-2001; 2001US-0324139P.
 PR 27-SEP-2001; 2001US-0325333P.
 PR 28-SEP-2001; 2001US-0325836P.
 PR 25-OCT-2001; 2001US-0338235P.
 PR 25-OCT-2001; 2001US-0343758P.
 PR 26-OCT-2001; 2001US-0340531P.
 PR 30-OCT-2001; 2001US-0340945P.
 PR 06-NOV-2001; 2001US-0333281P.
 PR 31-JUL-2002; 2002US-0399926P.
 XX (AFFI-) AFFINIUM PHARM INC.
 PA Edwards A, Dharamsi A, Vedadi M, Alam MZ, Awrey D, Beattie B;
 PI Canadien V, Domagala M, Kanagarajah D, Li Q, Mansoury K, Necakov S;
 PI Netherly K, Ng I, Pinder B, Sheldrick B, Vallee F, Viola C;
 PI Wrezel O;
 XX WPI; 2003-371794/35.
 DR New crystallized recombinant polypeptides and polynucleotides encoding
 PT them, useful in developing antimicrobial agents for treating or
 PT preventing infection or contamination, or for inducing an immunological
 PT response.
 XX Disclosure; SEQ ID NO 12; 172pp; English.
 PS The invention relates to a novel crystallised recombinant polypeptide
 XX (I). The polypeptide of the invention has at least one biological
 CC activity of ATP-dependent Clp protease, proline dipeptidase, chorismate
 CC mutase homology, branched-chain amino acid aminotransferase or serine
 CC hydroxymethyltransferase from Staphylococcus aureus, O-acetylserine
 CC sulhydrylase B from Escherichia coli, preprotein translocase secretion
 CC protein or tRNA methyltransferase from Helicobacter pylori, or 3-
 CC dehydroquinate synthase from Streptococcus pneumoniae. Nucleic acids
 CC encoding polypeptides of the invention are useful in antisense therapy,
 CC as diagnostic agents to detect the presence of the target DNA or RNA
 CC sequences to which the specifically bind, and in producing recombinant
 CC polypeptides. The polypeptides are useful for producing specific
 CC antibodies which protect against invasion of bacteria, in identifying
 CC compounds which modulate the action of the polypeptides, and in
 CC developing antimicrobial agents for treating or preventing infection or
 CC contamination. The nucleic acids and polypeptides may also be used for
 CC inducing an immunological response. Sequences given in ADH48561-ADH48641
 CC represent polypeptides and polynucleotides that are identified in the
 CC scope of the invention as microbial target sequences, peptide fragments
 CC of the proteins, and primers used for their amplification.
 XX Sequence 10 AA;
 SQ

Query Match 37.5%; Score 27; DB 7; Length 10;
 Best Local Similarity 55.6%; Pred. No. 2.8e+02;
 Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 NPYSAFQVD 10
 |||||
 DB 2 NPYSVILFD 10

RESULT 9
 ABP46828
 ID ABP46828 standard; peptide; 11 AA.
 XX
 AC ABP46828;
 XX
 DT 19-AUG-2002 (first entry)
 XX
 DE Human Blys binding scFv VH CDR3 SEQ ID 2839.
 XX
 KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX Homo sapiens.
 OS WO200202641-A1.
 PN 10-JAN-2002.
 PD 15-JUN-2001; 2001WO-US019110.
 XX 16-JUN-2000; 2000US-0212210P.
 PR 17-OCT-2000; 2000US-0240816P.
 PR 16-MAR-2001; 2001US-0276248P.
 PR 21-MAR-2001; 2001US-0277379P.
 PR 25-MAY-2001; 2001US-0293499P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 PI WPI; 2002-114799/15.
 DR Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
 PT diagnosis and treatment of cancers and immune disorders.
 PT Claim 2; Page 3062; 3148pp; English.
 XX This invention describes novel antibodies that immunospecifically bind to
 CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention
 XX Sequence 11 AA;
 SQ

Query Match 37.5%; Score 27; DB 5; Length 11;
 Best Local Similarity 57.1%; Pred. No. 3.1e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 PYSAFQV 9
 |||||
 DB 5 PYDAFDI 11

RESULT 10
ADG97655
ID ADG97655 standard; peptide; 11 AA.
AC ADG97655;
XX ADG97655;
XX 11-MAR-2004 (first entry)
XX scFV VHCDR3 peptide that immunospecifically binds Blys SeqID 2839.
DE antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
XX B cell proliferation; differentiation; scFv; myasthenia gravis;
XX multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KW carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
KW antiinflammatory; antiasthmatic; antiallergic; cytostatic.
XX Unidentified.
OS
XX WO2003055979-A2.
PN
XX 10-JUL-2003.
PD
XX 14-NOV-2002; 2002WO-US036496.
XX
XX 16-NOV-2001; 2001US-0331469P.
PR
XX 19-DEC-2001; 2001US-0340817P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
PI WPI; 2003-505530/47.
XX
XX Novel antibody that immunospecifically binds to a B lymphocyte stimulator
PT (Blys), useful for detecting and treating diseases or disorders e.g.
PT rheumatoid arthritis, asthma and leukemia.
XX
XX Example 1; SEQ ID NO 2839; 394pp; English.
PS
XX This invention relates to novel antibodies that immunospecifically bind
CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
CC chromosome 13q34 and encodes a protein that is a member of the tumour
CC necrosis factor superfamily and induces both in vivo and in vitro B cell
CC proliferation and differentiation. Specifically, it refers to single
CC chain antibody molecules (scFvs) derived, preferably, from the variable
CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
CC fragment thereof, of either human, murine, rat or monkey Blys. The
CC present invention refers to the use of such antibodies in various methods
CC for the detection, diagnosis and prognosis of diseases related to the
CC aberrant expression or inappropriate function of Blys or its receptor. As
CC such, these compositions are useful for identifying immune disorders
CC including myasthenia gravis and multiple sclerosis, inflammatory
CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC as AIDS and proliferative disorders including leukaemia, carcinoma and
CC lymphoma. Accordingly, they can be described as exhibiting various
CC activities such as antirheumatic, antiallergic and cytostatic. This
CC antiinflammatory, antiasthmatic, antiallergic and cytostatic. This
CC peptide sequence is a single chain antibody variable heavy CDR3 peptide
CC that immunospecifically binds Blys of the invention.
XX
SQ Sequence 11 AA;
Query Match 37.5%; Score 27; DB 7; Length 11;
Best Local Similarity 57.1%; Pred. No. 3.1e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 3 PYSAFQV 9
Db 5 PYDAFDI 11
RESULT 11
ADG44449

ID ADC44449 standard; peptide; 12 AA.
XX ADC44449;
AC ADC44449;
XX 18-DEC-2003 (first entry)
XX Endothelial cell binding peptide SEQ ID NO:177.
XX
XX endothelial cell binding protein; EGBP; anti-tumour; cytostatic;
KW vasotropic; antiporiatic; dermatological; ophthalmological;
KW antidiabetic; antiarthritic; vulnary; antiulcer; antiinflammatory;
KW antibacterial; gynaecological; angiogenesis.
XX Synthetic.
OS
XX WO2003037172-A2.
PN
XX 08-MAY-2003.
XX
XX 01-NOV-2002; 2002WO-US035258.
XX
XX 01-NOV-2001; 2001US-0334822P.
PR (GPCB-) GPC BIOTECH INC.
XX
XX Gyuris J, Lamphere L, Morris AJ, Tsaioun K;
PI WPI; 2003-482072/45.
XX
XX Novel synthetic or recombinant polypeptide useful for promoting, reducing
PT proliferation and/or migration of endothelial cells, and for modulating
PT angiogenesis, has endothelial cell binding protein sequences.
XX
PS Claim 3; SEQ ID NO 177; 126pp; English.
XX
XX The invention relates to a novel isolated, synthetic or recombinant
CC peptide or polypeptide which includes one or more endothelial cell
CC binding protein (EGBP) sequences. A peptide of the invention has anti-
CC tumour, cytostatic, vasotropic, antiporiatic, dermatological,
CC ophthalmological, antidiabetic, antiarthritic, vulnary, antiulcer,
CC antiinflammatory, antibacterial, and gynaecological activity. The peptide
CC is useful for promoting, reducing the proliferation and/or migration of
CC endothelial cells, by treating the cells with an EGBP agonist, which is
CC preferably the peptide, to promote proliferation and/or migration of the
CC treated cells, and for reducing or promoting angiogenesis, by treating
CC the cells with an EGBP antagonist, which is preferably the peptide of the
CC invention. A peptide of the invention is also useful for manufacturing a
CC medicament for promoting angiogenesis, by admixing an EGBP agonist or
CC EGBP antagonist to promote or reduce angiogenesis at one or more sites in
CC a treated mammal. The medicament is useful for promoting or reducing
CC angiogenesis. EGBP sequences are useful to alter the infectivity spectrum
CC of a viral particle. The present sequence represents an EGBP of the
CC invention.
XX
SQ Sequence 12 AA;
Query Match 37.5%; Score 27; DB 7; Length 12;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 SNFYSA 6
Db 1 SNFWSA 6
RESULT 12
AAR67117
ID AAR67117 standard; peptide; 14 AA.
XX
XX AAR67117;
AC
XX 25-MAR-2003 (revised)
DT 30-JUN-1995 (first entry)

KW allograft rejection; allergy; lyme disease; hepatitis; prostate cancer;
 KW glomerulonephritis; food hypersensitivity; malaria.
 XX Unidentified.
 XX WO9961916-A1.
 XX 02-DEC-1999.
 XX 28-MAY-1999; 99WO-US012066.
 XX 29-MAY-1998; 98US-0087192P.
 XX (EPIM-) EPIMUNE INC.
 XX Sette A, Southwood S, Sidney J;
 XX WPI; 2000-097143/08.
 XX New compositions containing immunogenic peptide epitopes for various HLA
 XX class II DR molecules useful for inducing helper T cell response.
 XX Claim 1; Page 46; 60pp; English.

CC The present invention relates to a new pharmaceutical composition
 CC comprising a unit dose form of a peptide, or analogue, comprising an
 CC epitope selected from those represented by peptides AAY9812-Y99339 which
 CC are derived from various antigens for various human leucocyte antigen
 CC class DR molecules, representative of the world wide population. The
 CC peptide/analogue binds to an HLA class II molecule at an IC-50 of less
 CC than or equal to 1,000 nM. The pharmaceutical can be used to induce a
 CC helper T cell response. The pharmaceutical focuses the immune response
 CC towards selected determinants and could therefore be used in cases of
 CC chronic viral diseases and cancer. Examples of diseases that can be
 CC treated using the peptide containing pharmaceutical include autoimmune
 CC diseases (rheumatoid arthritis, multiple sclerosis, and myasthenia
 CC gravis), allograft rejection, allergies, lyme disease, hepatitis, post-
 CC streptococcal endocarditis or glomerulonephritis and food
 CC hypersensitivities. The peptide epitopes can be used to enhance immune
 CC responses against other immunogens administered with the peptides.
 CC Diseases which can be treated using immunogenic mixtures include prostate
 CC cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, cervical
 CC carcinoma, lymphoma, and condyloma acuminatum. The peptides may also be
 CC used to make monoclonal antibodies useful as potential diagnostic or
 CC therapeutic agents. The peptides may also be useful as diagnostic
 CC reagents, for example, to determine the susceptibility of an individual
 CC to a treatment regimen. Also, the peptides may be used to predict which
 CC individuals will be at substantial risk of developing chronic infection.
 CC The selection of appropriate T and B cell epitopes should allow the
 CC development of epitope based vaccines particularly towards conserved
 CC epitopes of pathogens which are characterized by high sequence
 CC variability such as HIV, HCV and Malaria

XX Sequence 14 AA;

Query Match 37.5%; Score 27; DB 3; Length 14;
 Best Local Similarity 50.0%; Pred. No. 4.2e+02;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 YSAFQVDITTI 13
 Db 1 YAAFSQTTTL 10

RESULT 15

AAAY99305
 ID AAY99305 standard; peptide; 14 AA.

XX AAY99305;

XX 07-AUG-2000 (first entry)

DE HLA class II binding antigen epitope peptide #494.

XX Human leucocyte antigen; HLA class II; antigen epitope; pharmaceutical;
 KW immune response; chronic viral disease; cancer; autoimmune disease;
 KW rheumatoid arthritis; multiple sclerosis; myasthenia gravis; AIDS;
 KW allograft rejection; allergy; lyme disease; hepatitis; prostate cancer;
 KW glomerulonephritis; food hypersensitivity; malaria.
 XX Unidentified.
 XX WO9961916-A1.
 XX 02-DEC-1999.
 XX 28-MAY-1999; 99WO-US012066.
 XX 29-MAY-1998; 98US-0087192P.
 XX (EPIM-) EPIMUNE INC.
 XX Sette A, Southwood S, Sidney J;
 XX WPI; 2000-097143/08.

PT New compositions containing immunogenic peptide epitopes for various HLA
 PT class II DR molecules useful for inducing helper T cell response.
 XX Claim 1; Page 48; 60pp; English.

CC The present invention relates to a new pharmaceutical composition
 CC comprising a unit dose form of a peptide, or analogue, comprising an
 CC epitope selected from those represented by peptides AAY9812-Y99339 which
 CC are derived from various antigens for various human leucocyte antigen
 CC class DR molecules, representative of the world wide population. The
 CC peptide/analogue binds to an HLA class II molecule at an IC-50 of less
 CC than or equal to 1,000 nM. The pharmaceutical can be used to induce a
 CC helper T cell response. The pharmaceutical focuses the immune response
 CC towards selected determinants and could therefore be used in cases of
 CC chronic viral diseases and cancer. Examples of diseases that can be
 CC treated using the peptide containing pharmaceutical include autoimmune
 CC diseases (rheumatoid arthritis, multiple sclerosis, and myasthenia
 CC gravis), allograft rejection, allergies, lyme disease, hepatitis, post-
 CC streptococcal endocarditis or glomerulonephritis and food
 CC hypersensitivities. The peptide epitopes can be used to enhance immune
 CC responses against other immunogens administered with the peptides.
 CC Diseases which can be treated using immunogenic mixtures include prostate
 CC cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, cervical
 CC carcinoma, lymphoma, and condyloma acuminatum. The peptides may also be
 CC used to make monoclonal antibodies useful as potential diagnostic or
 CC therapeutic agents. The peptides may also be useful as diagnostic
 CC reagents, for example, to determine the susceptibility of an individual
 CC to a treatment regimen. Also, the peptides may be used to predict which
 CC individuals will be at substantial risk of developing chronic infection.
 CC The selection of appropriate T and B cell epitopes should allow the
 CC development of epitope based vaccines particularly towards conserved
 CC epitopes of pathogens which are characterized by high sequence
 CC variability such as HIV, HCV and Malaria

XX Sequence 14 AA;

Query Match 37.5%; Score 27; DB 3; Length 14;
 Best Local Similarity 50.0%; Pred. No. 4.2e+02;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 YSAFQVDITTI 13
 Db 1 YAAFSQTTTL 10

Search completed: November 14, 2004, 13:44:59
 Job time : 112.5 secs

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OM protein - protein search, using sw model

Run on: November 14, 2004, 13:17:28 ; Search time 122.5 Seconds
(without alignments)
65.757 Million cell updates/sec

Title: US-09-831-253F-7
Perfect score: 72
Sequence: 1 SNPSAFQVDITID 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 6764

Minimum DB seq length: 0
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_02: *
1: uniprot_eprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	28	38.9	9	2 Q7RA82	Q7RA82 plasmodium
2	26	36.1	13	2 Q79A22	Q79A22 borrelia bu
3	25	34.7	10	2 Q76NM5	Q76NM5 eurypharynx
4	25	34.7	10	2 BAB87140	BAB87140 euryphary
5	25	34.7	11	2 Q7M154	Q7M154 bacillus th
6	25	34.7	12	2 Q7XB05	Q7XB05 zea mays (m
7	25	34.7	13	2 Q7X761	Q7X761 zea mays (m
8	25	34.7	14	2 P81801	P81801 streptomyces
9	25	34.7	14	2 Q9R5I8	Q9R5I8 vibrio algi
10	24	33.3	8	2 Q9IU19	Q9IU19 influenza a
11	24	33.3	8	2 Q9IU21	Q9IU21 influenza a
12	24	33.3	12	2 Q9S550	Q9S550 streptococ
13	23	31.9	10	2 Q76MK9	Q76MK9 eurypharynx
14	23	31.9	10	2 Q9FS93	Q9FS93 silene pent
15	23	31.9	10	2 BAB87148	BAB87148 euryphary
16	23	31.9	10	2 BAB87156	BAB87156 euryphary
17	23	31.9	10	2 BAB87164	BAB87164 euryphary
18	23	31.9	13	2 Q9FS94	Q9FS94 silene pent
19	23	31.9	13	2 Q9FSA8	Q9FSA8 silene bacc
20	23	31.9	14	2 Q9FS91	Q9FS91 silene sedo
21	23	31.9	14	2 Q9FS95	Q9FS95 silene pent
22	23	31.9	14	2 Q9RSB1	Q9RSB1 silene aega
23	22	30.6	8	1 ALL3 CYDPO	P82154 cydia pomon
24	22	30.6	12	1 VESP_VESMA	Q7M3T3 vespa manda
25	22	30.6	14	2 Q55326	Q55326 synchococ
26	21	29.2	7	1 ALL5 CARMA	P81808 carcinus ma
27	21	29.2	13	2 Q7M0L4	Q7M0L4 bacillus ce
28	21	29.2	14	2 Q85576	Q85576 chlamydia t
29	21	29.2	14	2 Q9S3K6	Q9S3K6 chlamydia t
30	21	29.2	14	2 Q9S3K8	Q9S3K8 chlamydia t
31	21	29.2	14	2 Q9R8E6	Q9R8E6 chlamydia t

32	21	29.2	14	2 Q9R8E7	Q9R8E7 chlamydia t
33	21	29.2	14	2 Q9R8E8	Q9R8E8 chlamydia t
34	21	29.2	14	2 Q9R8E9	Q9R8E9 chlamydia t
35	21	29.2	14	2 Q9R8F0	Q9R8F0 chlamydia t
36	21	29.2	14	2 Q9R8F2	Q9R8F2 chlamydia t
37	21	29.2	14	2 Q9R8E5	Q9R8E5 chlamydia t
38	21	29.2	14	2 Q9R8F7	Q9R8F7 chlamydia t
39	21	29.2	14	2 Q9R8F9	Q9R8F9 chlamydia t
40	21	29.2	14	2 Q9R8G1	Q9R8G1 chlamydia t
41	21	29.2	14	2 Q9R8G3	Q9R8G3 chlamydia t
42	21	29.2	14	2 Q9R8G4	Q9R8G4 chlamydia t
43	21	29.2	14	2 Q9R8G6	Q9R8G6 chlamydia t
44	21	29.2	14	2 Q9R8G8	Q9R8G8 chlamydia t
45	21	29.2	14	2 Q9R8H0	Q9R8H0 chlamydia t

ALIGNMENTS

```
RESULT 1
Q7RA82
ID Q7RA82 PRELIMINARY; PRT; 9 AA.
AC Q7RA82;
DT 01-MAR-2004 (Tremblrel. 26, Created)
DT 01-MAR-2004 (Tremblrel. 26, Last sequence update)
DE Hypothetical protein (Fragment).
GN Name=PY06620;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_taxid=73239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=12368865;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perteu M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
parasite Plasmodium yoelii yoelii."
RL Nature 419:512-519(2002).
CC Nature 419:512-519(2002).
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
DR EMBL; AABL01002263; EAA18865.1; -.
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 9 AA; 1001 MW; 4687A5AB476455B7 CRC64;

Query Match 38.9%; Score 28; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNPS 5
Db |||||
3 SNPS 7

RESULT 2
Q79A22
ID Q79A22 PRELIMINARY; PRT; 13 AA.
AC Q79A22;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE MoxR protein (fragment).
```

GN Name=moxR;
 OS Borrelia burgdorferi (Lyme disease spirochete).
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
 OX NCBI_TaxID=139;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=212;
 RA Old I.G.;
 RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X95668; CAA64970.1; -.
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1484 MW; C7C2DF4CFD83A046 CRC64;
 Query Match 36.1%; Score 26; DB 2; Length 13;
 Best Local Similarity 40.0%; Pred. No. 9.2e+02;
 Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 5 SAFQVDITID 14
 Db ||| : :
 3 SGFOIDSEVE 12
 RESULT 3
 Q76MM5 PRELIMINARY; PRT; 10 AA.
 AC Q76MM5;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE NADH dehydrogenase subunit 2 (Fragment).
 GN Name=ND2;
 OS Eurypharynx pelicanoides (pelican eel).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes;
 OC Eurypharyngidae; Eurypharynx.
 OX NCBI_TaxID=55117;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=22967687; PubMed=12949142;
 RA Inoue J.G., Miya M., Tsukamoto K., Nishida M.;
 "Evolution of the deep-sea gulper eel mitochondrial genomes: large-scale gene rearrangements originated within the eels.";
 RL Mol. Biol. Evol. 20:1917-1924(2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.;
 Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB046477; BAB87140.1; -.
 DR GO; GO:0005739; C.mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1261 MW; 357BFE29C682DB47 CRC64;
 Query Match 34.7%; Score 25; DB 2; Length 10;
 Best Local Similarity 62.5%; Pred. No. 1.1e+03;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 NPYSAFQV 9
 Db ||| : :
 2 NPYVMFLV 9
 RESULT 4
 BAB87140 PRELIMINARY; PRT; 10 AA.
 AC BAB87140;
 DT 02-MAR-2004 (TREMBlrel. 27, Created)
 DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
 DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
 DE NADH dehydrogenase subunit 2 (Fragment).
 GN ND2.
 OS Eurypharynx pelicanoides (pelican eel).

OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes;
 OC Eurypharyngidae; Eurypharynx.
 OX NCBI_TaxID=55117;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A;
 RA Inoue J.G., Miya M., Tsukamoto K., Nishida M.;
 "Evolution of the Deep-Sea Gulper Eel Mitochondrial Genomes: Large-Scale Gene Rearrangements Originated Within the Eels.";
 RL Mol. Biol. Evol. 20:1917-1924(2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A;
 RA Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.;
 Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB046477; BAB87140.1; -.
 KW Mitochondrion.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1261 MW; 357BFE29C682DB47 CRC64;
 Query Match 34.7%; Score 25; DB 2; Length 10;
 Best Local Similarity 62.5%; Pred. No. 1.1e+03;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 NPYSAFQV 9
 Db ||| : :
 2 NPYVMFLV 9
 RESULT 5
 Q7M154 PRELIMINARY; PRT; 11 AA.
 AC Q7M154;
 DT 01-MAR-2004 (TREMBlrel. 26, Created)
 DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Parasporal crystal protein, wax moth-specific (Fragment).
 OS Bacillus thuringiensis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1428;
 RN [1]
 RP SEQUENCE.
 RA Chestukhina G.G., Kostina L.I., Zalunin I.A., Khodova O.M.,
 Stepanov V.M.;
 "Bacillus thuringiensis ssp. galleriae simultaneously produces two delta-endotoxins differing strongly in primary structure and entomocidal activity.";
 RL FEBS Lett. 232:249-251(1988).
 DR PIR; S00616; S00616.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1237 MW; C6FF9BD64764444D CRC64;
 Query Match 34.7%; Score 25; DB 2; Length 11;
 Best Local Similarity 80.0%; Pred. No. 1.2e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SNPYS 5
 Db : ||| :
 5 NNPYS 9
 RESULT 6
 Q7XB05 PRELIMINARY; PRT; 12 AA.
 AC Q7XB05;
 DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Phytoene synthase 2 (Fragment).
 GN Name=psy2;

OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Y-14;
 RX MEDLINE=22779048; PubMed=12897253;
 RA Palaisa K.A., Morgante M., Williams M., Rafalski A.;
 RT "Contrasting effects of selection on sequence diversity and linkage
 RT disequilibrium at two phytoene synthase loci.";
 RL Plant Cell 15:1795-1806(2003).
 DR EMBL; AY300568; AAP5307.1; -.
 FT NON_TER 1 1
 FT 12 12
 SQ SEQUENCE 12 AA; 1335 MW; 9B1E0AA0869C325 CRC64;
 Query Match 34.7%; Score 25; DB 2; Length 12;
 Best Local Similarity 54.5%; Pred. No. 1.3e+03;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 SNPYSAFOVDI 11
 Db :|:|:|
 1 SDTVSKFPVDI 11
 RESULT 7
 Q7X761 PRELIMINARY; PRT; 13 AA.
 ID Q7X761
 AC Q7X761;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Phytoene synthase 2 (Fragment).
 GN Name=psy2;
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=W-17, and W-50;
 RX MEDLINE=22779048; PubMed=12897253;
 RA Palaisa K.A., Morgante M., Williams M., Rafalski A.;
 RT "Contrasting effects of selection on sequence diversity and linkage
 RT disequilibrium at two phytoene synthase loci.";
 RL Plant Cell 15:1795-1806(2003).
 DR EMBL; AY300592; AAP5331.1; -.
 DR EMBL; AY300599; AAP5338.1; -.
 FT NON_TER 1 1
 FT 13 13
 SQ SEQUENCE 13 AA; 1449 MW; 9B1E0AA05615C325 CRC64;
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 Best Local Similarity 54.5%; Pred. No. 1.4e+03;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 SNPYSAFOVDI 11
 Db :|:|:|
 2 SDTVSKFPVDI 12
 RESULT 8
 P81801 PRELIMINARY; PRT; 14 AA.
 ID P81801
 AC P81801;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Puromycin-Hydrolyzing enzyme (EC 3.-.-.-) (Fragment).
 OS Streptomyces morookaensis.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1970;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=JCM4673 / KCC-S-0673;
 RX PubMed=9538199;
 RA Nishimura M., Matsuo H., Nakamura A., Sugiyama M.;
 RT "Purification and characterization of a puromycin-hydrolyzing enzyme
 RT from blastidin S-producing Streptomyces morookaensis.";
 RL J. Biochem. 123:247-252(1998).
 RN [2]
 RP CHARACTERIZATION, AND FUNCTION.
 RA Nishimura M., Matsuo H., Sugiyama M.;
 RT "Blastidin S-producing Streptomyces morookaensis possesses an enzyme
 RT activity with hydrolyzes puromycin.";
 RL FEMS Microbiol. Lett. 132:95-100(1995).
 CC -!- FUNCTION: INACTIVATES PUROMYCIN BY CATALYZING THE HYDROLYSIS OF
 CC THE AMIDE LINKAGE BETWEEN ITS AMINONUCLEOSIDE AND O-METHYL-L-
 CC TYROSINE MOETIES. THE OPTIMUM PH IS 8.0 AND THE OPTIMAL
 CC TEMPERATURE IS 45 DEGREES CELSIUS.
 CC -!- FUNCTION: MAY HAVE AMINOPEPTIDASE ACTIVITY.
 CC -!- ENZYME REGULATION: STIMULATED BY DTT. STRONGLY INHIBITED BY ZINC
 CC ION, FERROUS ION, CUPRIC ION, MERCURY ION, N-BROMOSUCCINIMIDE AND
 CC N-ETHYLMALIMIDE. PARTIALLY INHIBITED BY COBALT ION.
 CC -!- SUBUNIT: MONOMER.
 CC -!- MISCELLANEOUS: HAS AN ISOELECTRIC POINT OF 6.4.
 DR GO; GO:0004177; F:aminopeptidase activity; IEA.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 KW Aminopectidase; Hydrolase.
 FT NON_TER 14 14
 SQ SEQUENCE 14 AA; 1492 MW; 3F980730E45EF3D8 CRC64;
 Query Match 34.7%; Score 25; DB 2; Length 14;
 Best Local Similarity 55.6%; Pred. No. 1.5e+03;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 3 PYSAPQVDI 11
 Db :|:|:|
 5 PYGAWQSP 13
 RESULT 9
 Q9R518 PRELIMINARY; PRT; 14 AA.
 ID Q9R518
 AC Q9R518;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE L-2,4-diaminobutyrate decarboxylase (Fragment).
 OS Vibrio alginolyticus.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 OX NCBI_TaxID=663;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92381494; PubMed=1512577;
 RA Yamamoto S., Tsuzaki Y., Tougou K., Shinoda S.;
 RT "Purification and characterization of L-2,4-diaminobutyrate
 RT decarboxylase from Acinetobacter calcoaceticus.";
 RL J. Gen. Microbiol. 138:1461-1465(1992).
 DR PIR; B44854; B44854.
 SQ SEQUENCE 14 AA; 1643 MW; 9F1B13DD35168ABA CRC64;
 Query Match 34.7%; Score 25; DB 2; Length 14;
 Best Local Similarity 55.6%; Pred. No. 1.5e+03;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 5 SAFOVDITI 13
 Db :|:|:|
 2 TAFEVDSNI 10

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RESULT 10
Q91U19
ID Q91U19 PRELIMINARY; PRT; 8 AA.
AC Q91U19;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Nuclear export protein NS2 (Fragment).
OS Influenza A virus (A/Hong Kong/503/97(H5N1)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A; H5N1 subtype.
OX NCBI_TaxID=155224;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A/Hong Kong/503/97;
RA Shaw M.W., Cooper L.A., Xu X., Thompson W.W., Krauss S.L., Guan Y.,
RA Zhou N.N., Klimov A., Cox N.J., Webster R.G., Lim W., Shortridge K.F.,
RA Subbarao K.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF256192; AAK49326.1; -.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 869 MW; D9D9D5A5A2D1A455 CRC64;

Query Match 33.3%; Score 24; DB 2; Length 8;
Best Local Similarity 62.5%; Pred. No. 1.8e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SNPYSAFQ 8
DB ||| |
1 SNTVSSFQ 8

RESULT 11
Q91U21
ID Q91U21 PRELIMINARY; PRT; 8 AA.
AC Q91U21;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Nuclear export protein NS2 (Fragment).
OS Influenza A virus (A/Hong Kong/491/97(H5N1)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A; H5N1 subtype.
OX NCBI_TaxID=155223;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A/Hong Kong/491/97;
RA Shaw M.W., Cooper L.A., Xu X., Thompson W.W., Krauss S.L., Guan Y.,
RA Zhou N.N., Klimov A., Cox N.J., Webster R.G., Lim W., Shortridge K.F.,
RA Subbarao K.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF256191; AAK49324.1; -.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 869 MW; D9D9D5A5A2D1A455 CRC64;

Query Match 33.3%; Score 24; DB 2; Length 8;
Best Local Similarity 62.5%; Pred. No. 1.8e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SNPYSAFQ 8
DB ||| |
1 SNTVSSFQ 8

RESULT 12
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ID Q9S550 PRELIMINARY; PRT; 12 AA.
AC Q9S550;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)

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DE DexB (Fragment).
GN Name=dexB;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JD39;
RX MEDLINE=99214122; PubMed=10198036;
RA Iannelli F., Pearce B.J., Pozzi G.;
RT "The type 2 capsule locus of Streptococcus pneumoniae.";
RL J. Bacteriol. 181:2652-2654 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=JD39;
RA Pearce B.J., Iannelli F., Pozzi G.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF026471; AAD10169.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 12 AA; 1405 MW; 90A979D2B2B9CDDA CRC64;

Query Match 33.3%; Score 24; DB 2; Length 12;
Best Local Similarity 44.4%; Pred. No. 2e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 PYSAFQVDI 11
DB ||| |
3 PWDAPFCVEL 11

RESULT 13
Q76MK9
ID Q76MK9 PRELIMINARY; PRT; 10 AA.
AC Q76MK9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE NADH dehydrogenase subunit 2 (Fragment).
GN Name=ND2;
OS Eurypharynx pelecanoides (pelican eel).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes;
OC Eurypharyngidae; Eurypharynx.
OX NCBI_TaxID=55117;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22967687; PubMed=12949142;
RA Inoue J.G., Miya M., Tsukamoto K., Nishida M.;
RT "Evolution of the deep-sea gulper eel mitochondrial genomes: large-
RT scale gene rearrangements originated within the eels.";
RL Mol. Biol. Evol. 20:1917-1924 (2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB046485; BAB87156.1; -.
DR EMBL; AB046489; BAB87164.1; -.
DR EMBL; AB046481; BAB87148.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 1293 MW; 356FAE29C682DB47 CRC64;

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Best Local Similarity 66.7%; Pred. No. 2.5e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NPYSAF 7
DB ||| |
2 NPVVMF 7

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RESULT 14
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ID Q9FS93 PRELIMINARY; PRT; 10 AA.
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE RNA polymerase II (Fragment).
GN Name=rpb2;
OS Silene pentelica.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllaceae; Silene.
OX NCBI_TaxID=49735;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21419634; PubMed=11527472;
RA Popp M., Oxelman B.;
RT "Inferring the history of the polyploid Silene aegaea
RT (Caryophyllaceae) using plastid and homoeologous nuclear DNA
RT sequences."
RL Mol. Phylogenet. Evol. 20:474-481(2001).
DR EMBL; AJ296133; CAC13025.1; -.
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1108 MW; CFIAB6D1B2CAB1A9 CRC64;

Query Match 31.9%; Score 23; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 DITID 14
DB 5 DVTVD 9

RESULT 15
BAB87148
ID BAB87148 PRELIMINARY; PRT; 10 AA.
DT 02-MAR-2004 (TReMBLrel. 27, Created)
DT 02-MAR-2004 (TReMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TReMBLrel. 27, Last annotation update)
DE NADH dehydrogenase subunit 2 (Fragment).
GN ND2.
OS Eurypharynx pelecanoides (pelican eel).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes;
OC Eurypharyngidae; Eurypharynx.
OX NCBI_TaxID=55117;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B;
RA Inoue J.G., Miya M., Tsukamoto K., Nishida M.;
RT "Evolution of the Deep-Sea Gulper Eel Mitochondrial Genomes: Large-
RT Scale Gene Rearrangements Originated Within the Eels.";
RL Mol. Biol. Evol. 20:1917-1924(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=B;
RA Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB046481; BAB87148.1; -.
KW Mitochondrion.
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 1293 MW; 356FAE29C682DB47 CRC64;

Query Match 31.9%; Score 23; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.5e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 2 NPYSAP 7
 DB 2 NPYVWF 7

Search completed: November 14, 2004, 13:41:10
 Job time : 122.5 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2004, 12:03:21 ; Search time 33.0638 Seconds
(without alignments)
149.815 Million cell updates/sec

Title: US-09-831-253F-7

Perfect score: 72
Sequence: 1 SNPSAFQVDITID 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1568699 seqs, 353819137 residues

Total number of hits satisfying chosen parameters: 294451

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	37	51.4	17	9	US-09-071-838-173
2	37	51.4	17	14	US-10-213-513-173
3	32	44.4	15	10	US-09-988-493-305
4	32	44.4	15	14	US-10-014-340-802
5	32	44.4	15	17	US-10-700-330-264
6	29	40.3	15	14	US-10-285-394-332
7	29	40.3	20	14	US-10-162-538-25
8	29	40.3	22	9	US-09-864-761-43921
9	28	38.9	10	10	US-09-880-748-3097
10	28	38.9	10	14	US-10-293-418-3097
11	28	38.9	13	11	US-09-842-776A-30
12	28	38.9	19	14	US-10-230-880-125
13	28	38.9	23	15	US-10-211-462-91

14	27	37.5	11	10	US-09-880-748-2839	Sequence 2839, Ap
15	27	37.5	11	14	US-10-293-418-2839	Sequence 2839, Ap
16	27	37.5	12	14	US-10-286-457-177	Sequence 177, App
17	27	37.5	18	10	US-09-880-748-2736	Sequence 2736, Ap
18	27	37.5	18	14	US-10-293-418-2736	Sequence 2736, Ap
19	27	37.5	18	16	US-10-481-180-685	Sequence 685, App
20	27	37.5	19	9	US-09-864-761-43613	Sequence 43613, A
21	27	37.5	19	15	US-10-424-599-201443	Sequence 201443, A
22	27	37.5	19	16	US-10-481-180-692	Sequence 692, App
23	27	37.5	21	14	US-10-350-405-151	Sequence 151, App
24	27	37.5	23	16	US-10-481-180-714	Sequence 714, App
25	26.5	36.8	10	14	US-10-151-882-26	Sequence 26, Appl
26	26	36.1	7	9	US-09-927-180-3	Sequence 3, Appl
27	26	36.1	9	14	US-10-334-726-118	Sequence 118, App
28	26	36.1	9	14	US-10-334-726-220	Sequence 220, App
29	26	36.1	15	10	US-09-983-802-437	Sequence 437, App
30	26	36.1	15	10	US-09-984-490-437	Sequence 437, App
31	26	36.1	15	11	US-09-973-278-566	Sequence 566, App
32	26	36.1	15	14	US-10-411-120-102	Sequence 102, App
33	26	36.1	20	10	US-09-171-432A-70	Sequence 70, Appl
34	26	36.1	22	14	US-10-106-698-7411	Sequence 7411, Ap
35	26	36.1	22	14	US-10-029-386-31493	Sequence 31493, A
36	25	34.7	7	14	US-10-400-991-50	Sequence 50, Appl
37	25	34.7	9	10	US-09-995-529-83	Sequence 83, Appl
38	25	34.7	9	11	US-09-995-529-83	Sequence 83, Appl
39	25	34.7	10	10	US-09-572-404B-2428	Sequence 2428, Ap
40	25	34.7	10	16	US-10-327-598-519	Sequence 519, App
41	25	34.7	11	9	US-09-966-871-70	Sequence 70, Appl
42	25	34.7	11	13	US-10-039-645-70	Sequence 70, Appl
43	25	34.7	11	14	US-10-133-084-70	Sequence 70, Appl
44	25	34.7	11	15	US-10-458-860-70	Sequence 70, Appl
45	25	34.7	11	17	US-10-625-047-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1

US-09-071-838-173
; Sequence 173, Application US/09071838
; Patent No. US20020152501A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Yadegari, Ramin
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; TITLE OF INVENTION: Nucleic Acids That Control Seed and
; TITLE OF INVENTION: Fruit Development in Plants
; NUMBER OF SEQUENCES: 324
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,838
; FILING DATE: 01-MAY-1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 023070-086100US
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 173:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLSCULE TYPE: peptide
US-09-071-838-173

Query Match 51.4%; Score 37; DB 9; Length 17;
Best Local Similarity 50.0%; Pred. No. 9.1;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 SNPYSAFQVDITD 14
||| | : ||
Db 3 SNPYRKFTNTYTKD 16

RESULT 2

US-10-213-512-173
; Sequence 173, Application US/10213512
; Publication No. US20030110536A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Yadegari, Ramin
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Combinations of Nucleic Acids That Control Seed and
; TITLE OF INVENTION: Fruit Development in Plants
; FILE REFERENCE: 023070-086110US
; CURRENT APPLICATION NUMBER: US/10/213,512
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: US/09/177,206
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: US 09/071,838
; PRIOR FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 173
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-10-213-512-173

Query Match 51.4%; Score 37; DB 14; Length 17;
Best Local Similarity 50.0%; Pred. No. 9.1;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 SNPYSAFQVDITD 14
||| | : ||
Db 3 SNPYRKFTNTYTKD 16

RESULT 3

US-09-988-493-305
; Sequence 305, Application US/09988493
; Publication No. US2003006419A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyansele Athula Chandrasiri
; APPLICANT: O'Hare, Michael John
; APPLICANT: Page, Martin John
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Waterfield, Michael Derek
; TITLE OF INVENTION: Proteins, Genes, and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Breast Cancer
; FILE REFERENCE: 2543-1-024
; CURRENT APPLICATION NUMBER: US/09/988,493
; CURRENT FILING DATE: 2002-05-21

; PRIOR APPLICATION NUMBER: PCT/GB01/01219
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: GB 0006695.1
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: GB 0007265.2
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 305
; LENGTH: 15
; TYPE: PRT
; ORGANISM: homo sapien
US-09-988-493-305

Query Match 44.4%; Score 32; DB 10; Length 15;
Best Local Similarity 60.0%; Pred. No. 64;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 SAFOVDITD 14
||| | : ||
Db 5 SGFQIEETD 14

RESULT 4

US-10-014-340-802
; Sequence 802, Application US/10014340
; Publication No. US20030064411A1
; GENERAL INFORMATION:
; APPLICANT: Herath, et al
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Uses Therefor, Including
; TITLE OF INVENTION: Diagnosis and Treatment of Alzheimer's Disease
; FILE REFERENCE: 9195-078
; CURRENT APPLICATION NUMBER: US/10/014,340
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 802
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-340-802

Query Match 44.4%; Score 32; DB 14; Length 15;
Best Local Similarity 60.0%; Pred. No. 64;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 SAFOVDITD 14
||| | : ||
Db 5 SGFQIEETD 14

RESULT 5

US-10-700-330-264
; Sequence 264, Application US/10700330
; Publication No. US20040203022A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Mudiyansele Athula Chandrasiri Herath
; APPLICANT: Page, Martin John
; TITLE OF INVENTION: Proteins and Genes For Diagnosis And Treatment of ErbB2-Related (c
; FILE REFERENCE: 2543-1-031
; CURRENT APPLICATION NUMBER: US/10/700,330
; CURRENT FILING DATE: 2003-11-03
; PRIOR APPLICATION NUMBER: GB 0110886.9
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: GB 0128183.1
; PRIOR FILING DATE: 2001-11-23
; NUMBER OF SEQ ID NOS: 269
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 264
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-700-330-264

Query Match 44.4%; Score 32; DB 17; Length 15;
Best Local Similarity 60.0%; Pred. No. 64;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 SAFOVDITID 14
| | | | |
Db 5 SGFOIBETID 14

RESULT 6

US-10-285-394-332
; Sequence 332, Application US/10285394
; Publication No. US20030228583A1
; GENERAL INFORMATION:
; APPLICANT: FASULO, DAVID E.
; APPLICANT: HERATH, HERATH MUDIYANSELAGE ATHULA CHANDRASIRI
; APPLICANT: HOLT, GORDON DUANE
; APPLICANT: STIGER, THOMAS R.
; TITLE OF INVENTION: BIOMARKERS OF LIVER RESPONSE
; FILE REFERENCE: POA-003.01
; CURRENT APPLICATION NUMBER: US/10/285,394
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: 60/335,964
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 412
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 332
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-285-394-332

Query Match 40.3%; Score 29; DB 14; Length 15;
Best Local Similarity 54.5%; Pred. No. 2.3e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 YSAFOVDITID 14
| | | | |
Db 2 YPGSQDLID 12

RESULT 7

US-10-162-538-25
; Sequence 25, Application US/10162538
; Publication No. US20030113749A1
; GENERAL INFORMATION:
; APPLICANT: Brent, Roger
; McCoy, John M.
; Jesen, Timm H.
; Xu, Chanxing Wilson
; TITLE OF INVENTION: INTERACTION TRAP SYSTEMS FOR DETECTING
; PROTEIN
; INTERACTIONS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/162,538
; FILING DATE: 04-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: PCT/US01/00662

APPLICATION NUMBER: US/08/630,052
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/504,538
FILING DATE: July 20, 1995
APPLICATION NUMBER: 08/278,082
FILING DATE: July 20, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Karen F. Lech
REGISTRATION/DOCKET NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/311001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154

INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: No. US20030113749A1 Relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-10-162-538-25

Query Match 40.3%; Score 29; DB 14; Length 20;
Best Local Similarity 62.5%; Pred. No. 3.2e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 PYSAFOVD 10
| | | | |
Db 13 PHSVFNVVD 20

RESULT 8

US-09-864-761-43921
; Sequence 43921, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aemica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 43921
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC006227.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.72
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.71
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.86
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.77
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.61
US-09-864-761-43921

Query Match      40.3%; Score 29; DB 9; Length 22;
Best Local Similarity 54.5%; Pred. No. 3.5e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1 SNPSAFQVDI 11
DB      1 STPSSAFVSLS 11

RESULT 9
US-09-880-748-3097
; Sequence 3097, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3097
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-3097

Query Match      38.9%; Score 28; DB 10; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 NPYSAFQV 9
DB      3 SPYDAFDI 10

RESULT 10
US-10-293-418-3097
; Sequence 3097, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3097
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-3097

Query Match      38.9%; Score 28; DB 14; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 NPYSAFQV 9
DB      3 SPYDAFDI 10

RESULT 11
US-09-842-776A-30
; Sequence 30, Application US/09842776A
; Publication No. US2004002316A1
; GENERAL INFORMATION:
; APPLICANT: CONNEX GMBH
; TITLE OF INVENTION: NEW METHOD FOR DETECTING ACID-RESISTANT MICROORGANISMS
; FILE REFERENCE: 41735
; CURRENT APPLICATION NUMBER: US/09/842,776A
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: PCT/EP99/08212
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Complementarity determining region (CDR3) of an
; OTHER INFORMATION: antibody heavy chain directed to a beta-urease
; OTHER INFORMATION: epitope (alternative sequence)
US-09-842-776A-30

Query Match      38.9%; Score 28; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SNPYS 5
DB      6 SNPYS 10
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RESULT 12
US-10-230-880-125
; Sequence 125, Application US/10230880
; Publication No. US20030190705A1
; GENERAL INFORMATION:
; APPLICANT: WONG, HING C.
; APPLICANT: STINSON, JEFFREY L.
; APPLICANT: MOSQUERA, LUIS A.
; TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
; FILE REFERENCE: 71758/58066
; CURRENT APPLICATION NUMBER: US/10/230,880
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 125
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-230-880-125

Query Match 38.9%; Score 28; DB 14; Length 19;
Best Local Similarity 42.9%; Pred. No. 4.5e+02;
Matches 6; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 SNPYSAFQVDITD 14
DB 6 SNNYATFYADSVKD 19

RESULT 13
US-10-211-462-91
; Sequence 91, Application US/10211462
; Publication No. US20040033495A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Richard
; APPLICANT: Glynn, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Aziz, Natascha
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and
; FILE REFERENCE: 018501-006200US
; CURRENT APPLICATION NUMBER: US/10/211,462
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US 09/784,356
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/791,390
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: US 60/310,025
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/334,244
; PRIOR FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 230
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 91
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-211-462-91

Query Match 38.9%; Score 28; DB 15; Length 23;
Best Local Similarity 50.0%; Pred. No. 5.6e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 SNPYSAFQVD 10

Db 3 SIPYTVFQTN 12

RESULT 14
US-09-880-748-2839
; Sequence 2839, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2839
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2839

Query Match 37.5%; Score 27; DB 10; Length 11;
Best Local Similarity 57.1%; Pred. No. 3.7e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 PYSAFQV 9
DB 5 PYDAPDI 11

RESULT 15
US-10-293-418-2839
; Sequence 2839, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2839
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2839

Query Match 37.5%; Score 27; DB 14; Length 11;
Best Local Similarity 57.1%; Pred. No. 3.7e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PYSAFQV 9
||| :
Db 5 PYDAFDI 11

Search completed: November 14, 2004, 12:26:59
Job time : 33.0638 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:25 ; Search time 40.5106 Seconds
(without alignments)
123.973 Million cell updates/sec

Title: US-09-831-253F-7

Perfect score: 72

Sequence: 1 SNPYSAFQVDITD 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 718658

Minimum DB seq length: 0

Maximum DB seq length: 23

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	72	100.0	14	3 AAY92951	Aay92951 Transform
2	72	100.0	14	3 AAY93099	Aay93099 Transform
3	65	90.3	15	3 AAY92948	Aay92948 Transform
4	65	90.3	15	3 AAY93066	Aay93066 Transform
5	53	73.6	15	3 AAY93059	Aay93059 Transform
6	37	51.4	15	3 AAY93067	Aay93067 Transform
7	32	44.4	15	4 AAU68498	Aau68498 Human Bre
8	32	44.4	15	6 ABP99093	Abp99093 Erxb2 cel
9	32	44.4	15	6 ADA24180	Ada24180 Alzheimer
10	32	44.4	17	2 AAR42489	Aar42489 Canine ho
11	32	44.4	17	2 AAR67769	Aar67769 Peptide f
12	32	44.4	17	2 AAY23572	Aay23572 Peptide f
13	32	44.4	21	2 AAR34228	Aar34228 HTLV-I gp
14	32	44.4	22	2 AAY17925	Aay17925 Synthetic
15	30	41.7	15	8 ADL70819	Adl70819 pTP1B pho
16	30	41.7	15	8 ADL70905	Adl70905 pTP1B pho
17	30	41.7	15	8 ADL70907	Adl70907 pTP1B pho
18	30	41.7	15	8 ADL70906	Adl70906 pTP1B pho
19	30	41.7	15	8 ADL70908	Adl70908 pTP1B pho
20	30	41.7	17	7 ADD26370	Add26370 Staphyloc
21	30	41.7	20	2 AAU42169	Aau42169 T-cell ep
22	29	40.3	15	6 ABR75594	Abr75594 Liver res
23	29	40.3	15	7 ADN07473	Adn07473 Liver res
24	29	40.3	15	8 ADK90209	Adk90209 Human 191
25	29	40.3	20	2 AAW32131	Aaw32131 Interacti

ALIGNMENTS

RESULT 1

AA92951
ID AAY92951 standard; peptide; 14 AA.

XX AC

XX AAY92951;

DT 08-NOV-2000 (first entry)

XX Transforming growth factor inhibitory peptide #7.

DE Hepatotrophic; antagonist; transforming growth factor betal; TGF-b1;
KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.

XX Homo sapiens.

XX WO200031135-A1.

XX 02-JUN-2000.

XX 23-NOV-1999; 99WO-ES000375.

XX 24-NOV-1998; 98ES-00002465.

XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.

XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;

XX Borrás Cuesta F;

XX WPI; 2000-411935/35.

XX Peptides that antagonize binding of transforming growth factor betal.
XX useful for treatment of liver disease, especially cirrhosis, are partial
XX sequences of the factor or its receptors.

XX Claim 8; Page 82; 86pp; Spanish.

XX The invention relates to synthetic peptides that antagonise the binding
XX of transforming growth (TGF) factor betal (TGF-b1) to its receptor in
XX vivo which have partial amino acid sequences identical, or similar, with
XX those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
XX examples of the peptides of the invention. The peptides act by
XX competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
XX they are inhibitors of stimulation of collagen synthesis in liver cells
XX and inhibitors of synthesis of proteolytic enzymes able to degrade the
XX extracellular matrix. The peptides, their mimetopes and/or DNA (or
XX expression systems) encoding the peptides are used for treatment of liver
XX disease, specifically cirrhosis

```

XX SQ Sequence 14 AA;
Query Match 100.0%; Score 72; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNPYSAFQVDITID 14
Db 1 SNPYSAFQVDITID 14

RESULT 2
AAY93099
ID AAY93099 standard; peptide; 14 AA.
XX AC AAY93099;
XX DT 08-NOV-2000 (first entry)
XX DE Transforming growth factor inhibitory peptide P145.
XX KW Hepatotropic; antagonist; transforming growth factor beta1; TGF-beta1;
XX KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
XX KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX OS Homo sapiens.
XX PN WO200031135-A1.
XX PD 02-JUN-2000.
XX PF 23-NOV-1999; 99WO-ES000375.
XX PR 24-NOV-1998; 98ES-00002465.
XX PA (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
XX PI Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
XX PI Borrás Cuesta F;
XX WPI; 2000-411935/35.
XX PT Peptides that antagonize binding of transforming growth factor beta1,
XX PT useful for treatment of liver disease, especially cirrhosis, are partial
XX PT sequences of the factor or its receptors.
XX PS Claim 5; Page 81; 86pp; Spanish.
XX CC The invention relates to synthetic peptides that antagonise the binding
XX CC of transforming growth (TGF) factor beta1 (TGF-beta1) to its receptor in
XX CC vivo which have partial amino acid sequences identical, or similar, with
XX CC those of TGF-beta1 and/or its receptors. Peptides AAY92945-Y93133 represent
XX CC examples of the peptides of the invention. The peptides act by
XX CC competitive inhibition of the binding of TGF-beta1 to its receptors, e.g.
XX CC they are inhibitors of stimulation of collagen synthesis in liver cells
XX CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
XX CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
XX CC expression systems) encoding the peptides are used for treatment of liver
XX CC disease, specifically cirrhosis
XX SQ Sequence 15 AA;
Query Match 90.3%; Score 65; DB 3; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.9e-05;
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNPYSAFQVDITID 14
Db 1 SNPYSAFQVDITID 14

RESULT 4
AAY93066
ID AAY93066 standard; peptide; 15 AA.
XX AC AAY93066;
XX DT 08-NOV-2000 (first entry)
XX DE Transforming growth factor inhibitory peptide P106.
XX KW Hepatotropic; antagonist; transforming growth factor beta1; TGF-beta1;
XX KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
XX KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX
```


CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
CC examples of the peptides of the invention. The peptides act by
CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
CC they are inhibitors of stimulation of collagen synthesis in liver cells
CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
CC expression systems) encoding the peptides are used for treatment of liver
CC disease, specifically cirrhosis
XX
SQ Sequence 15 AA;

Query Match 51.4%; Score 37; DB 3; Length 15;
Best Local Similarity 77.8%; Pred. No. 5.8;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 AFQVDITID 14
| | | | | : |
Db 1 AFQVDITID 9

RESULT 7

AAU68498

ID AAU68498 standard; peptide; 15 AA.

XX AC

AAU68498;

DT 16-JAN-2002 (first entry)

XX DT

DE Human Breast cancer-associated protein isoform, BPI-279 peptide #3.

XX DE

KW Human; Breast cancer-associated protein isoform; breast cancer;

XX KW

KW immunogen; cytostatic; BPI; tryptic digest peptide.

XX KW

XX OS Homo sapiens.

XX OS

PN WO200171357-A2.

XX PN

XX PD 27-SEP-2001.

XX PD

PF 20-MAR-2001; 2001WO-GB001219.

XX PF

XX PR 20-MAR-2000; 2000GB-00006695.

XX PR

XX PR 24-MAR-2000; 2000GB-00007265.

XX PR

PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX PA

XX PI Herath HMAC, O'hare MJ, Page MJ, Parekh RB, Waterfield MD;

XX PI

XX PS WPI; 2001-611532/70.

XX PS

XX PT Identifying proteins for clinical screening, diagnosis and prognosis of
XX PT breast cancer, comprises detecting Breast Cancer-Associated Protein
XX PT Isoforms (BPIs) using two-dimensional electrophoresis.

XX PT

XX PS Claim 9; Page 53; 197pp; English.

XX PS

XX CC The invention relates to diagnosing, determining the stage or severity,
XX CC or identifying the risk of a subject developing cancer (especially breast
XX CC cancer), or monitoring the effect of therapy on a subject with cancer,
XX CC comprising analysing a test sample using two-dimensional electrophoresis
XX CC and detecting Breast Cancer-Associated Protein Isoforms (BPIs). The
XX CC methods disclosed are used for the diagnosis and prognosis of breast
XX CC cancer, for determining the severity of breast cancer, and for
XX CC identifying a subject at risk of developing breast cancer, and monitoring
XX CC the effect of therapy administered to a subject. Antibodies raised
XX CC against the binding domain of a BPI, the binding domain of a BPI, a
XX CC nucleic acid encoding a BPI, or a nucleic acid that inhibits the function
XX CC of a BPI can be incorporated into a pharmaceutical composition for
XX CC treating or preventing breast cancer. The methods use sensitive and
XX CC specific biomarkers provide early diagnosis of breast cancer, and the
XX CC compositions are more potent, specific, and has a more rapid effect with
XX CC fewer side effects than other prior art methods. The present sequence is
XX CC a tryptic digest peptide from a BPI of the invention

XX SQ

Sequence 15 AA;

Query Match 44.4%; Score 32; DB 4; Length 15;
Best Local Similarity 60.0%; Pred. No. 51;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 SAFOVDITID 14
| | | | | : |
Db 5 SGFQIEETID 14

RESULT 8

ABP99093

ID ABP99093 standard; peptide; 15 AA.

XX XX

AC ABP99093;

XX AC

DT 18-MAR-2003 (first entry)

XX DT

DE ErbB2 cell overexpression EOPI-97 peptide SEQ ID NO:264.

XX DE

KW ErbB2; cancer; oncogene; ErbB2 overexpression-associated protein isoform;
KW EOPI; EOP; ErbB2 overexpression feature; cytostatic; vaccine;
KW gene therapy.

XX KW

XX OS Homo sapiens.

XX OS

PN WO200290991-A2.

XX PN

PD 14-NOV-2002.

XX PD

XX PF 02-MAY-2002; 2002WO-GB002047.

XX PF

XX PR 03-MAY-2001; 2001GB-00010886.

XX PR

XX PR 23-NOV-2001; 2001GB-00028183.

XX PR

XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX PA

XX PI Herath HMAC, Page MJ;

XX PI

XX DR WPI; 2003-103531/09.

XX DR

XX PT Diagnosing and treating ErbB2-related cancer, comprises generating ErbB2
XX PT Overexpression features (EOFs) from test samples from a subject by
XX PT electrophoresis, and comparing the EOFs in the sample with a
XX PT predetermined reference range.

XX PT

XX PS Claim 3; Page 21; 106pp; English.

XX PS

XX CC The present invention describes a method for screening or diagnosing
XX CC ErbB2-related cancer. The method comprises generating ErbB2
XX CC overexpression features (EOFs) from test samples of body fluid from the
XX CC subject by electrophoresis, and comparing the EOFs in the test sample
XX CC with that from normal subjects or with an expression reference feature
XX CC (ERF) in the test sample. Also described: (1) an antibody capable of
XX CC immunospecific binding to an ErbB2 overexpression protein isoform (EOPI);
XX CC (2) pharmaceutical compositions comprising an EOPI, a nucleic acid
XX CC encoding an EOPI, an amount of the above antibody or its fragment, and a
XX CC carrier; (3) a kit comprising one or more antibodies and/or EOPIs cited
XX CC above, other reagents and instructions for use; (4) methods of treating
XX CC or preventing ErbB2-related cancer; (5) methods of screening for or
XX CC identifying agents that interact with or modulate the expression or
XX CC activity of, one or more EOPIs, EOPI fragment, EOPI-related polypeptides,
XX CC or EOPI-fusion proteins; (6) a method for modulating the activity of one
XX CC or more of the ErbB2 EOPIs, comprising administering to a subject an
XX CC agent identified by the method of (5); and (7) a method for identifying
XX CC targets for therapeutic modulation of ErbB2-related cancer. EOPIs have
XX CC cytostatic activity and can be used in vaccines and gene therapy. The
XX CC method is useful in screening, diagnosing, preventing or treating ErbB2-
XX CC related cancer, determining the stage or severity of ErbB2-related
XX CC cancer, identifying a subject at risk of developing ErbB2-related cancer,
XX CC monitoring the effect of therapy administered to a subject with ErbB2-

CC related cancer, and for drug screening or drug development. The kit is
 CC useful in carrying out the above methods. ABP98940 to ABP99206 represent
 CC specifically claimed EOPIS from the present invention
 XX
 SQ Sequence 15 AA;

Query Match 44.4%; Score 32; DB 6; Length 15;
 Best Local Similarity 60.0%; Pred. No. 51;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 SAFOVDITID 14
 | | | | |
 Db 5 SGFOIETID 14

RESULT 9

ADA24180
 ID ADA24180 standard; peptide; 15 AA.

AC ADA24180;

XX 20-NOV-2003 (first entry)

XX Alzheimer's disease-associated protein isoform tryptic peptide #789.
 XX human; Alzheimer's disease; vascular dementia; Lewy body dementia;
 KW schizophrenia; Parkinson's disease; multiple sclerosis; depression;
 KW Alzheimer's disease-associated protein isoform; ADPI.

XX Homo sapiens.

XX US2003064411-A1.

XX 03-APR-2003.

XX 10-DEC-2001; 2001US-00014340.

XX 08-DEC-2000; 2000US-0254431P.

XX (HERA/) HERATH H M A C.

XX (PARE/) PAREKH R B.

XX (ROHL/) ROHLFF C.

XX Herath HMAC, Parekh RB, Rohlf C;

XX WPI; 2003-540784/51.

XX Screening, diagnosis or prognosis of Alzheimer's disease in subject,
 PT involves analyzing test sample of brain tissue from subject, and
 PT comparing feature in test sample with that of person(s) free from
 PT Alzheimer's disease.

XX Disclosure; SEQ ID NO 789; 115pp; English.

XX The invention relates to a method of screening or diagnosing Alzheimer's
 CC disease in a subject. The method is useful for screening, diagnosis or
 CC prognosis of Alzheimer's disease in a subject for determining the stage
 CC of severity of Alzheimer's disease in a subject, for identifying a
 CC subject at risk of developing Alzheimer's disease, or for monitoring the
 CC effect of therapy administered to a subject having Alzheimer's disease.
 CC The method is also useful in treating vascular dementia, Lewy body
 CC dementia, schizophrenia, Parkinson's disease, multiple sclerosis or
 CC depression. The inventive method identifies sensitive and specific
 CC biomarkers for the diagnosis of Alzheimer's disease in living subjects.
 CC It provides therapeutic agents for Alzheimer's disease that works
 CC quickly, potentially, specifically with fewer side effects. The present
 CC sequence represents the amino acid sequence of a Alzheimer's disease-
 CC associated protein isoform tryptic peptide.

XX Sequence 15 AA;

Query Match 44.4%; Score 32; DB 6; Length 15;
 Best Local Similarity 60.0%; Pred. No. 51;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 5 SAFOVDITID 14
 | | | | |
 Db 5 SGFOIETID 14

RESULT 10

AAR42489
 ID AAR42489 standard; protein; 17 AA.

XX AAR42489;

XX 25-MAR-2003 (revised)

DT 02-JUN-1994 (first entry)

XX Canine hookworm NIF tryptic fragment T24.

XX neutrophil inhibitory factor; NIF; glycoprotein; endoparasite; nematode;
 KW parasitic worm; canine hookworm; peritoneal inflammation.

XX Ancylostoma caninum.

XX WO9323063-A1.

XX 25-NOV-1993.

XX 11-MAY-1993; 93WO-US0004502.

XX 11-MAY-1992; 92US-00881721.

XX 24-DEC-1992; 92US-00996972.

XX (CORV-) CORVAS INT INC.

XX Moyle M, Foster DL, Vlasuk GP;

XX WPI; 1993-386208/48.

XX New neutrophil inhibitory factor from parasitic worms - for preventing
 PT and treating inflammation, also derived nucleic acid, vectors,
 PT transformed hosts and antibodies.

XX Example 9; Fig 7; 114pp; English.

XX Neutrophil Inhibitory Factor was isolated from canine hookworms. The NIF
 CC was digested with either endoprotease AspN, LysC or trypsin and the
 CC resulting proteolytic fragments were sequenced. See AAR42489- AAR42493
 CC for the trypsin fragments. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 17 AA;

Query Match 44.4%; Score 32; DB 2; Length 17;
 Best Local Similarity 75.0%; Pred. No. 59;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 SAFOVDIT 12
 | | | | |

Db 1 SAFELDIT 8

RESULT 11

AAR67769
 ID AAR67769 standard; protein; 17 AA.

XX AAR67769;

XX 25-MAR-2003 (revised)

DT 27-FEB-1995 (first entry)

XX Peptide fragment of neutrophil inhibitory factor (NIF).

XX Primer; neutrophil inhibitory factor; NIF; inflammation; adhesion;
 KW endothelial cells; inflammatory response.

```

XX OS Ancylostoma caninum.
XX PN WO9414973-A1.
XX PD 07-JUL-1994.
XX PF 23-DEC-1993; 93WO-US012626.
XX PR 24-DEC-1992; 92US-00996972.
XX PR 11-MAY-1993; 93US-00060433.
XX PR 10-NOV-1993; 93US-00151064.
XX PA (CORV-) CORVAS INT INC.
XX PI Moyle M, Foster DL, Vlasuk GP;
XX WI 1994-234706/28.
XX PT Neutrophil inhibitory factor peptide(s) - derived from nematodes, useful
XX for therapy of inflammatory responses.
XX PS Example 9; Fig 7; 239pp; English.
XX CC Neutrophil inhibitory factors can be used in compositions to inhibit
XX CC neutrophil activity e.g. adhesion to vascular endothelial cells, and
XX CC which are useful in the therapy of conditions which involve abnormal or
XX CC undesired inflammatory responses. This is a peptide fragment of a
XX CC neutrophil inhibitory factor from canine hookworm which was designated T-
XX CC 24 and obtained by trypsin digestion of the factor. (Updated on 25-MAR-
XX CC 2003 to correct PN field.)
XX SQ Sequence 17 AA;
Query Match 44.4%; Score 32; DB 2; Length 17;
Best Local Similarity 75.0%; Pred. No. 59;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 5 SAFQVDIT 12
DB 1 SAFELDIT 8
RESULT 12
AAY23572
ID AAY23572 standard; peptide; 17 AA.
XX AC AAY23572;
XX DT 03-SEP-1999 (first entry)
XX DE Peptide fragment of canine hookworm NIF.
XX KW Neutrophil inhibitory factor; NIF; mutant; shock; stroke;
XX KW allograft rejection; vasculitis; autoimmune diabetes; ARDS;
XX KW rheumatoid arthritis; inflammatory skin disease; myocardial infarction;
XX KW inflammatory bowel disease; adult respiratory distress syndrome;
XX KW ischemia-reperfusion injury; acute inflammation; bacterial infection;
XX KW vaccine; parasitic worm infection; antihelminic.
XX OS Ancylostoma caninum.
XX PN US5919900-A.
XX PD 06-JUL-1999.
XX PF 26-MAY-1995; 95US-00450497.
XX PR 11-MAY-1992; 92US-00881721.
XX PR 24-DEC-1992; 92US-00996972.
XX PR 11-MAY-1993; 93US-00060433.
XX PR 10-NOV-1993; 93US-00151064.
XX PR 23-DEC-1993; 93US-00173510.
XX PA (CORV-) CORVAS INT INC.
XX PI Moyle M, Foster DL;
XX WI 1999-403975/34.
XX PT Mutant Neutrophil Inhibitory Factors useful for treating inflammatory
XX conditions and especially to prevent or decrease inflammatory responses.
XX PS Example 9; Fig 7A; 131pp; English.
XX CC The specification describes mutant Neutrophil Inhibitory Factors (NIFs),
XX CC where at least 1 of the Asp residues at positions 18, 87, 110, 130, 197,
XX CC or 223 in the wild type sequence (see AAY23591) is replaced by a Gln
XX CC residue. NIFs may be useful for treating shock, stroke, acute and chronic
XX CC allograft rejection, vasculitis, autoimmune diabetes, rheumatoid
XX CC arthritis, inflammatory skin diseases, inflammatory bowel disease, adult
XX CC respiratory distress syndrome (ARDS), ischemia-reperfusion injury
XX CC following myocardial infarction, and acute inflammation caused by
XX CC bacterial infection such as sepsis or bacterial meningitis. NIFs or NIF
XX CC fragments may be used as vaccines against parasitic worm infection. Anti-
XX CC NIF antibodies may be useful for detecting infection of a mammalian host
XX CC by a parasitic worm, as antihelminic agents, and in the detection and
XX CC isolation of NIF from tissue homogenates, cloned cells etc. NIFs may be
XX CC useful for the detection of NIF mimics or antagonists in other compounds.
XX CC Other NIF agonists and inhibitors may also be used as antihelminic
XX CC agents. AAY23572-90 represent peptide fragments of a canine hookworm NIF,
XX CC obtained after proteolytic digestion
XX SQ Sequence 17 AA;
Query Match 44.4%; Score 32; DB 2; Length 17;
Best Local Similarity 75.0%; Pred. No. 59;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 5 SAFQVDIT 12
DB 1 SAFELDIT 8
RESULT 13
AAR34228
ID AAR34228 standard; peptide; 21 AA.
XX AC AAR34228;
XX DT 25-MAR-2003 (revised)
XX DT 04-AUG-1993 (first entry)
XX DE HTLV-I gp46 external envelope glycoprotein fragment 4.
XX KW Human T-cell leukaemia virus; hydrophilic; conjugate; aggregate;
XX KW diagnosis; antibodies.
XX OS Synthetic.
XX PN WO9306843-A1.
XX PD 15-APR-1993.
XX PF 08-OCT-1992; 92WO-US008405.
XX PR 08-OCT-1991; 91US-00771553.
XX PA (UYDU-) UNIV DUKE.
XX PI Palker TJ, Haynes BF;
XX WI 1993-134125/16.
XX PT Antigenic determinant peptide(s) of HTLV envelope glyco:protein - useful
XX for detecting anti-HTLV-I and -II antibodies and as vaccine against HTLV.

```

[illegible]

Db |:|:|
 6 YNAYQVD 12

Search completed: November 14, 2004, 12:02:14
Job time : 42.5106 secs

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OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:25 ; Search time 8.6383 Seconds
(without alignments)
155.938 Million cell updates/sec

Title: US-09-831-253F-7
Perfect score: 72
Sequence: 1 SNPYSAFQVDITD 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 4495

Minimum DB seq length: 0
Maximum DB seq length: 23

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	43.1	22	2 C39800	calcium-activated
2	31	43.1	23	2 PS0446	potassium channel
3	30	41.7	23	2 A48968	exo-poly-alpha-gal
4	27	37.5	16	2 S16376	L-serine dehydrata
5	27	37.5	21	2 S69371	duodenase - bovine
6	26	36.1	17	2 A58946	formylmethanofuran
7	26	36.1	22	2 S05236	exoenzyme C3 - Clo
8	25	34.7	11	2 S00616	paraspinal crystal
9	25	34.7	14	2 B44854	L-2,4-diaminobuty
10	23	31.9	13	2 A54326	glandular kallikre
11	22	30.6	12	2 A61360	vespakinin M - hor
12	22	30.6	14	2 PS0371	hypothetical prote
13	22	30.6	15	2 A61612	allatostatin - tob
14	22	30.6	17	2 A61334	trypsin (EC 3.4.21
15	22	30.6	18	2 S43834	DNA topoisomerase
16	22	30.6	19	2 A61110	68K collagen-bind
17	22	30.6	20	2 A85659	hypothetical prote
18	21.5	29.9	11	2 A35646	mast cell proteina
19	21	29.2	21	2 A40795	glycoprotein H-a -
20	21	29.2	12	2 S36899	ribosomal protein
21	21	29.2	13	2 FC2369	unidentified 85k p
22	21	29.2	16	2 A48301	glutamate-1-semial
23	21	29.2	20	2 S27351	lysophospholipase
24	21	29.2	23	2 PH1361	Ig heavy chain DJ
25	21	29.2	23	2 PH1729	Ig heavy chain V r
26	20	27.8	9	2 S10784	enamelin i - bovin
27	20	27.8	11	2 FT0229	Ig heavy chain CDR
28	20	27.8	14	2 A59018	MUC1 enhancer bind
29	20	27.8	15	2 S08209	hypothetical prote

30	20	27.8	17	2 A48179	methane monooxygen
31	20	27.8	18	2 A45138	arsenite oxidase I
32	20	27.8	20	2 I79432	MHC class II histo
33	20	27.8	22	2 B33174	sormatin - sorghum
34	20	27.8	23	2 A44524	pregnancy-specific
35	19	26.4	9	2 S36898	ribosomal protein
36	19	26.4	13	2 G22565	R-phycoerythrin ga
37	19	26.4	14	2 PT0077	proteochondroitin c
38	19	26.4	14	2 A28018	very late antigen-
39	19	26.4	15	2 G24417	interphotoreceptor
40	19	26.4	17	2 PH1802	T cell receptor al
41	19	26.4	18	2 A61392	brain-associated s
42	19	26.4	18	2 S59490	translation elonga
43	19	26.4	19	2 D24417	interphotoreceptor
44	19	26.4	19	2 B26930	ermG leader peptid
45	19	26.4	20	2 A53875	creatine kinase (E

ALIGNMENTS

RESULT 1

C39800

Calcium-activated potassium channel, alternate exon B - fruit fly (Drosophila melanogaster)

C;Species: Drosophila melanogaster

C;Date: 27-Mar-1992 #sequence_revision 27-Mar-1992 #text_change 09-Jul-2004

C;Accession: C39800

R;Atkinson, N.S.; Robertson, G.A.; Ganetzky, B.

Science 253, 551-555, 1991

A;Title: A component of calcium-activated potassium channels encoded by the Drosophila

A;Reference number: A39800; MUID:91313401; PMID:1857984

A;Accession: C39800

A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tr

A;Molecule type: mRNA

A;Residues: 1-22 <ATK>

A;Cross-references: UNIPROT:Q03720

C;Genetics:

A;Gene: FlyBase:slo

A;Cross-references: FlyBase:FBgn0003429

Query Match 43.1%; Score 31; DB 2; Length 22;

Best Local Similarity 44.4%; Pred. No. 35;

Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNPYSAFQV 9

Db 6 ANPYAGYQL 14

RESULT 2

PS0446

potassium channel protein Slo 11 - fruit fly (Drosophila melanogaster) (fragment)

C;Species: Drosophila melanogaster

C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004

C;Accession: PS0446

R;Adelman, J.P.; Shen, K.Z.; Kavanaugh, M.P.; Warren, R.A.; Wu, Y.N.; Lagrutta, A.; Bon

Neuron 9, 209-216, 1992

A;Title: Calcium-activated potassium channels expressed from cloned complementary DNAs.

A;Reference number: JH0697; MUID:92360298; PMID:1497890

A;Accession: PS0446

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-23 <ADE>

A;Cross-references: UNIPROT:Q03720

C;Comment: This potassium channel is activated by calcium.

C;Genetics:

A;Gene: FlyBase:slo

A;Cross-references: FlyBase:FBgn0003429

C;Keywords: alternative splicing; ion channel; potassium channel; transmembrane protein

Query Match 43.1%; Score 31; DB 2; Length 23;

Best Local Similarity 44.4%; Pred. No. 37;

Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNPYSAFQV 9
:||||:|
Db 7 ANPYAGYQL 15

RESULT 3
A48968
exo-poly-alpha-galacturonidase (EC 3.2.1.82) - Clostridium thermosaccharolyticum (frag
N/Alternate names: exo-poly-alpha-galacturonate hydrolase
C/Species: Clostridium thermosaccharolyticum, Clostridium tartarivorum
C/Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 06-Dec-1996
C/Accession: A48968
R/Van Rijssel, M.; Gervig, G.J.; Hansen, T.A.
Appl. Environ. Microbiol. 59, 828-836, 1993
A/Title: Isolation and characterization of an extracellular glycosylated protein complex
A/Reference number: A48968; MUID:93243739; PMID:8481009
A/Accession: A48968
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-23 <VAN>
A/Note: sequence extracted from NCBI backbone (NCBIP:130462)
C/Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 41.7%; Score 30; DB 2; Length 23;
Best Local Similarity 45.5%; Pred. No. 56;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 YSAFQVDITD 14
:||||:|
Db 3 YAAFEYDXTFN 13

RESULT 4
S16376
L-serine dehydratase beta chain - Peptostreptococcus asaccharolyticus
C/Species: Peptostreptococcus asaccharolyticus
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C/Accession: S16376
R/Grabowski, R.; Buckel, W.
Eur. J. Biochem. 195, 89-94, 1991
A/Title: Purification and properties of an iron-sulfur-containing and pyridoxal-phosphat
A/Reference number: S16224; MUID:91293139; PMID:2065681
A/Accession: S16376
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-16 <EUR>
A/Cross-references: UNIPROT:P33074

Query Match 37.5%; Score 27; DB 2; Length 16;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 YSAFQV 9
:||||:|
Db 1 YSAFEV 6

RESULT 5
S69371
duodenase - bovine (fragment)
C/Species: Bos primigenius taurus (cattle)
C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C/Accession: S69371
R/Zamolodchikova, T.S.; Vorotyntseva, T.I.; Antonov, V.K.
Eur. J. Biochem. 227, 866-872, 1995
A/Title: Duodenase, a new serine protease of unusual specificity from bovine duodenal mu
A/Reference number: S69371; MUID:95172075; PMID:7867648
A/Accession: S69371
A/Molecule type: protein
A/Residues: 1-21 <ZAM>
A/Cross-references: UNIPROT:Q9GLN2
C/Superfamily: trypsin; trypsin homology

Query Match 37.5%; Score 27; DB 2; Length 21;
Best Local Similarity 71.4%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SNPYSAF 7
:||||:|
Db 11 SRPYMAF 17

RESULT 6
AS8946
formylmethanofuran dehydrogenase (EC 1.2.99.5) (molybdenum) chain C - Methanobacterium t
N/Alternate names: formylmethanofuran dehydrogenase (molybdenum) chain B [misidentificat
C/Species: Methanobacterium thermoautotrophicum
C/Date: 16-Apr-1999 #sequence_revision 16-Apr-1999 #text_change 04-Feb-2000
C/Accession: AS8946
R/Hochheimer, A.; Schmitz, R.A.; Thauer, R.K.; Hedderich, R.
Eur. J. Biochem. 234, 910-920, 1995
A/Title: The tungsten formylmethanofuran dehydrogenase from Methanobacterium thermoautot
A/Reference number: S63519; MUID:96163477; PMID:8575452
A/Accession: AS8946
A/Molecule type: protein
A/Residues: 1-17 <HOC>
A/Note: the authors identify this peptide as the amino terminus of chain B, but it appea
C/Keywords: iron-sulfur protein; metalloprotein; molybdenum; molybdopterin; oxidoreduct

Query Match 36.1%; Score 26; DB 2; Length 17;
Best Local Similarity 41.7%; Pred. No. 2.1e+02;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 PYSAFQVDITD 14
:||||:|
Db 6 PTSDPQIGLEAD 17

RESULT 7
S05236
exoenzyme C3 - Clostridium botulinum (fragment)
C/Species: Clostridium botulinum
C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C/Accession: S05236
R/Torata, S.; Yokosawa, N.; Yokosawa, H.; Ishii, S.I.; Oguma, K.
FEBS Lett. 252, 83-87, 1989
A/Title: Immuno-crossreactivity between botulinum neurotoxin type C1 or D and exoenzyme
A/Reference number: S05236; MUID:89338716; PMID:2474453
A/Accession: S05236
A/Molecule type: protein
A/Residues: 1-22 <TOR>
A/Cross-references: UNIPROT:Q7M0L1

Query Match 36.1%; Score 26; DB 2; Length 22;
Best Local Similarity 45.5%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 SNPYSAFQVDI 11
:||||:|
Db 3 SNTYQEFNTNI 13

RESULT 8
S00616
parasporal crystal protein, wax moth-specific - Bacillus thuringiensis (strain galleria
N/Alternate names: delta-endotoxin; parasporal crystal protein positive chain
C/Species: Bacillus thuringiensis
C/Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C/Accession: S00616
R/Chestukhina, G.G.; Kostina, L.I.; Zalunin, I.A.; Khodova, O.M.; Stepanov, V.M.
FEBS Lett. 232, 249-251, 1988
A/Title: Bacillus thuringiensis ssp. galleriae simultaneously produces two delta-endotox
A/Reference number: S00615
A/Accession: S00616
A/Molecule type: protein

A;Residues: 1-11 <CHE>

A;Cross-references: UNIPROT:Q7M154

C;Comment: This toxin is effective against the larvae of Galleria melonella (greater wax moth)

C;Superfamily: parasporal crystal protein

C;Keywords: delta-endotoxin

Query Match 34.7%; Score 25; DB 2; Length 11;

Best Local Similarity 80.0%; Pred. No. 2e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNPYS 5

Db 5 NNPYS 9

RESULT 9

B44854

L-2,4-diaminobutyrate decarboxylase (EC 4.1.1.1) - Vibrio alginolyticus (fragment)

C;Species: Vibrio alginolyticus

C;Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C;Accession: B44854; B41817

R;Yamamoto, S.; Tsuzaki, Y.; Tougou, K.; Shinoda, S.

J. Gen. Microbiol. 138, 1461-1465, 1992

A;Title: Purification and characterization of L-2,4-diaminobutyrate decarboxylase from *Vibrio alginolyticus*

A;Reference number: A44854; MUID:92381494; PMID:1512577

A;Accession: B44854

A;Molecule type: protein

A;Residues: 1-14 <YAM>

A;Cross-references: UNIPROT:Q9F518

A;Note: sequence extracted from NCBI backbone (NCBIP:112332)

C;Keywords: carbon-carbon lyase; carboxy-lyase

Query Match 34.7%; Score 25; DB 2; Length 14;

Best Local Similarity 55.6%; Pred. No. 2.6e+02;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 SAFOVDITI 13

Db 2 TAPEVDSNI 10

RESULT 10

A54326

glandular kallikrein-1 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 29-Aug-1994 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995

C;Accession: A54326

R;Riegman, P.H.; Vlietstra, R.J.; van der Korput, H.A.; Romijn, J.C.; Trapman, J.

Mol. Cell. Endocrinol. 76, 181-190, 1991

A;Title: Identification and androgen-regulated expression of two major human glandular kallikreins

A;Reference number: A54326; MUID:92324494; PMID:1726490

A;Accession: A54326

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-13 <RIE>

A;Experimental source: prostate

A;Note: sequence extracted from NCBI backbone (NCBIP:108060)

Query Match 31.9%; Score 23; DB 2; Length 13;

Best Local Similarity 80.0%; Pred. No. 5.5e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNPYS 5

Db 2 SHPYS 6

RESULT 11

A61360

vespakinin M - hornet (Vespa mandarinia)

C;Species: Vespa mandarinia

C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004

C;Accession: A61360

R;Kishimura, H.; Yasuhara, T.; Yoshida, H.; Nakajima, T.

Chem. Pharm. Bull. 24, 2896-2897, 1976

A;Title: Vespakinin-M, a novel bradykinin analogue containing hydroxyproline, in the venom of *Vespa mandarinia*

A;Reference number: A61360; MUID:77114342; PMID:1017116

A;Accession: A61360

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-12 <KIS>

A;Cross-references: UNIPROT:Q7M3T3

C;Superfamily: unassigned animal peptides

C;Keywords: hydroxyproline; venom

F;4/Modified site: 4-hydroxyproline (Pro) #status experimental

Query Match 30.6%; Score 22; DB 2; Length 12;

Best Local Similarity 42.9%; Pred. No. 7.7e+02;

Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 YSAFQVD 10

Db 6 FSPFRID 12

RESULT 12

PS0371

hypothetical protein (psaC region) - *Synechococcus* sp. (fragment)

C;Species: *Synechococcus* sp.

C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 08-Oct-1999

C;Accession: PS0371

R;Rhiel, E.; Stirewalt, V.L.; Gasparich, G.E.; Bryant, D.A.

Gene 112, 123-128, 1992

A;Title: The psaC genes of *Synechococcus* sp. PCC7002 and *Cyanophora paradoxa*: cloning a

A;Reference number: JS0694; MUID:92201692; PMID:1551590

A;Accession: PS0371

A;Molecule type: DNA

A;Residues: 1-14 <RHI>

A;Cross-references: GB:M86238; NID:GL54574; PIDN:AAA27351.1; PID:G552030

Query Match 30.6%; Score 22; DB 2; Length 14;

Best Local Similarity 50.0%; Pred. No. 9.2e+02;

Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 7 FQVDIT 12

Db 4 FKLDVT 9

RESULT 13

A61612

allatostatatin - tobacco hornworm

C;Species: *Manduca sexta* (tobacco hornworm)

C;Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004

C;Accession: A61612

R;Kramer, S.J.; Toschi, A.; Miller, C.A.; Kataoka, H.; Quistad, G.B.; Li, J.P.; Carney,

Proc. Natl. Acad. Sci. U.S.A. 88, 9458-9462, 1991

A;Title: Identification of an allatostatatin from the tobacco hornworm *Manduca sexta*.

A;Reference number: A61612; MUID:92052112; PMID:1946359

A;Accession: A61612

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-15 <KRA>

A;Cross-references: UNIPROT:P42559

C;Keywords: neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 30.6%; Score 22; DB 2; Length 15;

Best Local Similarity 66.7%; Pred. No. 9.9e+02;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NPVSF 7

Db 10 NPISCF 15

RESULT 14

A61334
 trypsin (EC 3.4.21.4) 1 - starfish (*Dermasterias imbricata*) (fragment)
 C:Species: *Dermasterias imbricata*
 C>Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 09-Jul-2004
 C:Accession: A61334
 R:Estell, D.A.; Laskowski Jr., M.
 Biochemistry 19, 124-131, 1980
 A:Title: *Dermasterias imbricata* trypsin 1: an enzyme which rapidly hydrolyzes the reaction
 A:Reference number: A61334; MUID:80109692; PMID:7352972
 A:Accession: A61334
 A:Molecule type: protein
 A:Residues: 1-17 <EST>
 A:Cross-references: UNIPROT:O7M433
 C:Comment: This isoform is novel in that it readily dissociates from bovine pancreatic B
 inhibited.
 C:Superfamily: trypsin; trypsin homology
 C:Keywords: hydrolase; protein digestion; serine proteinase

Query Match 30.6%; Score 22; DB 2; Length 17;
 Best Local Similarity 66.7%; Pred. No. 1.1e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SNPYSA 6

Db 11 SRPYQA 16

RESULT 15

S43834
 DNA topoisomerase (EC 5.99.1.2) - *Klebsiella* sp. (ATCC 15380) (fragment)
 C:Species: *Klebsiella* sp.
 A:Variety: ATCC 15380
 C>Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 07-May-1999
 C:Accession: S43834
 R:lynnch, A.S.; Tyrrell, R.; Smerdon, S.J.; Briggs, G.S.; Wilkinson, A.J.
 Biochem. J. 299, 129-136, 1994
 A:Title: Characterization of the CysB protein of *Klebsiella aerogenes*: direct evidence b
 A:Reference number: S43834; MUID:94220019; PMID:8166630
 A:Accession: S43834
 A>Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-18 <LVN>
 A:Experimental source: ATCC 15380
 C:Genetics:
 A:Gene: topI
 C:Function:
 A:Description: catalyzes ATP-independent transient breakage of DNA phosphodiester bonds
 rejoining; this reaction will lead to the conversion of one topological isomer of DNA to
 C:Superfamily: bacterial type I DNA topoisomerase
 C:Keywords: DNA binding; DNA replication; isomerase; zinc finger

Query Match 30.6%; Score 22; DB 2; Length 18;
 Best Local Similarity 57.1%; Pred. No. 1.2e+03;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 YSAFQVD 10

Db 4 WSAFFID 10

Search completed: November 14, 2004, 12:03:13
 Job time : 8.6383 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:26 ; Search time 11.0213 Seconds
(without alignments)
84.242 Million cell updates/sec

Title: US-09-831-253F-7

Perfect score: 72
Sequence: 1 SNPYSAFOVDITID 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 202416

Minimum DB seq length: 0
Maximum DB seq length: 23

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	51.4	17	3	US-09-177-249-173
2	32	44.4	17	1	US-08-173-510B-63
3	32	44.4	17	1	US-08-458-218-61
4	32	44.4	17	2	US-08-450-497-63
5	32	44.4	17	4	US-08-060-433C-13
6	32	44.4	22	1	US-08-116-733-5
7	29	40.3	20	3	US-08-630-052-25
8	28	38.9	21	4	US-09-270-767-56843
9	27	37.5	14	2	US-08-934-222-110
10	27	37.5	14	2	US-08-933-402-110
11	27	37.5	14	2	US-09-207-621-110
12	27	37.5	14	2	US-08-532-818-110
13	27	37.5	14	3	US-09-231-797-110
14	27	37.5	14	3	US-08-934-224-110
15	27	37.5	14	3	US-08-933-843-110
16	27	37.5	14	3	US-08-934-223-110
17	27	37.5	14	3	US-09-413-492-110
18	27	37.5	17	1	US-08-435-925C-7
19	27	37.5	17	1	US-08-435-925C-8
20	27	37.5	21	1	US-08-290-373B-7
21	27	37.5	21	1	US-08-127-499A-18
22	27	37.5	21	1	US-08-482-847-18
23	26	36.1	7	1	US-08-281-193-3
24	26	36.1	7	1	US-08-422-106-3
25	26	36.1	7	2	US-08-735-716-3
26	26	36.1	7	2	US-08-555-568B-3
27	26	36.1	7	3	US-09-519-223-3

28	26	36.1	7	4	US-09-927-180-3	Sequence 3, Appli
29	26	36.1	7	5	PCT-US95-08069-3	Sequence 3, Appli
30	26	36.1	15	3	US-09-227-357-437	Sequence 437, App
31	26	36.1	22	1	US-08-399-696-89	Sequence 89, Appl
32	25	34.7	8	3	US-08-444-818-304	Sequence 304, App
33	25	34.7	8	3	US-08-444-818-305	Sequence 305, App
34	25	34.7	15	5	PCT-US91-09422-27	Sequence 27, Appl
35	25	34.7	16	3	US-08-847-844A-75	Sequence 75, Appl
36	25	34.7	18	4	US-09-250-609-39	Sequence 39, Appl
37	25	34.7	18	4	US-09-250-611-39	Sequence 39, Appl
38	25	34.7	20	3	US-08-612-973-56	Sequence 56, Appl
39	25	34.7	20	3	US-08-927-597-56	Sequence 56, Appl
40	25	34.7	20	4	US-08-635-886C-15	Sequence 15, Appl
41	25	34.7	20	4	US-08-974-690C-15	Sequence 15, Appl
42	25	34.7	20	4	US-08-974-685-15	Sequence 15, Appl
43	25	34.7	20	4	US-08-861-153A-10	Sequence 10, Appl
44	25	34.7	21	3	US-08-907-468-11	Sequence 11, Appl
45	24.5	34.0	17	3	US-08-652-877-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-177-249-173
; Sequence 173, Application US/09177249
; Patent No. 6229064
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Yadegari, Ramin
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit
; FILE REFERENCE: 023070-086120US
; CURRENT APPLICATION NUMBER: US/09/177,249
; CURRENT FILING DATE: 1998-10-22
; EARLIER APPLICATION NUMBER: US 09/071,838
; EARLIER FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 173
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-09-177-249-173

Query Match 51.4%; Score 37; DB 3; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.9;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 SNPYSAFOVDITID 14
||||| : : :
Db 3 SNPYRKFKNYTKD 16

RESULT 2
US-08-173-510B-63
; Sequence 63, Application US/08173510B
; Patent No. 5747296
; GENERAL INFORMATION:
; APPLICANT: MATTHEW MOYLE, ET AL.
; TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles

STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,510B
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/151,064
FILING DATE: 10-NOV-1993
APPLICATION NUMBER: 08/060,433
FILING DATE: 11-MAY-1993
APPLICATION NUMBER: 07/996,972
FILING DATE: 24-DEC-1992
APPLICATION NUMBER: 07/881,721
FILING DATE: 11-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 205/073
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 AMINO ACIDS
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE
US-08-173-510B-63

Query Match 44.4%; Score 32; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 16;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 SAFQVDIT 12
|||:|
Db 1 SAFELDIT 8

RESULT 3
US-08-458-218-61
Sequence 61, Application US/08458218
Patent No. 5789178
GENERAL INFORMATION:
APPLICANT: MATTHEW MOYLE ET AL.
TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS
NUMBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,218
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/151,064
FILING DATE: 10-NOVEMBER-1993
APPLICATION NUMBER: 08/060,433
FILING DATE: 11-MAY-1993
APPLICATION NUMBER: 07/881,721
FILING DATE: 11-MAY-1992
APPLICATION NUMBER: 07/996,972
FILING DATE: 24-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 203/226
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 AMINO ACIDS
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE
US-08-458-218-61

Query Match 44.4%; Score 32; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 16;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 SAFQVDIT 12
|||:|
Db 1 SAFELDIT 8

RESULT 4
US-08-450-497-63
Sequence 63, Application US/08450497
Patent No. 5919900
GENERAL INFORMATION:
APPLICANT: MATTHEW MOYLE, ET AL.
TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,497
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/173,510
FILING DATE: 23-DEC-1993
APPLICATION NUMBER: 08/151,064
FILING DATE: 10-NOV-1993
APPLICATION NUMBER: 08/060,433
FILING DATE: 11-MAY-1993
APPLICATION NUMBER: 07/996,972
FILING DATE: 24-DEC-1992
APPLICATION NUMBER: 07/881,721
FILING DATE: 11-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 205/073

TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 AMINO ACIDS
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE
US-08-450-497-63

Query Match 44.4%; Score 32; DB 2; Length 17;
Best Local Similarity 75.0%; Pred. No. 16;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 SAFQVDIT 12
|||:||||
Db 1 SAFELDIT 8

RESULT 5
US-08-060-433C-13
Sequence 13, Application US/08060433C
Patent No. 6756211
GENERAL INFORMATION:
APPLICANT: MATTHEW MOYLE ET AL.
TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44
MEDIUM TYPE: Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/060,433C
FILING DATE: 11 May 1993
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/881,721
FILING DATE: 11 May 1992
APPLICATION NUMBER: 07/996,972
FILING DATE: 24 December 1992
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 200/271
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 AMINO ACIDS
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE
US-08-060-433C-13

Query Match 44.4%; Score 32; DB 4; Length 17;
Best Local Similarity 75.0%; Pred. No. 16;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 SAFQVDIT 12

Db 1 SAFELDIT 8
|||:||||

RESULT 6
US-08-116-733-5
Sequence 5, Application US/08116733
Patent No. 5516632
GENERAL INFORMATION:
APPLICANT: PALKER, Thomas J.
APPLICANT: HAYNES, Barton F.
TITLE OF INVENTION: SYNTHETIC PEPTIDES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/116,733
FILING DATE: 07-SEP-1993
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1579-33
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-116-733-5

Query Match 44.4%; Score 32; DB 1; Length 22;
Best Local Similarity 54.5%; Pred. No. 22;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 SNPYSAFQVDI 11
|||:||||
Db 1 SSPYWKQHDV 11

RESULT 7
US-08-630-052-25
Sequence 25, Application US/08630052
Patent No. 639296
GENERAL INFORMATION:
APPLICANT: Brent, Roger
APPLICANT: McCoy, John M.
APPLICANT: Jessen, Timm H.
APPLICANT: Xu, Chanxing Wilson
TITLE OF INVENTION: INTERACTION TRAP SYSTEMS FOR DETECTING PROTEIN
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,052
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/504,538
FILING DATE: July 20, 1995
APPLICATION NUMBER: 08/278,082
FILING DATE: July 20, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Karen F. Lech
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/311001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-630-052-25

Query Match 40.3%; Score 29; DB 3; Length 20;
Best Local Similarity 62.5%; Pred. No. 71;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 PYSAFQVD 10
|:|:|:
Db 13 PHSVFND 20

RESULT 8
US-09-270-767-56843
Sequence 56843, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 56843
LENGTH: 21
TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-56843

Query Match 38.9%; Score 28; DB 4; Length 21;
Best Local Similarity 27.3%; Pred. No. 1.2e+02;
Matches 3; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 4 YSAFQVDITD 14
|:|:|:
Db 7 YXKFNDVSLN 17

RESULT 9
US-08-934-222-110
Sequence 110, Application US/08934222
Patent No. 5928896

GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
CONSTRAINING GROUPS WHICH FLANK A PROTEIN-PROTEIN INTERACTION
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,222
FILING DATE: 19-SEPT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isaacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-934-222-110

Query Match 37.5%; Score 27; DB 2; Length 14;
Best Local Similarity 57.1%; Pred. No. 1.1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAPQ 8
|:|:|:
Db 1 NPTVTFQ 7

RESULT 10
US-08-933-402-110
Sequence 110, Application US/08933402
Patent No. 5948887
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
CONSTRAINING GROUPS WHICH FLANK A PROTEIN-PROTEIN INTERACTION
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,402
FILING DATE: 19-SEPT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isaacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-933-402-110

Query Match 37.5%; Score 27; DB 2; Length 14;
Best Local Similarity 57.1%; Pred. No. 1.1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8
Db 1 NPWTVFQ 7

RESULT 11

US-09-207-621-110
Sequence 110, Application US/09207621
Patent No. 5952465
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/207,621
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isaacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148

INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-207-621-110

Query Match 37.5%; Score 27; DB 2; Length 14;
Best Local Similarity 57.1%; Pred. No. 1.1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8
Db 1 NPWTVFQ 7

RESULT 12

US-08-532-818-110
Sequence 110, Application US/08532818
Patent No. 5965698
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/532,818
FILING DATE: 03-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isaacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-532-818-110

Query Match 37.5%; Score 27; DB 2; Length 14;
Best Local Similarity 57.1%; Pred. No. 1.1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8
Db 1 NPWTVFQ 7

RESULT 13

US-09-231-797-110

; Sequence 110, Application US/09231797
; Patent No. 6084066

; GENERAL INFORMATION:

; APPLICANT: EVANS, Herbert J.

; APPLICANT: KINI, R. Manjunatha

; TITLE OF INVENTION: Polypeptides That Include Conformation-

; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction

; NUMBER OF SEQUENCES: 153

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: Suite 500, 3000 K Street NW

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20007

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/231,797

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/532,818

; FILING DATE: 03-MAY-1996

; APPLICATION NUMBER: PCT/US94/04294

; FILING DATE: 21-APR-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: U.S. 08/143,364

; FILING DATE: 29-OCT-1993

; APPLICATION NUMBER: U.S. 08/051,741

; FILING DATE: 23-APR-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Isaacson, John P.

; REGISTRATION NUMBER: 33,751

; REFERENCE/DOCKET NUMBER: 040433/0148

; INFORMATION FOR SEQ ID NO: 110:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 14 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; US-09-231-797-110

Query Match

Best Local Similarity 37.5%; Score 27; DB 3; Length 14;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8

Db 1 NPWTVFQ 7

RESULT 14

US-08-934-224-110

; Sequence 110, Application US/08934224

; Patent No. 6100044

; GENERAL INFORMATION:

; APPLICANT: EVANS, Herbert J.

; APPLICANT: KINI, R. Manjunatha

; TITLE OF INVENTION: Polypeptides That Include Conformation-

; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction

; NUMBER OF SEQUENCES: 153

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: Suite 500, 3000 K Street NW

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20007

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/934,224

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/532,818

; FILING DATE: 03-MAY-1996

; APPLICATION NUMBER: PCT/US94/04294

; FILING DATE: 21-APR-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: U.S. 08/143,364

; FILING DATE: 29-OCT-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: U.S. 08/051,741

; FILING DATE: 23-APR-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Isaacson, John P.

; REGISTRATION NUMBER: 33,751

; REFERENCE/DOCKET NUMBER: 040433/0148

; INFORMATION FOR SEQ ID NO: 110:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 14 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; US-08-934-224-110

Query Match

Best Local Similarity 37.5%; Score 27; DB 3; Length 14;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8

Db 1 NPWTVFQ 7

RESULT 15

US-08-933-843-110

; Sequence 110, Application US/08933843

; Patent No. 6111069

; GENERAL INFORMATION:

; APPLICANT: EVANS, Herbert J.

; APPLICANT: KINI, R. Manjunatha

; TITLE OF INVENTION: Polypeptides That Include Conformation-

; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction

; NUMBER OF SEQUENCES: 153

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: Suite 500, 3000 K Street NW

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20007

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/933,843

; FILING DATE: 19-SEPT-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/532,818

; FILING DATE: 03-MAY-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: U.S. 08/143,364

; FILING DATE: 29-OCT-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: U.S. 08/051,741

; FILING DATE: 23-APR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Isacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-933-843-110

Query Match 37.5%; Score 27; DB 3; Length 14;
Best Local Similarity 57.1%; Pred.No. 1.1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8
||:|
Db 1 NPWTVFQ 7

Search completed: November 14, 2004, 12:08:49
Job time : 11.0213 secs

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QY 2 NPYSAPQ 8
||: ||
Db 1 NPWTVPQ 7

RESULT 2

US-08-933-402-110
; Sequence 110, Application US/08933402
; Patent No. 5948887
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
; TITLE OF INVENTION: Site
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/933,402
; FILING DATE: 19-SEPT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isaacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-933-402-110

Query Match 37.5%; Score 27; DB 2; Length 14;
Best Local Similarity 57.1%; Pred.No. 1.le+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAPQ 8
||: ||
Db 1 NPWTVPQ 7

RESULT 3

US-09-207-621-110
; Sequence 110, Application US/09207621
; Patent No. 5952465
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
; TITLE OF INVENTION: Site
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW

; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/207,621
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
; APPLICATION NUMBER: PCT/US94/04294
; FILING DATE: 21-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isaacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-09-207-621-110

Query Match 37.5%; Score 27; DB 2; Length 14;
Best Local Similarity 57.1%; Pred.No. 1.le+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAPQ 8
||: ||
Db 1 NPWTVPQ 7

RESULT 4

US-08-532-818-110
; Sequence 110, Application US/08532818
; Patent No. 5965698
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
; TITLE OF INVENTION: Site
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/532,818
; FILING DATE: 03-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/04294
; FILING DATE: 21-APR-1994
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isaacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-532-818-110

Query Match 37.5%; Score 27; DB 2; Length 14;
Best Local Similarity 57.1%; Pred. No. 1.1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8
||: ||
DB 1 NPWTVFQ 7

RESULT 5

US-09-231-797-110
Sequence 110, Application US/09231797
Patent No. 6084066
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction S
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/231,797
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isaacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-231-797-110

Query Match 37.5%; Score 27; DB 3; Length 14;

Best Local Similarity 57.1%; Pred. No. 1.1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8
||: ||
DB 1 NPWTVFQ 7

RESULT 6

US-08-934-224-110
Sequence 110, Application US/08934224
Patent No. 6100044
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,224
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isaacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-934-224-110

Query Match 37.5%; Score 27; DB 3; Length 14;
Best Local Similarity 57.1%; Pred. No. 1.1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8
||: ||
DB 1 NPWTVFQ 7

RESULT 7

US-08-933-843-110
Sequence 110, Application US/08933843
Patent No. 6111069
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-

```

; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
; TITLE OF INVENTION: Site
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/933,843
; FILING DATE: 19-SEPT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isaacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-933-843-110

Query Match 37.5%; Score 27; DB 3; Length 14;
Best Local Similarity 57.1%; Pred. No. 1.le+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8
Db 1 NPWTVFQ 7

RESULT 8
US-08-934-223-110
; Sequence 110, Application US/08934223
; Patent No. 6147189
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
; TITLE OF INVENTION: Site
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,223
; FILING DATE:

; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
; TITLE OF INVENTION: Site
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,223
; FILING DATE:

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/532,818
; FILING DATE: 03-MAY-1996
; APPLICATION NUMBER: PCT/US94/04294
; FILING DATE: 21-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isaacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-934-223-110

Query Match 37.5%; Score 27; DB 3; Length 14;
Best Local Similarity 57.1%; Pred. No. 1.le+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8
Db 1 NPWTVFQ 7

RESULT 9
US-09-413-492-110
; Sequence 110, Application US/09413492
; Patent No. 6258550
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
; TITLE OF INVENTION: Site
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/413,492
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
; APPLICATION NUMBER: PCT/US94/04294
; FILING DATE: 21-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isaacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 110:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-09-413-492-110

Query Match 37.5%; Score 27; DB 3; Length 14;
Best Local Similarity 57.1%; Pred. No. 1.1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8
||:|:
Db 1 NPWTVFQ 7

RESULT 10
US-08-281-193-3
; Sequence 3, Application US/08281193
; Patent No. 5466595
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 15
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/281,193
; FILING DATE:
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
US-08-281-193-3

Query Match 36.1%; Score 26; DB 1; Length 7;
Best Local Similarity 57.1%; Pred. No. 3.8e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8
||:|:
Db 1 NPHSGFR 7

RESULT 11
US-08-422-106-3
; Sequence 3, Application US/08422106
; Patent No. 5589170
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 15
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,106
; FILING DATE: 14-APR-1995
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
US-08-422-106-3

; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
US-08-422-106-3

Query Match 36.1%; Score 26; DB 1; Length 7;
Best Local Similarity 57.1%; Pred. No. 3.8e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8
||:|:
Db 1 NPHSGFR 7

RESULT 12
US-08-735-716-3
; Sequence 3, Application US/08735716
; Patent No. 5840511
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 15
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/735,716
; FILING DATE: 23-OCT-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/281,193
; FILING DATE: 27-JUL-1994
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
US-08-735-716-3

Query Match 36.1%; Score 26; DB 2; Length 7;
Best Local Similarity 57.1%; Pred. No. 3.8e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8
||:|:
Db 1 NPHSGFR 7

RESULT 13
US-08-555-568B-3
; Sequence 3, Application US/08555568B
; Patent No. 5976854
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts

COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/555,568B
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-08-555-568B-3

Query Match 36.1%; Score 26; DB 2; Length 7;
Best Local Similarity 57.1%; Pred. No. 3.8e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAPQ 8
Db 1 NPHSGFR 7

RESULT 14
US-09-519-223-3
; Sequence 3, Application US/09519223
; Patent No. 6274140
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/519,223
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-09-519-223-3
Query Match 36.1%; Score 26; DB 3; Length 7;
Best Local Similarity 57.1%; Pred. No. 3.8e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2 NPYSAPQ 8
Db 1 NPHSGFR 7
RESULT 15
US-09-927-180-3
; Sequence 3, Application US/09927180
; Patent No. 6645736
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
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; FILING DATE: 09-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/519,223
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-927-180-3
Query Match 36.1%; Score 26; DB 4; Length 7;
Best Local Similarity 57.1%; Pred. No. 3.8e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAPQ 8
Db 1 NPHSGFR 7

Search completed: November 14, 2004, 13:46:48
Job time : 28.5 secs

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OM protein - protein search, using sw model

Run on: November 14, 2004, 13:45:09 ; Search time 94.5 Seconds
(without alignments)
52.418 Million cell updates/sec

Title: US-09-831-253F-7
Perfect score: 72
Sequence: 1 SNPSAFQVDITID 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1568699 seqs, 353819137 residues

Total number of hits satisfying chosen parameters: 222219

Minimum DB seq length: 0
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

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- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
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- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	38.9	10	US-09-880-748-3097	Sequence 3097, Ap
2	28	38.9	10	US-10-293-418-3097	Sequence 3097, Ap
3	28	38.9	13	US-09-842-776A-30	Sequence 30, Appl
4	27	37.5	11	US-09-880-748-2839	Sequence 2839, Ap
5	27	37.5	11	US-10-293-418-2839	Sequence 2839, Ap
6	27	37.5	12	US-10-286-457-177	Sequence 177, Appl
7	26.5	36.8	10	US-10-151-882-26	Sequence 26, Appl
8	26	36.1	7	US-09-927-180-3	Sequence 3, Appl
9	26	36.1	9	US-10-334-726-118	Sequence 118, Appl
10	26	36.1	9	US-10-334-726-220	Sequence 220, Appl
11	25	34.7	7	US-10-400-931-50	Sequence 50, Appl
12	25	34.7	9	US-09-995-529-83	Sequence 83, Appl
13	25	34.7	9	US-09-995-529-83	Sequence 83, Appl

14	25	34.7	10	US-09-572-404B-2428	Sequence 2428, Ap
15	25	34.7	10	US-10-327-598-519	Sequence 519, Appl
16	25	34.7	11	US-09-966-871-70	Sequence 70, Appl
17	25	34.7	11	US-10-039-645-70	Sequence 70, Appl
18	25	34.7	11	US-10-139-084-70	Sequence 70, Appl
19	25	34.7	11	US-10-458-860-70	Sequence 70, Appl
20	25	34.7	11	US-10-625-047-8	Sequence 8, Appl
21	25	34.7	12	US-10-073-118-30	Sequence 30, Appl
22	25	34.7	12	US-10-128-520-34	Sequence 34, Appl
23	25	34.7	13	US-09-855-604-602	Sequence 602, Appl
24	25	34.7	13	US-09-855-604-792	Sequence 792, Appl
25	25	34.7	14	US-10-365-738-15	Sequence 15, Appl
26	24	33.3	8	US-10-182-452A-319	Sequence 319, Appl
27	24	33.3	8	US-10-182-452A-1072	Sequence 1072, Ap
28	24	33.3	8	US-10-182-452A-1073	Sequence 1073, Ap
29	24	33.3	8	US-10-182-452A-1074	Sequence 1074, Ap
30	24	33.3	8	US-10-182-452A-1085	Sequence 1085, Ap
31	24	33.3	8	US-10-182-452A-1086	Sequence 1086, Ap
32	24	33.3	8	US-10-182-452A-1087	Sequence 1087, Ap
33	24	33.3	8	US-10-182-452A-1104	Sequence 1104, Ap
34	24	33.3	8	US-10-182-452A-1105	Sequence 1105, Ap
35	24	33.3	8	US-10-182-452A-1106	Sequence 1106, Ap
36	24	33.3	8	US-10-182-452A-1112	Sequence 1112, Ap
37	24	33.3	8	US-10-182-452A-1113	Sequence 1113, Ap
38	24	33.3	8	US-10-182-452A-1282	Sequence 1282, Ap
39	24	33.3	10	US-09-572-404B-2193	Sequence 2193, Ap
40	24	33.3	10	US-10-200-708-99	Sequence 99, Appl
41	24	33.3	11	US-10-014-340-453	Sequence 453, Appl
42	24	33.3	12	US-10-652-407-11	Sequence 11, Appl
43	24	33.3	14	US-09-880-748-2619	Sequence 2619, Ap
44	24	33.3	14	US-10-293-418-2619	Sequence 2619, Ap
45	23.5	32.6	10	US-10-149-138-4377	Sequence 4377, Ap

ALIGNMENTS

RESULT 1

US-09-880-748-3097
; Sequence 3097, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3097
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-3097

Query Match 38.9%; Score 28; DB 10; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 NPYSAFQV 9

|||

3 SPYDAFDI 10

DB

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RESULT 2
US-10-293-418-3097
; Sequence 3097, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3097
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-3097

Query Match      38.9%; Score 28; DB 14; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 NPYSAFQV 9
DB      3 SPYDAFDI 10

RESULT 3
US-09-842-776A-30
; Sequence 30, Application US/09842776A
; Publication No. US20040023316A1
; GENERAL INFORMATION:
; APPLICANT: CONNEX GMBH
; TITLE OF INVENTION: NEW METHOD FOR DETECTING ACID-RESISTANT MICROORGANISMS
; FILE REFERENCE: 41735
; CURRENT APPLICATION NUMBER: US/09/842,776A
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: PCT/EP99/08212
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Complementarity determining region (CDR3) of an
; OTHER INFORMATION: antibody heavy chain directed to a beta-urease
; OTHER INFORMATION: epitope (alternative sequence)
US-09-842-776A-30

Query Match      38.9%; Score 28; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 SNPYS 5
DB      6 SNPYS 10

RESULT 4
US-09-880-748-2839
; Sequence 2839, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2839
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2839

Query Match      37.5%; Score 27; DB 10; Length 11;
Best Local Similarity 57.1%; Pred. No. 3.7e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      3 PYSFAQV 9
DB      5 PYDAFDI 11

RESULT 5
US-10-293-418-2839
; Sequence 2839, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2839
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-10-293-418-2839

Query Match 37.5%; Score 27; DB 14; Length 11;
Best Local Similarity 57.1%; Pred. No. 3.7e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PYSAFQV 9
Db 5 PYDAFDI 11

RESULT 6

US-10-286-457-177
; Sequence 177, Application US/10286457
; Publication No. US20030166004A1
; GENERAL INFORMATION:
; APPLICANT: JENO GYURIS et al.
; TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY
; FILE REFERENCE: GPCI-P01-178
; CURRENT APPLICATION NUMBER: US/10/286,457
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 60/334822
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 684
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 177
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence isolated from random peptide libraries, based
; OTHER INFORMATION: ability to selectively bind to endothelial cells
US-10-286-457-177

Query Match 37.5%; Score 27; DB 14; Length 12;
Best Local Similarity 83.3%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNPWSA 6
Db 1 SNPWSA 6

RESULT 7

US-10-151-882-26
; Sequence 26, Application US/10151882
; Publication No. US20030059862A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
; FILE REFERENCE: PF554
; CURRENT APPLICATION NUMBER: US/10/151,882
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293,100
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-151-882-26

Query Match 36.8%; Score 26.5; DB 14; Length 10;
Best Local Similarity 60.0%; Pred. No. 4.1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Qy 1 SNP-YSAFOV 9
Db 1 SNPQYDAFDI 10

RESULT 8

US-09-927-180-3

; Sequence 3, Application US/09927180
; Patent No. US20020106364A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; Title of Invention: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/927,180
; FILING DATE: 09-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/519,223
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEetical: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-927-180-3

Query Match 36.1%; Score 26; DB 9; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.4e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 NPYSAFQ 8
Db 1 NPHSGFR 7

RESULT 9

US-10-334-726-118
; Sequence 118, Application US/10334726
; Publication No. US20030211521A1
; GENERAL INFORMATION:
; APPLICANT: TAYLOR-PAPADIMITROU, JOYCE
; TITLE OF INVENTION: BREAST CANCER ANTIGEN
; FILE REFERENCE: 1090-36
; CURRENT APPLICATION NUMBER: US/10/334,726
; CURRENT FILING DATE: 2003-01-02
; PRIOR APPLICATION NUMBER: US/09/645,446
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: PCT/GB99/00866
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: GB 9805877.9
; PRIOR FILING DATE: 1998-09-20
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 118
; LENGTH: 9

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:predicted
; OTHER INFORMATION: peptide
US-10-334-726-118

Query Match 36.1%; Score 26; DB 14; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAF 7
Db 3 NPNLNF 8

RESULT 10
US-10-334-726-220
; Sequence 220, Application US/10334726
; Publication No. US20030211521A1
; GENERAL INFORMATION:
; APPLICANT: TAYLOR-PAPADIMITROU, JOYCE
; TITLE OF INVENTION: BREAST CANCER ANTIGEN
; FILE REFERENCE: 1090-36
; CURRENT APPLICATION NUMBER: US/10/334,726
; PRIOR FILING DATE: 2003-01-02
; PRIOR APPLICATION NUMBER: US/09/645,446
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: PCT/GB99/00866
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: GB 9805877.9
; PRIOR FILING DATE: 1998-09-20
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 220
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:predicted
; OTHER INFORMATION: peptide
US-10-334-726-220

Query Match 36.1%; Score 26; DB 14; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAF 7
Db 4 NPNLNF 9

RESULT 11
US-10-400-991-50
; Sequence 50, Application US/10400991
; Publication No. US20030224417A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Weich, Nadine S.
; APPLICANT: Hunter, John J.
; APPLICANT: White, David
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Williamson, Mark J.
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Chun, Miyoung
; TITLE OF INVENTION: 1400, 2838, 14618, 15334, 14274, 32164,
; TITLE OF INVENTION: 39404, 38911, 26904, 31237, 18057, 16405, 32705, 23224,
; TITLE OF INVENTION: 27423, 32700, 32712 AND 12216. NOVEL SEVEN-TRANSMEMBRANE
; TITLE OF INVENTION: PROTEINS/G-PROTEIN COUPLES RECEPTORS
; FILE REFERENCE: NP103-0240NM1
; CURRENT APPLICATION NUMBER: US/10/400,991
; CURRENT FILING DATE: 2003-03-27

; PRIOR APPLICATION NUMBER: US 10/190,469
; PRIOR FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: US 09/439,159
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 09/137,063
; PRIOR FILING DATE: 1998-08-20
; PRIOR APPLICATION NUMBER: US 10/167,192
; PRIOR FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 09/420,187
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 09/173,869
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 10/339,056
; PRIOR FILING DATE: 2003-01-09
; PRIOR APPLICATION NUMBER: US 09/377,429
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: US 09/136,726
; PRIOR FILING DATE: 1998-08-19
; PRIOR APPLICATION NUMBER: US 09/911,583
; PRIOR FILING DATE: 2001-07-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino Acid Fragment
US-10-400-991-50

Query Match 34.7%; Score 25; DB 14; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 PYSAFQ 8
Db 1 PYSLPE 6

RESULT 12
US-09-995-529-83
; Sequence 83, Application US/09995529
; Publication No. US2003009655A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody mutation
US-09-995-529-83

Query Match 34.7%; Score 25; DB 10; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNPYS 5
Db 5 SNPYT 9

RESULT 13

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US-09-995-529-83
; Sequence 83, Application US/09995529
; Publication No. US20040091482A9
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; FILE OF INVENTION: Related Methods
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody mutation
US-09-995-529-83

Query Match          34.7%; Score 25; DB 11; Length 9;
Best Local Similarity 80.0%; Pred.No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNPYS 5
Db 5 SNPYT 9

RESULT 14
US-09-572-404B-2428
; Sequence 2428, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human Patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 2428
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in API2 OR IAP2 OR MIHB at 171-180 and may inter
; OTHER INFORMATION: with Sequence 2427 in this patent.
US-09-572-404B-2428

Query Match          34.7%; Score 25; DB 10; Length 10;
Best Local Similarity 80.0%; Pred.No. 7.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNPYS 5
Db 4 TNPYS 8

RESULT 15
US-10-327-598-519
; Sequence 519, Application US/10327598
; Publication No. US20040181039A1
; GENERAL INFORMATION:
; APPLICANT: Krah, Eugene
; APPLICANT: Guo, Honliang
; APPLICANT: Aiyappa, Ashok
; APPLICANT: Lawton, Robert
; TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, and
; TITLE OF INVENTION: for Making and Using Them
; FILE REFERENCE: 01-799-A
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; CURRENT APPLICATION NUMBER: US/10/327,598
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/344,874
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 1139
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 519
; LENGTH: 10
; TYPE: PRT
; ORGANISM: canis familiaris;
US-10-327-598-519

Query Match          34.7%; Score 25; DB 16; Length 10;
Best Local Similarity 57.1%; Pred.No. 7.7e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNPYSAF 7
Db 3 SRPFNAF 9

Search completed: November 14, 2004, 14:01:10
Job time : 95.5 secs
```

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OM protein - protein search, using sw model

Run on: November 14, 2004, 13:46:55 ; Search time 188 Seconds
(without alignments)
27.545 Million cell updates/sec

Title: US-09-831-253F-5

Perfect score: 48

Sequence: 1 TSLMIWTMM 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1598

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	39.6	8	2 O85406	O85406 coxiella bu
2	19	39.6	9	2 Q8NHL3	Q8NHL3 homo sapien
3	18	37.5	8	2 Q8IVK3	Q8IVK3 homo sapien
4	18	37.5	8	2 Q9H3Y3	Q9H3Y3 homo sapien
5	18	37.5	9	2 Q38366	Q38366 bacterioph
6	18	37.5	9	2 Q801K0	Q801K0 illicura mil
7	18	37.5	9	2 Q801K1	Q801K1 chiroxiphia
8	18	37.5	9	2 Q801K2	Q801K2 antilophia
9	17	35.4	8	2 Q99MN0	Q99MN0 mus musculu
10	17	35.4	9	2 Q71EB9	Q71EB9 homo sapien
11	17	35.4	9	2 AAQ08824	AAQ08824 homo sapi
12	16	33.3	8	2 Q86SLO	Q86SLO homo sapien
13	16	33.3	9	2 Q94VC6	Q94VC6 varanus pil
14	16	33.3	9	2 Q9R5M1	Q9R5M1 staphylococ
15	16	33.3	9	2 Q8X4G1	Q8X4G1 escherichia
16	15	31.2	6	1 E101 LITRU	P82096 litoria rub
17	15	31.2	7	1 WWA1_ACHFU	P35919 achatina fu
18	15	31.2	7	1 WWA2_ACHFU	P35921 achatina fu
19	15	31.2	7	1 WWA3_ACHFU	P35920 achatina fu
20	15	31.2	7	2 Q95945	Q95945 saccharomyc
21	15	31.2	8	2 Q70Y57	Q70Y57 fuerstia af
22	15	31.2	8	2 P77556	P77556 escherichia
23	15	31.2	8	2 CAD45547	CAD45547 fuerstia
24	15	31.2	9	2 Q6LDP7	Q6LDP7 rattus norv
25	15	31.2	9	2 Q69100	Q69100 human herpe
26	15	31.2	9	2 AAAG3501	AAAG3501 rattus no
27	14	29.2	7	2 Q8JEB1	Q8JEB1 human immun
28	14	29.2	8	1 C125 CYPDO	P83661 cyphononyx
29	14	29.2	8	1 COW2_CONPU	P58785 conus purpu
30	14	29.2	8	2 Q94VC1	Q94VC1 varanus rud
31	14	29.2	8	2 Q9SAY7	Q9SAY7 dioscorea t

RESULT 1

O85406 PRELIMINARY; PRT; 8 AA.
AC O85406;
DT 01-NOV-1998 (TREMELrel. 08, Created)
DT 01-NOV-1998 (TREMELrel. 08, Last sequence update)
DE Hypothetical protein (Fragment).
OS Coxiella burnetii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Coxiellaceae; Coxiella.
OX NCBI_TaxID=777;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Nine Mile Phase I;
RX MEDLINE=98348442; PubMed=9683477;
RA Willems H., Jaeger C., Baljer G.;
RT "Physical and genetic map of the obligate intracellular bacterium
Coxiella burnetii.";
RL J. Bacteriol. 180:3816-3822(1998).
DR EMBL; AF064963; AAD09947.1; -;
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 8 AA; 993 MW; 04655AA453772727 CRC64;

Query Match 39.6%; Score 19; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 LMW 6
DB 1 LLLW 4

RESULT 2

Q8NHL3 PRELIMINARY; PRT; 9 AA.
AC Q8NHL3;
DT 01-OCT-2002 (TREMELrel. 22, Created)
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DE Killer-cell immunoglobulin-like receptor KIR2DL5.3 (Fragment).
GN Name=KIR2DL5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20540100; PubMed=11086080;
RA Vilches C., Gardiner C.M., Parham P.;
RT "Gene structure and promoter variation of expressed and nonexpressed
variants of the KIR2DL5 gene.";
RL J. Immunol. 165:6416-6421(2000).

32 14 29.2 8 2 Q7M0L0 Q7M0L0 clostridium
33 14 29.2 8 2 Q6R7U6 Q6R7U6 gnyptetosc
34 14 29.2 8 2 AAS09897 AAS09897 gnyptetosc
35 14 29.2 8 2 AAS09898 AAS09898 gnyptetosc
36 13 27.1 7 2 Q9BRV4 Q9BRV4 homo sapien
37 13 27.1 8 2 Q7RBP6 Q7RBP6 plasmodium
38 13 27.1 8 2 O18854 O18854 canis famli
39 13 27.1 8 2 Q7M124 Q7M124 kluyvera ci
40 13 27.1 8 2 P79940 P79940 xenopus lae
41 13 27.1 8 2 Q98TU5 Q98TU5 xenopus lae
42 13 27.1 8 2 AAB33374 AAB33374 homo sapi
43 13 27.1 9 1 LITR_PHYRO P08946 phyllomedus
44 13 27.1 9 2 Q95953 Q95953 homo sapien
45 13 27.1 9 2 Q15891 Q15891 homo sapien

ALIGNMENTS

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DR EMBL; AF260137; AAG38010.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 9
SQ SEQUENCE 9 AA; 968 MW; 9DEF85A2D2C69735 CRC64;

Query Match 39.6%; Score 19; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 SLMWVSM 8
DB 2 SLMWVSM 8

RESULT 3
Q81VK3 PRELIMINARY; PRT; 8 AA.
AC Q81VK3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Steering2 (Fragment).
OS Homo sapiens (Human).
GN Name=STEERIN2;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Peeters P.J., Verhasselt P., Moechars D.W., Luyten W.H.M.L.,
RA Geysen J.J.G.H.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ488208; CAD32561.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 1030 MW; E8A7245417737726 CRC64;

Query Match 37.5%; Score 18; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 MIV 6
DB 1 MLW 3

RESULT 4
Q9H3Y3 PRELIMINARY; PRT; 9 AA.
AC Q9H3Y3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE DJ839B11.1 (Novel protein with a Kunitz/Bovine pancreatic trypsin
DE inhibitor domain and WAP-type (Whey Acidic Protein) 'four-disulfide
DE core' domains) (Fragment).
GN Name=dJ461P17.1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lloyd D.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL121778; CAB76844.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1036 MW; 2C417B01B412D1B3 CRC64;

Query Match 37.5%; Score 18; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 IWTM 8
DB 1 MWTV 4

RESULT 5
Q38366 PRELIMINARY; PRT; 9 AA.
AC Q38366;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE E gene product (Fragment).
OS Bacteriophage phi-X174.
OC Viruses; ssDNA viruses; Microviridae; Microvirus.
OX NCBI_TaxID=10847;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88118956; PubMed=2963134;
RA Buckley K.J., Hayashi M.;
RT "Role of premature translational termination in the regulation of
RT expression of the phi X174 lysis gene.";
RL J. Mol. Biol. 198:599-607(1987).
DR EMBL; X07809; CAA30668.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1207 MW; C093B37731B36412 CRC64;

Query Match 37.5%; Score 18; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 WTM 8
DB 4 WTL 6

RESULT 6
Q801KO PRELIMINARY; PRT; 9 AA.
AC Q801KO;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Beta fibrinogen (Fragment).
GN Name=beta fibrinogen;
OS Illicura militaris (pin-tailed manakin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Tyrannidae; Illicura.
OX NCBI_TaxID=208056;
RN [1]
RP SEQUENCE FROM N.A.
RA Marini M.A., Hackett S.J.;
RT "A Multifaceted Approach to the Characterization of an Intergeneric
RT Hybrid Manakin (Pipridae) from Brazil.";
RL Auk 119:1114-1120(2002).
DR EMBL; AV136617; AAN16894.1; -.
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 992 MW; 8620B37878744AB1 CRC64;

Query Match 37.5%; Score 18; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 WTM 8
DB 7 WTL 9

RESULT 7
Q801K1 PRELIMINARY; PRT; 9 AA.
AC Q801K1;
```



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DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Beta fibrinogen (Fragment).
GN Name=beta fibrinogen;
OS Chiroxiphia caudata.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archostralia; Aves; Neognathae; Passeriformes; Pipridae; Chiroxiphia.
OX NCBI_TaxID=196027;
RN [1]
RP SEQUENCE FROM N.A.
RA Marini M.A., Hackett S.J.;
RT "A Multifaceted Approach to the Characterization of an Intergeneric
RT Hybrid Manakin (Pipridae) from Brazil.";
RL Auk 119:1114-1120(2002).
DR EMBL; AY136616; AAN16893.1; -.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 992 MW; 8620B378744AB1 CRC64;

Query Match 37.5%; Score 18; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 WTM 8
DB 7 WTL 9

RESULT 8
Q801K2 PRELIMINARY; PRT; 9 AA.
AC Q801K2;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Beta fibrinogen (Fragment).
GN Name=beta fibrinogen;
OS Antilophia galeata (Hemeted manakin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archostralia; Aves; Neognathae; Passeriformes; Tyrannidae; Antilophia.
OX NCBI_TaxID=208054;
RN [1]
RP SEQUENCE FROM N.A.
RA Marini M.A., Hackett S.J.;
RT "A Multifaceted Approach to the Characterization of an Intergeneric
RT Hybrid Manakin (Pipridae) from Brazil.";
RL Auk 119:1114-1120(2002).
DR EMBL; AY136615; AAN16892.1; -.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 992 MW; 8620B378744AB1 CRC64;

Query Match 37.5%; Score 18; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 WTM 8
DB 7 WTL 9

RESULT 9
Q99MN0 PRELIMINARY; PRT; 8 AA.
AC Q99MN0;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Adenosine deaminase tRNA-specific 1 (Fragment).
GN Name=Adat1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ;
RX MEDLINE=21231131; PubMed=11331948;
RA Maas S., Kim Y.G., Rich A.;
RT "Genomic clustering of tRNA-specific adenosine deaminase ADAT1 and two
RT tRNA synthetases.";
RL Mamm. Genome 12:387-393(2001).
DR EMBL; AF328904; AAK19310.1; -.
FT NON_TER 8 8
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 936 MW; F4D05B1AADC1B376 CRC64;

Query Match 35.4%; Score 17; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 IWT 7
DB 1 MWT 3

RESULT 10
Q71EB9 PRELIMINARY; PRT; 9 AA.
AC Q71EB9;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Tumor antigen CML66 short isoform (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14688378;
RA Yan Y., Phan L., Yang F., Talpaz M., Yang Y., Xiong Z., Ng B.,
RA Timchenko N.A., Wu C.J., Ritz J., Wang H., Yang X.-P.;
RT "A novel mechanism of alternative promoter and splicing regulates the
RT epitope generation of tumor antigen CML66-L.";
RL J. Immunol. 172:651-660(2004).
DR EMBL; AF521134; AAQ08824.1; -.
FT NON_TER 9 9
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1128 MW; 55BCA37866D73B57 CRC64;

Query Match 35.4%; Score 17; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 WTM 8
DB 7 WSM 9

RESULT 11
AAQ08824 PRELIMINARY; PRT; 9 AA.
AC AAQ08824;
DT 02-MAR-2004 (TReMBLrel. 27, Created)
DT 02-MAR-2004 (TReMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TReMBLrel. 27, Last annotation update)
DE Tumor antigen CML66 short isoform (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14688378;
RA Yan Y., Phan L., Yang F., Talpaz M., Yang Y., Xiong Z., Ng B.,
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RA Timchenko N.A., Wu C.J., Ritz J., Wang H., Yang X.-F.;
 RT "A Novel Mechanism of Alternative Promoter and Splicing Regulates the
 RL Epitope Generation of Tumor Antigen CML66-L.";
 RL J. Immunol. 172:651-660(2004).
 DR EMBL, AF521134; AAQ08824.1; -.
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 1128 MW; 55BCA37866D73B57 CRC64;

Query Match 35.4%; Score 17; DB 2; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.8e+06;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 WTM 8
 | |
 Db 7 WSM 9

RESULT 12
 Q86SLO PRELIMINARY; PRT; 8 AA.
 AC Q86SLO; DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Flavocytochrome b-558 alpha polypeptide (Fragment).
 GN Names=Cyba;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22615572; PubMed=12729892;
 RA Moreno M.U., San Jose G., Orbe J., Paramo J.A., Beloqui O., Diez J.,
 RA Zalba G.;
 RT "Preliminary characterisation of the promoter of the human p22phox
 RT gene: identification of a new polymorphism associated with
 RT hypertension.";
 RL FEBS Lett. 542:27-31(2003).
 DR EMBL, AV128666; AAM96953.1; -.
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA; 965 MW; FF9DC37B1046D876 CRC64;

Query Match 33.3%; Score 16; DB 2; Length 8;
 Best Local Similarity 66.7%; Pred. No. 1.8e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 WTM 8
 | |
 Db 6 WAM 8

RESULT 13
 Q94VC6 PRELIMINARY; PRT; 9 AA.
 AC Q94VC6; DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN Names=COI;
 OS Varanus pilbarensis.
 OS Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Anguilliformia; Varanidae; Varanus.
 OX NCBI_TaxID=62048;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Aet J.C.;
 RA "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
 RL Cladistics 17:211-226(2001).
 DR EMBL, AF407518; AAL10108.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.

KW Mitochondrion.
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 1064 MW; 874CA5A36411A735 CRC64;

Query Match 33.3%; Score 16; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 SLMIWT 7
 | |
 Db 2 SLTRWS 7

RESULT 14
 Q9R5M1 PRELIMINARY; PRT; 9 AA.
 AC Q9R5M1; DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE 66 kDa cell surface adhesin for heparan sulfate (Fragment).
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92176005; PubMed=1541563;
 RA Liang O.D., Acencio F., Fransson L.A., Wadstrom T.;
 RT "Binding of heparan sulfate to Staphylococcus aureus.";
 RL Infect. Immun. 60:899-906(1992).
 DR PIR; A43848; A43848.
 FT NON_TER 1 1
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 990 MW; 2289DDD7337861B3 CRC64;

Query Match 33.3%; Score 16; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WT 7
 | |
 Db 2 WT 3

RESULT 15
 Q8X4G1 PRELIMINARY; PRT; 9 AA.
 AC Q8X4G1; DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE 22947 protein.
 GN OrderedLocustNames=z2947;
 OS Escherichia coli O157:H7.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=83334;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
 RX MEDLINE=21074935; PubMed=11206551;
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
 RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
 RA Grobbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamoudis K.,
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
 RA Welch R.A., Blattner F.R.;
 RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7";
 RL Nature 409:529-533(2001).
 DR EMBL; AF005411; AAG56883.1; -.
 DR PIR; G85802; G85802.
 KW Complete proteome.
 SQ SEQUENCE 9 AA; 1107 MW; 8F6CB72699D1B841 CRC64;

Query Match 33.3%; Score 16; DB 2; Length 9;
Best Local Similarity 50.0%; Pred.No. 1.8e+06;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 MIWTNM 9
| : |
Db 1 MTYTEM 6

Search completed: November 14, 2004, 14:07:05
Job time : 189 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2004, 14:07:12 ; Search time 137 Seconds
(without alignments)
23.244 Million cell updates/sec

Title: US-09-831-253F-5
Perfect score: 48
Sequence: 1 TSLMIWTMM 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1568699 seqs, 353819137 residues

Total number of hits satisfying chosen parameters: 133040

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US06_PCT_NEW_PUB.pep.*
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18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	54.2	9	US-09-796-744-10	Sequence 10, Appl
2	26	54.2	9	US-10-231-452-7	Sequence 7, Appl
3	25	52.1	8	US-08-979-847-170	Sequence 170, App
4	25	52.1	8	US-10-114-104-170	Sequence 170, App
5	25	52.1	9	US-10-182-252A-632	Sequence 632, App
6	25	52.1	9	US-10-182-252A-657	Sequence 657, App
7	24	50.0	5	US-10-441-626-35	Sequence 35, Appl
8	24	50.0	5	US-10-441-625-35	Sequence 35, Appl
9	24	50.0	6	US-10-441-626-38	Sequence 38, Appl
10	24	50.0	6	US-10-441-625-38	Sequence 38, Appl
11	24	50.0	7	US-10-651-165-170	Sequence 170, App
12	24	50.0	8	US-08-979-847-169	Sequence 169, App
13	24	50.0	8	US-10-114-104-169	Sequence 169, App

14	24	50.0	9	15	US-10-182-252A-3	Sequence 3, Appl
15	24	50.0	9	15	US-10-182-252A-215	Sequence 215, App
16	24	50.0	9	15	US-10-182-252A-617	Sequence 617, App
17	24	50.0	9	15	US-10-182-252A-631	Sequence 631, App
18	24	50.0	9	15	US-10-182-252A-656	Sequence 656, App
19	24	50.0	9	15	US-10-182-252A-658	Sequence 658, App
20	24	50.0	9	15	US-10-182-252A-685	Sequence 685, App
21	24	50.0	9	15	US-10-182-252A-1216	Sequence 1216, App
22	23	47.9	7	14	US-10-052-578-216	Sequence 216, App
23	23	47.9	7	14	US-10-053-520-216	Sequence 216, App
24	23	47.9	7	14	US-10-053-498B-216	Sequence 216, App
25	23	47.9	7	15	US-10-258-146A-74	Sequence 74, Appl
26	23	47.9	7	15	US-10-328-353-219	Sequence 219, App
27	23	47.9	7	16	US-10-258-144-109	Sequence 109, App
28	23	47.9	8	15	US-10-462-452-475	Sequence 475, App
29	23	47.9	8	15	US-10-601-953-604	Sequence 604, App
30	23	47.9	8	16	US-10-322-266-476	Sequence 476, App
31	23	47.9	9	10	US-09-845-042-27	Sequence 27, Appl
32	23	47.9	9	15	US-10-182-252A-630	Sequence 630, App
33	23	47.9	9	15	US-10-182-252A-655	Sequence 655, App
34	22	45.8	6	14	US-10-348-167-40	Sequence 40, Appl
35	22	45.8	8	8	US-08-979-847-171	Sequence 171, App
36	22	45.8	8	14	US-10-190-082-595	Sequence 595, App
37	22	45.8	8	14	US-10-114-104-171	Sequence 171, App
38	22	45.8	9	9	US-09-751-798-5	Sequence 5, Appl
39	22	45.8	9	9	US-09-751-798-6	Sequence 6, Appl
40	22	45.8	9	9	US-09-780-053-145	Sequence 145, App
41	22	45.8	9	9	US-09-766-889A-51	Sequence 51, Appl
42	22	45.8	9	9	US-09-766-889A-52	Sequence 52, Appl
43	22	45.8	9	10	US-09-995-529-133	Sequence 133, App
44	22	45.8	9	10	US-09-833-039-122	Sequence 122, App
45	22	45.8	9	11	US-09-995-529-133	Sequence 133, App

ALIGNMENTS

RESULT 1
US-09-796-744-10
; Sequence 10, Application US/09796744
; Patent No. US20020098527A1
; GENERAL INFORMATION:
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: SHOJI, EMI
; APPLICANT: SAKURADA, MIKKIKO
; APPLICANT: FURUYA, AKIKO
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: NIWA, RINPEI
; APPLICANT: SHIBATA, KENJI
; APPLICANT: YAMASAKI, MOTOO
; TITLE OF INVENTION: GENE RECOMBINANT ANTIBODY AND ANTIBODY FRAGMENT THEREOF
; FILE REFERENCE: 249-170
; CURRENT APPLICATION NUMBER: US/09/796,744
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: JP 2000-59508
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: JP 2000-401563
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-796-744-10

Query Match 54.2%; Score 26; DB 9; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 SLMIWT 7
||: ||

Db 4 SLLFWT 9

RESULT 2

US-10-231-452-7

; Sequence 7, Application US/10231452

; Publication No. US20030175273A1

; GENERAL INFORMATION:

; APPLICANT: SHITARA, KENYA

; APPLICANT: NAKAMURA, KAZUYASU

; APPLICANT: HOSAKA, EMI

; APPLICANT: TANAKA, AKIKO

; APPLICANT: KOIKE, MASAMICHI

; TITLE OF INVENTION: HUMAN CDR GRAFTED ANTIBODY AND ANTIBODY FRAGMENT THEREOF

; FILE REFERENCE: 249-273

; CURRENT APPLICATION NUMBER: US/10/231,452

; CURRENT FILING DATE: 2003-04-18

; PRIOR APPLICATION NUMBER: JP 2001-265144

; PRIOR FILING DATE: 2001-08-31

; NUMBER OF SEQ ID NOS: 78

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 7

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Mus musculus

US-10-231-452-7

Query Match 54.2%; Score 26; DB 14; Length 9;

Best Local Similarity 66.7%; Pred. No. 1.4e+06;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 SLMWT 7

Db 4 SLLFWT 9

RESULT 3

US-08-979-847-170

; Sequence 170, Application US/08979847

; Publication No. US20030039664A1

; GENERAL INFORMATION:

; APPLICANT: PERRON, HERVE

; APPLICANT: BESEME, FREDERIC

; APPLICANT: BEDIN, FREDERIC

; APPLICANT: PARANHOS-BACCALA, GLAUCIA

; APPLICANT: KOMURIAN-PRADEL, FLORENCE

; APPLICANT: JOLIVET-REYNAUD, COLETTE

; APPLICANT: MANDRAND, BERNARD

; APPLICANT: GARSON, JEREMY

; APPLICANT: TUKE, PHILIP

; TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS

; TITLE OF INVENTION: ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLACTIC AND THERAPEUTIC PURPOSES

; NUMBER OF SEQUENCES: 210

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OLIFF & BERRIDGE, PLC

; STREET: P.O. BOX 19928

; CITY: ALEXANDRIA

; STATE: VA

; COUNTRY: USA

; ZIP: 22320

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/979,847

FILING DATE: 26-NOV-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/979,847

FILING DATE: 26-NOV-1997

ATTORNEY/AGENT INFORMATION:

NAME: BERRIDGE, WILLIAM P.

REGISTRATION NUMBER: 30,024

TELEPHONE: 703-836-6400

TELEFAX: 703-836-2787

INFORMATION FOR SEQ ID NO: 78

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

; REFERENCE/DOCKET NUMBER: WPB 39046A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-836-6400

; TELEFAX: 703-836-2787

; INFORMATION FOR SEQ ID NO: 170:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-979-847-170

Query Match 52.1%; Score 25; DB 8; Length 8;

Best Local Similarity 50.0%; Pred. No. 1.4e+06;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 TSLMIWTM 8

Db 1 TSQLTWT 8

RESULT 4

US-10-114-104-170

; Sequence 170, Application US/10114104

; Publication No. US20030198647A1

; GENERAL INFORMATION:

; APPLICANT: PERRON, HERVE

; APPLICANT: BESEME, FREDERIC

; APPLICANT: BEDIN, FREDERIC

; APPLICANT: PARANHOS-BACCALA, GLAUCIA

; APPLICANT: KOMURIAN-PRADEL, FLORENCE

; APPLICANT: JOLIVET-REYNAUD, COLETTE

; APPLICANT: MANDRAND, BERNARD

; APPLICANT: GARSON, JEREMY

; APPLICANT: TUKE, PHILIP

; TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS

; TITLE OF INVENTION: ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLACTIC AND THERAPEUTIC PURPOSES

; NUMBER OF SEQUENCES: 210

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OLIFF & BERRIDGE, PLC

; STREET: P.O. BOX 19928

; CITY: ALEXANDRIA

; STATE: VA

; COUNTRY: USA

; ZIP: 22320

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/114,104

FILING DATE: 03-Apr-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/979,847

FILING DATE: 26-NOV-1997

ATTORNEY/AGENT INFORMATION:

NAME: BERRIDGE, WILLIAM P.

REGISTRATION NUMBER: 30,024

REFERENCE/DOCKET NUMBER: WPB 39046A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-836-6400

TELEFAX: 703-836-2787

INFORMATION FOR SEQ ID NO: 170:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

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; SEQUENCE DESCRIPTION: SEQ ID NO: 170:
US-10-114-104-170
Query Match      52.1%; Score 25; DB 14; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 TSLMIWTM 8
   |||: |||
Db 1 TSQLTWTV 8

RESULT 5
US-10-182-252A-632
; Sequence 632, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUUS, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEMOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; TITLE OF INVENTION: CONTROL OF HIV INFECTIONS
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 632
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-632

Query Match      52.1%; Score 25; DB 15; Length 9;
Best Local Similarity 28.6%; Pred. No. 1.4e+06;
Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 2 SLMIWTM 8
   :|||:
Db 3 AIVVWTL 9

RESULT 6
US-10-182-252A-657
; Sequence 657, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUUS, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEMOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; TITLE OF INVENTION: CONTROL OF HIV INFECTIONS
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28

; SEQUENCE DESCRIPTION: SEQ ID NO: 179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: PatentIn Ver. 2.1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-657

Query Match      52.1%; Score 25; DB 15; Length 9;
Best Local Similarity 28.6%; Pred. No. 1.4e+06;
Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 2 SLMIWTM 8
   :|||:
Db 3 AIVVWTL 9

RESULT 7
US-10-441-626-35
; Sequence 35, Application US/10441626
; Publication No. US20030186418A1
; GENERAL INFORMATION:
; APPLICANT: Gualfetti, Peter
; APPLICANT: Mitchinson, Colin
; APPLICANT: Phillips, Jay Ian
; TITLE OF INVENTION: No. US20030186418A1el Variant EGIII-Like Cellulase
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: GC631
; CURRENT APPLICATION NUMBER: US/10/441,626
; CURRENT FILING DATE: 2003-05-19
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: BOX2
US-10-441-626-35

Query Match      50.0%; Score 24; DB 14; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 LMIW 6
   ||||
Db 2 LMIW 5

RESULT 8
US-10-441-625-35
; Sequence 35, Application US/10441625
; Publication No. US20030203467A1
; GENERAL INFORMATION:
; APPLICANT: Gualfetti, Peter
; APPLICANT: Mitchinson, Colin
; APPLICANT: Phillips, Jay Ian
; TITLE OF INVENTION: Novel Variant EGIII-Like Cellulase
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: GC631
; CURRENT APPLICATION NUMBER: US/10/441,625
; CURRENT FILING DATE: 2003-05-19
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: BOX2
US-10-441-625-35

Query Match 50.0%; Score 24; DB 14; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LMIW 6
|||
DB 2 LMIW 5
|||

RESULT 9

US-10-441-626-38
; Sequence 38, Application US/10441626
; Publication No. US20030186418A1
; GENERAL INFORMATION:
; APPLICANT: Gualfetti, Peter
; APPLICANT: Mitchinson, Colin
; APPLICANT: Phillips, Jay Ian
; TITLE OF INVENTION: No. US20030186418A1el Variant EGIII-Like Cellulase
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: GC631
; CURRENT APPLICATION NUMBER: US/10/441,626
; CURRENT FILING DATE: 2003-05-19
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: BOX2'
US-10-441-626-38

Query Match 50.0%; Score 24; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LMIW 6
|||
DB 3 LMIW 6
|||

RESULT 10

US-10-441-625-38
; Sequence 38, Application US/10441625
; Publication No. US20030203467A1
; GENERAL INFORMATION:
; APPLICANT: Gualfetti, Peter
; APPLICANT: Mitchinson, Colin
; APPLICANT: Phillips, Jay Ian
; TITLE OF INVENTION: Novel Variant EGIII-Like Cellulase
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: GC631
; CURRENT APPLICATION NUMBER: US/10/441,625
; CURRENT FILING DATE: 2003-05-19
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: BOX2'
US-10-441-625-38

Query Match 50.0%; Score 24; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LMIW 6
|||

DB 3 LMIW 6

RESULT 11

US-10-651-165-170
; Sequence 170, Application US/10651165
; Publication No. US20040047877A1
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; TITLE OF INVENTION: VIRUS
; FILE REFERENCE: 2551-94
; CURRENT APPLICATION NUMBER: US/10/651,165
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US/08/974,690C
; PRIOR FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 170
; LENGTH: 7
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-10-651-165-170

Query Match 50.0%; Score 24; DB 15; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 MIWTMM 9
|||
DB 2 MAWDMW 7
|||

RESULT 12

US-08-979-847-169
; Sequence 169, Application US/08979847
; Publication No. US20030039664A1
; GENERAL INFORMATION:
; APPLICANT: PERRON, HERVE
; APPLICANT: BESEME, FREDERIC
; APPLICANT: BEDIN, FREDERIC
; APPLICANT: PARANHOS-BACCALA, GLAUCIA
; APPLICANT: KOMURIAN-PRADEL, FLORENCE
; APPLICANT: JOLIVET-REYNAUD, COLETTE
; APPLICANT: MANDRAND, BERNARD
; APPLICANT: GARSON, JEREMY
; APPLICANT: TUKE, PHILIP
; TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
; TITLE OF INVENTION: ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLACTIC
; TITLE OF INVENTION: THERAPEUTIC PURPOSES
; NUMBER OF SEQUENCES: 210
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OLIFF & BERRIDGE, PLC
; STREET: P.O. BOX 19928
; CITY: ALEXANDRIA
; STATE: VA
; COUNTRY: USA
; ZIP: 22320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/979,847
; FILING DATE: 26-NOV-1997
; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 39046A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
TELEFAX: 703-836-2787
INFORMATION FOR SEQ ID NO: 169:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-979-847-169

Query Match 50.0%; Score 24; DB 8; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TSLMIWT 7
||: ||
Db 2 TSQLTWT 8

RESULT 13

US-10-114-104-169
Sequence 169, Application US/10114104
Publication No. US20030198647A1
GENERAL INFORMATION:

APPLICANT: PERRON, HERVE
BESEME, FREDERIC
BEDIN, FREDERIC
PARANHOS-BACCALA, GLAUCIA
KOMURIAN-PRADEL, FLORENCE
JOLIVET-REYNAUD, COLETTE
MANDRAND, BERNARD
GARSON, JEREMY
TUIKE, PHILIP
TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYL
THERAPEUTIC PURPOSES

NUMBER OF SEQUENCES: 210

CORRESPONDENCE ADDRESS:

ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
STATE: VA
COUNTRY: USA
ZIP: 22320

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/114,104

FILING DATE: 03-Apr-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/979,847

FILING DATE: 26-NOV-1997

ATTORNEY/AGENT INFORMATION:

NAME: BERRIDGE, WILLIAM P.

REGISTRATION NUMBER: 30,024

REFERENCE/DOCKET NUMBER: WPB 39046A

TELEPHONE: 703-836-6400

TELEFAX: 703-836-2787

INFORMATION FOR SEQ ID NO: 169:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 169:
US-10-114-104-169

Query Match 50.0%; Score 24; DB 14; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TSLMIWT 7
||: ||
Db 2 TSQLTWT 8

RESULT 14

US-10-182-252A-3
Sequence 3, Application US/10182252A
Publication No. US20040072162A1
GENERAL INFORMATION:

APPLICANT: FOMSGAARD, ANDERS
BRUNAK, SOREN
APPLICANT: BUUS, SOREN
CORBET, SYLVIE
APPLICANT: LAUEMOLLER, SANNE LISE
APPLICANT: HANSEN, JAN
TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
CONTROL OF HIV INFECTIONS
FILE REFERENCE: 030307/0205
CURRENT APPLICATION NUMBER: US/10/182,252A
CURRENT FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: PCT/DK01/00059
PRIOR FILING DATE: 2001-01-29
PRIOR APPLICATION NUMBER: EP 00610017.6
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/179,333
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 1388
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 9
TYPE: PPT
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: HIV peptide

US-10-182-252A-3

Query Match 50.0%; Score 24; DB 15; Length 9;
Best Local Similarity 28.6%; Pred. No. 1.4e+06;
Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 2 SLMIWTM 8
::: ||
Db 3 AIVVWII 9

RESULT 15

US-10-182-252A-215
Sequence 215, Application US/10182252A
Publication No. US20040072162A1
GENERAL INFORMATION:

APPLICANT: FOMSGAARD, ANDERS
BRUNAK, SOREN
APPLICANT: BUUS, SOREN
CORBET, SYLVIE
APPLICANT: LAUEMOLLER, SANNE LISE
APPLICANT: HANSEN, JAN
TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
CONTROL OF HIV INFECTIONS
FILE REFERENCE: 030307/0205
CURRENT APPLICATION NUMBER: US/10/182,252A
CURRENT FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: PCT/DK01/00059

```
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 215
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-215

Query Match      50.0%; Score 24; DB 15; Length 9;
Best Local Similarity 28.6%; Pred. No. 1.4e+06;
Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      2 SLMIWTM 8
Db      3 AIVVTV 9
```

Search completed: November 14, 2004, 14:18:57
Job time : 137 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2004, 13:45:55 ; Search time 156 Seconds
(without alignments)
20.696 Million cell updates/sec

Title: US-09-831-253F-5
Perfect score: 48
Sequence: 1 TSLMIWTMM 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 202273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 313949

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	9	3	AAY93096 Transform
2	48	100.0	9	3	AAY92949 Transform
3	28	58.3	9	8	ADK08459 Human pap
4	28	58.3	9	8	ADK08095 Human pap
5	27	56.2	9	6	ABU64837 Human NV-
6	26	54.2	8	8	ADK08449 Human pap
7	26	54.2	8	8	ADK08088 Human pap
8	26	54.2	9	4	AA67672 Complemen
9	26	54.2	9	6	ABR40267 Murine pe
10	26	54.2	9	7	AD227682 Mouse ant
11	26	54.2	9	8	ADK08458 Human pap
12	25	52.1	8	4	ABP14228 HIV A02 s
13	25	52.1	8	4	ABP19690 HIV B62 s
14	25	52.1	8	7	AD84465 MSRV-1 PO
15	25	52.1	8	8	ADG14911 MSRV-1 PO
16	25	52.1	9	4	AAW22772 HIV pepti
17	25	52.1	9	4	AAW22747 HIV pepti
18	25	52.1	9	4	ABP16598 HIV A24 s
19	25	52.1	9	4	ABP14239 HIV A02 s
20	25	52.1	9	4	ABP18424 HIV B58 s
21	25	52.1	9	4	ABP22273 HIV A03 m
22	25	52.1	9	4	ABP11937 HIV A01 s
23	25	52.1	9	4	ABP19680 HIV B62 s
24	24	50.0	5	3	AAB13397 EGIII-lik
25	24	50.0	5	5	AAU77443 BOX2 pept

26	24	50.0	5	5	AAU87811	Aau87811 Endogluca
27	24	50.0	6	3	AAB13398	Aab13398 EGIII-lik
28	24	50.0	6	5	AAU77075	Aau77075 Endogluca
29	24	50.0	6	5	AAU77444	Aau77444 BOX2, pep
30	24	50.0	6	5	AAU87812	Aau87812 Endogluca
31	24	50.0	8	2	AAV33692	Aav33692 Maize 33k
32	24	50.0	8	4	ABP18425	Abp18425 HIV B58 s
33	24	50.0	8	4	ABP22274	Abp22274 HIV A03 m
34	24	50.0	8	4	ABP16588	Abp16588 HIV A24 s
35	24	50.0	8	4	ABP19683	Abp19683 HIV B62 s
36	24	50.0	8	4	ABP16597	Abp16597 HIV A24 s
37	24	50.0	8	4	ABP11934	Abp11934 HIV A01 s
38	24	50.0	8	4	ABP14227	Abp14227 HIV A02 s
39	24	50.0	8	4	AAJ00551	Aaj00551 Hepatitis
40	24	50.0	8	4	AAJ01013	Aaj01013 Hepatitis
41	24	50.0	8	4	AAJ01178	Aaj01178 Hepatitis
42	24	50.0	8	4	AAJ01692	Aaj01692 Hepatitis
43	24	50.0	8	7	ADB84464	Adb84464 MSRV-1 PO
44	24	50.0	8	7	ABW00710	Abw00710 Chrysoespo
45	24	50.0	8	8	ADG14910	Adg14910 MSRV-1 PO

ALIGNMENTS

RESULT 1
AAY93096
ID AAY93096 standard; peptide; 9 AA.
XX
AC AAY93096;
XX
DT 08-NOV-2000 (first entry)
XX
DE Transforming growth factor inhibitory peptide P142.
XX
KW Hepatotrophic; antagonist; transforming growth factor betaf; TGF-b1;
KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX
OS Homo sapiens.
XX
PN WO200031135-A1.
XX
PD 02-JUN-2000.
XX
PF 23-NOV-1999; 99WO-ES000375.
XX
PR 24-NOV-1998; 98ES-00002465.
XX
PA (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
XX
PI Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
PI Borrás Cuesta F;
XX
DR WPI; 2000-411935/35.
XX
PT Peptides that antagonize binding of transforming growth factor betaf,
PT useful for treatment of liver disease, especially cirrhosis, are partial
PT sequences of the factor or its receptors.
XX
PS Disclosure; Page 31; 86pp; Spanish.
XX
CC The invention relates to synthetic peptides that antagonise the binding
CC of transforming growth (TGF) factor betaf (TGF-b1) to its receptor in
CC vivo which have partial amino acid sequences identical, or similar, with
CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
CC examples of the peptides of the invention. the peptides act by
CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
CC they are inhibitors of stimulation of collagen synthesis in liver cells
CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
CC expression systems) encoding the peptides are used for treatment of liver
CC disease, specifically cirrhosis

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XX SQ Sequence 9 AA;
Query Match 100.0%; Score 48; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLMIWTMM 9
   |||||
Db 1 TSLMIWTMM 9

RESULT 2
AAY92949
ID AAY92949 standard; peptide; 9 AA.
XX AC AAY92949;
XX DT 08-NOV-2000 (first entry)
XX DE Transforming growth factor inhibitory peptide #5.
XX KW Hepatotropic; antagonist; transforming growth factor betaf; TGF-b1;
XX KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
XX KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX OS Homo sapiens.
XX PN WO200031135-A1.
XX PD 02-JUN-2000.
XX PF 23-NOV-1999; 99WO-ES000375.
XX PR 24-NOV-1998; 98ES-00002465.
XX PA (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
XX PI Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
XX PI Borras Cuesta F;
XX WPI; 2000-411935/35.
XX PT Peptides that antagonize binding of transforming growth factor betaf,
XX PT useful for treatment of liver disease, especially cirrhosis, are partial
XX PT sequences of the factor or its receptors.
XX PS Claim 6; Page 81; 86pp; Spanish.
XX CC The invention relates to synthetic peptides that antagonise the binding
XX CC of transforming growth (TGF) factor betaf (TGF-b1) to its receptor in
XX CC vivo which have partial amino acid sequences identical, or similar, with
XX CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
XX CC examples of the peptides of the invention. The peptides act by
XX CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
XX CC they are inhibitors of stimulation of collagen synthesis in liver cells
XX CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
XX CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
XX CC expression systems) encoding the peptides are used for treatment of liver
XX CC disease, specifically cirrhosis
XX SQ Sequence 9 AA;
Query Match 100.0%; Score 48; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLMIWTMM 9
   |||||
Db 1 TSLMIWTMM 9

RESULT 3
ADK08459
ID ADK08459 standard; peptide; 9 AA.
XX AC ADK08459;
XX DT 06-MAY-2004 (first entry)
XX DE Human papillomavirus peptide #514.
XX KW pathogenic virus; alternative reading frame; antigenic determinant;
XX KW virucide; vaccine; therapeutic agent; infection; HPV.
XX OS Human papillomavirus.
XX PN WO2004011650-A2.
XX PD 05-FEB-2004.
XX PF 24-JUL-2003; 2003WO-EP008112.
XX PR 24-JUL-2002; 2002AT-00001124.
XX PR 11-JUL-2003; 2003EP-00450171.
XX PA (INTE-) INTERCELL AG.
XX PI Mattner F, Schmidt W, Habel A;
XX WPI; 2004-169243/16.
XX CC New polypeptide encoded by an alternative reading frame of a pathogenic
XX CC virus comprising an antigenic determinant, useful for treating or
XX CC preventing an infection with the pathogenic virus.
XX PS Claim 18; Page 179; 220pp; English.
XX CC This invention relates to a novel polypeptide encoded by an alternative
XX CC reading frame of a pathogenic virus, where the polypeptide starts with a
XX CC methionine amino acid residue, which comprises an antigenic determinant
XX CC and more than 7 amino acid residues. The invention may be useful for the
XX CC production of compounds with a virucide activity or the development of a
XX CC vaccine. The polypeptide or its fragments may be useful as a therapeutic
XX CC agent. It is also useful for the manufacture of a medicament for treating
XX CC or preventing an infection with the pathogenic virus. The present
XX CC sequence is that of a human papillomavirus (HPV) epitope peptide of the
XX CC invention.
XX SQ Sequence 9 AA;
Query Match 58.3%; Score 28; DB 8; Length 9;
Best Local Similarity 37.5%; Pred. No. 1.7e+06;
Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 2 SLMWTMM 9
   :||:
Db 2 ALVLTLL 9

RESULT 4
ADK08095
ID ADK08095 standard; peptide; 9 AA.
XX AC ADK08095;
XX DT 06-MAY-2004 (first entry)
XX DE Human papillomavirus peptide #150.
XX KW pathogenic virus; alternative reading frame; antigenic determinant;
XX KW virucide; vaccine; therapeutic agent; infection; HPV.
XX OS Human papillomavirus.
XX PN WO2004011650-A2.

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XX PD 05-FEB-2004.
XX PF 24-JUL-2003; 2003WO-EF008112.
XX PR 24-JUL-2002; 2002AT-00001124.
XX PR 11-JUL-2003; 2003EP-00450171.
XX PA (INTE-) INTERCELL AG.
XX PI Mattner F, Schmidt W, Habel A;
XX DR WPI; 2004-169243/16.
XX PT New polypeptide encoded by an alternative reading frame of a pathogenic
XX PT virus comprising an antigenic determinant, useful for treating or
XX PT preventing an infection with the pathogenic virus.
XX PS Claim 18; Page 175; 220pp; English.
XX CC This invention relates to a novel polypeptide encoded by an alternative
XX CC reading frame of a pathogenic virus, where the polypeptide starts with a
XX CC methionine amino acid residue, which comprises an antigenic determinant
XX CC and more than 7 amino acid residues. The invention may be useful for the
XX CC production of compounds with a virucide activity or the development of a
XX CC vaccine. The polypeptide or its fragments may be useful as a therapeutic
XX CC agent. It is also useful for the manufacture of a medicament for treating
XX CC or preventing an infection with the pathogenic virus. The present
XX CC sequence is that of a human papillomavirus (HPV) epitope peptide of the
XX CC invention.
XX SQ Sequence 9 AA;
    Query Match 58.3%; Score 28; DB 8; Length 9;
    Best Local Similarity 37.5%; Pred No. 1.7e+06;
    Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 2 SLMIWTMM 9
Db :|||:
2 ALVLWTLL 9
RESULT 5
ABU64837.
ID ABU64837 standard; peptide; 9 AA.
AC ABU64837;
XX 14-MAY-2003 (first entry)
XX Human NY-ESO-1 HLA binding motif #21.
XX Human; antigen; NY-ESO-1; cancer; SEREX; cytostatic; immunosuppressive;
XX serological identification of antigens by recombinant expression cloning;
XX melanoma; hepatoma; lymphoma; breast cancer; prostate cancer;
XX lung cancer; ovarian cancer; thyroid cancer; bladder cancer; infection;
XX autoimmune disorder; cancer marker; CTL; cytolytic T cell line;
XX human leukocyte antigen; HLA binding motif.
XX OS Homo sapiens.
XX US2002164665-A1.
XX 07-NOV-2002.
XX 17-DEC-2001; 2001US-00023182.
XX 03-OCT-1996; 96US-00725182.
XX 15-SEP-1997; 97US-00937263.
XX 29-DEC-2000; 2000US-00751798.
XX (STOC/) STOCKERT E.
XX (JAGE/) JAGER E.

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PA (CHEN/) CHEN Y.
PA (SCAN/) SCANLAN M.
PA (ALEX/) ALEXANDER K.
XX (OLDL/) OLD L J.
XX Stockert E, Jager E, Chen Y, Scanlan M, Alexander K, Old LJ;
XX WPI; 2003-298695/29.
XX New antibody that binds to the cancer associated antigen NY-ESO-1, useful
XX PT for treating cancer, e.g. melanoma, hepatoma, lymphoma, or breast,
XX PT prostate, lung, ovarian, thyroid or bladder cancer, infections or
XX PT autoimmune disorders.
XX Example 13; Page 6; 18pp; English.
XX The invention relates to an isolated antibody or binding fragment of an
XX CC antibody, which binds with a protein that is encoded by an isolated
XX CC nucleic acid molecule the complementary sequence of which hybridises
XX CC under stringent conditions to a nucleic acid molecule comprising the
XX CC nucleotides 54-593 of the human cancer marker NY-ESO-1 cDNA appearing as
XX CC ABX96656. Also included are a hybridoma cell line producing the novel
XX CC monoclonal antibody, screening for cancer in a sample (by contacting the
XX CC sample with the isolated antibody, and determining binding of the novel
XX CC antibody to a target as an indicator of cancer), determining antibodies
XX CC against a cancer-associated antigen in a sample, determining
XX CC regression/progression/onset of a cancerous condition (by monitoring a
XX CC sample from a patient with the cancerous condition from parameters such
XX CC as NY-ESO-1 protein or a peptide derived from NY-ESO-1 protein, with the
XX CC antibody that binds to it, where the amount of the parameter is
XX CC indicative of progression, regression or onset of cancerous conditions),
XX CC and treating a subject afflicted with a cancerous condition by
XX CC administering to the subject an antibody that specifically binds to NY-
XX CC ESO-1 protein or to an ESO-1 derived peptide (e.g. a peptide identified
XX CC as stimulating a CTL (cytolytic T cell line) identified by SEREX
XX CC (serological identification of antigens by recombinant expression
XX CC cloning) expressed on a cancerous cell associated with the cancerous
XX CC condition) where the antibody is coupled to an anticancer agent. The
XX CC antibody is useful for treating cancer, e.g. melanoma, hepatoma,
XX CC lymphoma, or breast, prostate, lung, ovarian, thyroid or bladder cancer,
XX CC infections or autoimmune disorders. The present sequence represents an
XX CC HLA (human leukocyte antigen) binding peptide derived from human NY-ESO-1
XX SQ Sequence 9 AA;
    Query Match 56.2%; Score 27; DB 6; Length 9;
    Best Local Similarity 66.7%; Pred. No. 1.7e+06;
    Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 2 SLMIWT 7
Db :|||:
4 SLLMWT 9
RESULT 6
ADK08449
ID ADK08449 standard; peptide; 8 AA.
XX AC ADK08449;
XX 06-MAY-2004 (first entry)
XX Human papillomavirus peptide #504.
XX pathogenic virus; alternative reading frame; antigenic determinant;
XX virucide; vaccine; therapeutic agent; infection; HPV.
XX Human papillomavirus.
XX WO2004011650-A2.
XX 05-FEB-2004.

```

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PF 24-JUL-2003; 2003WO-EP008112.
XX
PR 24-JUL-2002; 2002AT-00001124.
PR 11-JUL-2003; 2003EP-00450171.
XX
PA (INTE-) INTERCELL AG.
XX
PI Mattner F, Schmidt W, Habel A;
XX
DR WPI; 2004-169243/16.
XX
XX New polypeptide encoded by an alternative reading frame of a pathogenic
PT virus comprising an antigenic determinant, useful for treating or
PT preventing an infection with the pathogenic virus.
XX
PS Claim 18; Page 178; 220pp; English.
XX
CC This invention relates to a novel polypeptide encoded by an alternative
CC reading frame of a pathogenic virus, where the polypeptide starts with a
CC methionine amino acid residue, which comprises an antigenic determinant
CC and more than 7 amino acid residues. The invention may be useful for the
CC production of compounds with a virucide activity or the development of a
CC vaccine. The polypeptide or its fragments may be useful as a therapeutic
CC agent. It is also useful for the manufacture of a medicament for treating
CC or preventing an infection with the pathogenic virus. The present
CC sequence is that of a human papillomavirus (HPV) epitope peptide of the
CC invention.
XX
XX Sequence 8 AA;
XX
Query Match 54.2%; Score 26; DB 8; Length 8;
Best Local Similarity 42.9%; Pred. No. 1.7e+06;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
OY 2 SLMIWTM 8
DB :|:|:|:
2 ALVLWTL 8
RESULT 8
AAG67672
ID AAG67672 standard; peptide; 9 AA.
XX
AC AAG67672;
XX
XX 26-NOV-2001 (first entry)
DT
XX
DE Complementarity determining region 3 of light chain variable region.
XX
XX Gene recombinant antibody; CCR4; Th2-mediated immune disease;
KW blood cancer; bronchial asthma; atrophic dermatitis; leukemia.
XX
OS Mus musculus.
XX
PN WO200164754-A1.
XX
XX 07-SEP-2001.
PD
XX
XX 02-MAR-2001; 2001WO-JP001656.
PF
XX
PR 03-MAR-2000; 2000JP-00059508.
PR 28-DEC-2000; 2000JP-00401563.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
PA
XX
PI Shitara K, Hanai N, Shoji E, Sakurada M, Furuya A, Nakamura K;
PI Niwa R, Shibata K, Yamasaki M;
XX
XX WPI; 2001-565496/63.
DR
XX
PT Gene-recombinant antibody, its fragment and encoded DNAs, applicable in
PT diagnosis and development of drugs for Th2-mediated immune diseases and
PT blood cancer, and in reducing or eliminating cells.
XX
PS Claim 15; Page 101; 116pp; Japanese.
XX
CC The specification describes a gene recombinant antibody that can
CC specifically react with the extracellular domain of human CCR4. The
CC antibody and its fragment are applicable in diagnosis and development of
CC drugs for Th2-mediated immune diseases and blood cancer including
CC bronchial asthma, atrophic dermatitis and leukemia. The present sequence
CC represents a complementarity determining region (CDR) of the light chain
CC variable region of an antibody directed against human CCR4
XX
XX Sequence 9 AA;
XX
Query Match 54.2%; Score 26; DB 4; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
PF 24-JUL-2003; 2003WO-EP008112.
XX
PR 24-JUL-2002; 2002AT-00001124.
PR 11-JUL-2003; 2003EP-00450171.
XX
PA (INTE-) INTERCELL AG.
XX
PI Mattner F, Schmidt W, Habel A;
XX
DR WPI; 2004-169243/16.
XX
XX New polypeptide encoded by an alternative reading frame of a pathogenic
PT virus comprising an antigenic determinant, useful for treating or
PT preventing an infection with the pathogenic virus.
XX
PS Claim 18; Page 178; 220pp; English.
XX
CC This invention relates to a novel polypeptide encoded by an alternative
CC reading frame of a pathogenic virus, where the polypeptide starts with a
CC methionine amino acid residue, which comprises an antigenic determinant
CC and more than 7 amino acid residues. The invention may be useful for the
CC production of compounds with a virucide activity or the development of a
CC vaccine. The polypeptide or its fragments may be useful as a therapeutic
CC agent. It is also useful for the manufacture of a medicament for treating
CC or preventing an infection with the pathogenic virus. The present
CC sequence is that of a human papillomavirus (HPV) epitope peptide of the
CC invention.
XX
XX Sequence 8 AA;
XX
Query Match 54.2%; Score 26; DB 8; Length 8;
Best Local Similarity 42.9%; Pred. No. 1.7e+06;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
OY 2 SLMIWTM 8
DB :|:|:|:
2 ALVLWTL 8
RESULT 7
ADK08088
ID ADK08088 standard; peptide; 8 AA.
XX
AC ADK08088;
XX
XX 06-MAY-2004 (first entry)
DT
XX
DE Human papillomavirus peptide #143.
XX
KW pathogenic virus; alternative reading frame; antigenic determinant;
KW virucide; vaccine; therapeutic agent; infection; HPV.
XX
OS Human papillomavirus.
XX
PN WO2004011650-A2.
XX
XX 05-FEB-2004.
PD
XX
XX 24-JUL-2003; 2003WO-EP008112.
PF
XX
PR 24-JUL-2002; 2002AT-00001124.
PR 11-JUL-2003; 2003EP-00450171.
XX
XX (INTE-) INTERCELL AG.
PA
XX
PI Mattner F, Schmidt W, Habel A;
XX
DR WPI; 2004-169243/16.
XX
XX New polypeptide encoded by an alternative reading frame of a pathogenic
PT virus comprising an antigenic determinant, useful for treating or
PT preventing an infection with the pathogenic virus.
XX
XX

```

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 SLMIWT 7
||: ||
4 SLLFWT 9

DB

RESULT 9
ABR40267
ID ABR40267 standard; peptide; 9 AA.
XX
AC ABR40267;
XX
DT 24-JUN-2003 (first entry)
XX
DE Murine peptide SEQ ID NO: 7.
XX
KW Mouse; CDR-grafted antibody; CC chemokine receptor 4; CCR4; cytostatic;
KW antiallergic; antiinflammatory; immunomodulator; cancer; immune disease.
XX
OS Mus musculus:
XX
PN WO2003018635-A1.
XX
PD 06-MAR-2003.
XX
PF 30-AUG-2002; 2002WO-JP008828.
XX
PR 31-AUG-2001; 2001JP-00265144.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Shitara K, Nakamura K, Hosaka E, Tanaka A, Koike M;
DR WPI; 2003-278645/27.
XX
PT Human CDR-grafted antibodies and their fragments specifically reacting
PT with extracellular regions of human CCR4 and cytotoxic to cells
PT expressing it, applicable in diagnosis and drugs for e.g. cancer.
XX
PS Claim 21; Page 109; 144pp; Japanese.
XX
CC The invention relates to a novel human CDR-grafted antibody, or its
CC fragment. The antibody or fragment reacts specifically with the
CC extracellular region of human CC chemokine receptor 4 (CCR4) but shows no
CC reactivity toward human platelets. The antibody of the invention has
CC cytostatic, antiallergic, antiinflammatory and immunomodulator activity.
CC The antibodies and their fragments are applicable in the diagnosis and
CC treatment of e.g. cancer and immune diseases. The present sequence is
CC used in the exemplification of the invention
XX
SQ Sequence 9 AA;

Query Match 54.2%; Score 26; DB 6; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 SLMIWT 7
||: ||
4 SLLFWT 9

DB

RESULT 10
ADE27682
ID ADE27682 standard; peptide; 9 AA.
XX
AC ADE27682;
XX
DT 29-JAN-2004 (first entry)
XX
DE Mouse anti-CCR4 antibody light chain CDR3.
XX
KW antiinflammatory; diagnosis; interstitial pneumonia; anti-CCR4 antibody;

Query Match 54.2%; Score 26; DB 6; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 SLMIWT 7
||: ||
4 SLLFWT 9

DB

RESULT 10
ADE27682
ID ADE27682 standard; peptide; 9 AA.
XX
AC ADE27682;
XX
DT 29-JAN-2004 (first entry)
XX
DE Mouse anti-CCR4 antibody light chain CDR3.
XX
KW antiinflammatory; diagnosis; interstitial pneumonia; anti-CCR4 antibody;

Query Match 54.2%; Score 26; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 SLMIWT 7
||: ||
4 SLLFWT 9

DB

RESULT 11
ADK08458
ID ADK08458 standard; peptide; 9 AA.
XX
AC ADK08458;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human papillomavirus peptide #513.
XX
KW pathogenic virus; alternative reading frame; antigenic determinant;
KW virucide; vaccine; therapeutic agent; infection; HPV.
XX
OS Human papillomavirus.
XX
PN WO2004011650-A2.
XX
PD 05-FEB-2004.
XX
PF 24-JUL-2003; 2003WO-EP008112.
XX
PR 24-JUL-2002; 2002AT-00001124.
XX
PR 11-JUL-2003; 2003EP-00450171.
XX
PA (INTE-) INTERCELL AG.
XX
PI Mattner F, Schmidt W, Habel A;

anti-CCR3 antibody; Th1 cell infiltration; Th2 cell infiltration;
complementarity determining region.
Mus sp.
WO2003072134-A1.
04-SEP-2003.
28-FEB-2003; 2003WO-JP002372.
28-FEB-2002; 2002JP-00054764.
(KYOW) KYOWA HAKKO KOGYO KK.
Ueda R, Sato S, Yoshinouchi T, Niimi T, Shimizu S, Bimoto T;
WPI; 2003-671855/63.
Agents containing anti-CCR4 and/or anti-CCR3 antibody for diagnosis,
prevention and treatment of interstitial pneumonia.
Claim 12; SEQ ID NO 7; 145pp; Japanese.
The invention relates to diagnostic reagents and agents for treatment and
prevention of interstitial pneumonia containing anti-CCR4 antibody and/or
anti-CCR3 antibody. The reagents are used for the diagnosis, prevention
and treatment of interstitial pneumonia. The invention provides a method
for distinguishing atypical from typical idiopathic interstitial
pneumonia, since the former involves infiltration of mainly Th1 cells
while the latter involves infiltration of both Th1 and Th2 cells with a
majority of the latter. This sequence represents the complementarity
determining region 3 (CDR3) from the mouse anti-CCR4 antibody light chain
variable region.
Sequence 9 AA;

Query Match 54.2%; Score 26; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 SLMIWT 7
||: ||
4 SLLFWT 9

DB

RESULT 11
ADK08458
ID ADK08458 standard; peptide; 9 AA.
XX
AC ADK08458;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human papillomavirus peptide #513.
XX
KW pathogenic virus; alternative reading frame; antigenic determinant;
KW virucide; vaccine; therapeutic agent; infection; HPV.
XX
OS Human papillomavirus.
XX
PN WO2004011650-A2.
XX
PD 05-FEB-2004.
XX
PF 24-JUL-2003; 2003WO-EP008112.
XX
PR 24-JUL-2002; 2002AT-00001124.
XX
PR 11-JUL-2003; 2003EP-00450171.
XX
PA (INTE-) INTERCELL AG.
XX
PI Mattner F, Schmidt W, Habel A;

XX WPI; 2004-169243/16.
 XX New polypeptide encoded by an alternative reading frame of a pathogenic
 PT virus comprising an antigenic determinant, useful for treating or
 PT preventing an infection with the pathogenic virus.
 XX
 PS Claim 18; Page 179; 220pp; English.
 XX This invention relates to a novel polypeptide encoded by an alternative
 CC reading frame of a pathogenic virus, where the polypeptide starts with a
 CC methionine amino acid residue, which comprises an antigenic determinant
 CC and more than 7 amino acid residues. The invention may be useful for the
 CC production of compounds with a virucide activity or the development of a
 CC vaccine. The polypeptide or its fragments may be useful as a therapeutic
 CC agent. It is also useful for the manufacture of a medicament for treating
 CC or preventing an infection with the pathogenic virus. The present
 CC sequence is that of a human papillomavirus (HPV) epitope peptide of the
 CC invention.
 XX
 SQ Sequence 9 AA;
 Query Match 54.2%; Score 26; DB 8; Length 9;
 Best Local Similarity 42.9%; Pred. No. 1.7e+06;
 Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 2 SLMIWTM 8
 Db 3 ALVLWTL 9
 : : : : :
 : : : : :
 RESULT 12
 ID ABP14228
 AC ABP14228 standard; peptide; 8 AA.
 XX
 AC ABP14228;
 XX
 DT 11-SEP-2003 (revised)
 DT 15-JUL-2002 (first entry)
 XX
 DE HIV A02 super motif vpu peptide #11.
 XX
 XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
 KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
 KW vaccine; HIV infection; immunisation; virucide.
 KW
 XX Human immunodeficiency virus 1.
 OS
 XX WO200124810-A1.
 PN
 XX 12-APR-2001.
 PD
 XX 05-OCT-2000; 2000WO-US027766.
 XX
 PF 05-OCT-1999; 99US-00412863.
 XX
 PR (EPIM-) EPIMMUNE INC.
 PA
 XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX
 XX WPI; 2001-354887/37.
 DR
 XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1.
 PT
 XX Claim 32; Page 159; 448pp; English.
 PS
 XX The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
 CC be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine

CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines. An
 CC additional advantage of an group-based vaccine approach is the ability to
 CC combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP11501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)
 XX
 XX Sequence 8 AA;
 SQ
 Query Match 52.1%; Score 25; DB 4; Length 8;
 Best Local Similarity 25.0%; Pred. No. 1.7e+06;
 Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
 QY 2 SLMIWTMM 9
 Db 1 AIVVWTV 8
 : : : : :
 : : : : :
 RESULT 13
 ID ABP19690
 AC ABP19690 standard; peptide; 8 AA.
 XX
 AC ABP19690;
 XX
 DT 11-SEP-2003 (revised)
 DT 15-JUL-2002 (first entry)
 XX
 DE HIV B62 super motif vpu peptide #28.
 XX
 KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
 KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
 KW vaccine; HIV infection; immunisation; virucide.
 KW
 XX Human immunodeficiency virus 1.
 OS
 XX WO200124810-A1.
 PN
 XX 12-APR-2001.
 PD
 XX 05-OCT-2000; 2000WO-US027766.
 XX
 PF 05-OCT-1999; 99US-00412863.
 XX
 PR (EPIM-) EPIMMUNE INC.
 PA
 XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX
 XX WPI; 2001-354887/37.
 DR
 XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1.
 PT
 XX Claim 32; Page 272; 448pp; English.
 PS
 XX The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
 CC be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine

CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines. An
 CC additional advantage of an group-based vaccine approach is the ability to
 CC combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP1501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 8 AA;

Query Match 52.1%; Score 25; DB 4; Length 8;
 Best Local Similarity 25.0%; Pred. No. 1.7e+06;
 Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 2 SLMIWTMM 9
 DB 1 AIVWTV 8

RESULT 14
 ADB84465
 ID ADB84465 standard; peptide; 8 AA.

AC ADB84465;

DT 04-DEC-2003 (first entry)

DE MSRV-1 POL2B octapeptide #27.

XX MSRV; multiple sclerosis; rheumatoid arthritis; gag; pol;
 KW reverse transcriptase; ribonuclease H; antigen; immunogen.

XX Multiple sclerosis associated retrovirus.

XX US2003039664-A1.

PD 27-FEB-2003.

PF 26-NOV-1997; 97US-00979847.

PR 26-NOV-1996; 96US-00756429.

XX (PERR/) PERRON H.
 PA (BESE/) BESEME F.
 PA (BEDI/) BEDIN F.
 PA (PARA/) PARANHOS-BACCALA G.
 PA (KOMU/) KOMURIAN-PRADEL F.
 PA (JOLI/) JOLIVET-REYNAUD C.
 PA (MAND/) MANDRAND B.
 PA (GARS/) GARSON J A.
 PA (TUKP/) TUKP P W.

XX Perron H, Beseme F, Bedin F, Paranhos-Baccala G;
 PI Komurian-Pradel F, Jollivet-Reynaud C, Mandrand B, Garson JA, Tuke PW;
 XX WPI; 2003-512253/48.

XX New isolated or purified nucleic acid associated with multiple sclerosis
 PT retrovirus, useful for detecting a virus associated with
 PT multiple sclerosis or rheumatoid arthritis in a biological sample.

XX Example 11; Fig 31; 193pp; English.

XX The invention relates to an isolated or purified nucleic acid from a
 CC virus associated with multiple sclerosis and/or rheumatoid arthritis,

CC multiple sclerosis-associated virus (MSRV)-1. The nucleic acids comprise
 CC pol, gag or reverse transcriptase genes (or their fragments) encoding the
 CC proteins or defined peptides (including immunodominant peptides,
 CC antigenic peptides or conserved motifs). Also included are a process for
 CC detecting a virus associated with multiple sclerosis or rheumatoid
 CC arthritis in a biological sample, a nucleic acid probe for the detection
 CC of a virus associated with multiple sclerosis or rheumatoid arthritis, a
 CC primer for the amplification by polymerisation of a nucleic acid of a
 CC viral material associated with multiple sclerosis or rheumatoid
 CC arthritis, a polypeptide exhibiting an inhibitory activity on the
 CC proteolytic, reverse transcriptase or ribonuclease H activity from MSRV,
 CC and an antibody directed against the MSRV-1 virus obtained by
 CC immunologically reacting a human or animal body or cells with an
 CC immunogenic agent consisting of the antigenic polypeptide defined above.
 CC The nucleic acids are useful for detecting a biological sample a virus
 CC associated with multiple sclerosis or rheumatoid arthritis, or for
 CC detecting in a biological sample, the presence of or exposure to a virus
 CC associated with multiple sclerosis or rheumatoid arthritis. The present
 CC sequence is an MSRV immunogenic or antigenic peptide (or a conserved
 CC peptide motif). Note: The SEQ ID numbers for the sequences as displayed
 CC in the main body of the patent do not match the SEQ ID numbers in the
 CC sequence listing. Consequently those sequences mentioned in the claims
 CC may not be the sequences the authors intended to claim.

XX Sequence 8 AA;

Query Match 52.1%; Score 25; DB 7; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.7e+06;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 TSLMIWTMM 8
 DB 1 TSQLTWTV 8

RESULT 15
 ADG14911

ID ADG14911 standard; peptide; 8 AA.

XX ADG14911;

DT 26-FEB-2004 (first entry)

XX MSRV-1 POL2B peptide #29.

DE pol gene; retrovirus; multiple sclerosis; rheumatoid arthritis.

XX Multiple sclerosis associated retrovirus.

XX US2003198647-A1.

PD 23-OCT-2003.

PF 03-APR-2002; 2002US-00114104.

PR 26-NOV-1996; 96US-00756429.

PR 26-NOV-1997; 97US-00979847.

XX (INNR) BIO MERIEUX.

XX Perron H, Beseme F, Bedin F, Paranhos-Baccala G;
 PI Komurian-Pradel F, Jollivet-Reynaud C, Mandrand B, Garson JA, Tuke PW;
 XX WPI; 2004-032461/03.

XX New isolated nucleic acid and their fragments having the pol gene of a
 PT retrovirus, useful for diagnosing, preventing and/or treating multiple
 PT sclerosis and/or rheumatoid arthritis.

XX Disclosure; SEQ ID NO 170; 193pp; English.

XX The invention relates to an isolated nucleic acid which comprises the pol
 CC gene of a retrovirus associated with multiple sclerosis or rheumatoid

CC arthritis. The methods and compositions of the present invention are
CC useful for diagnosing, preventing and/or treating multiple sclerosis
CC and/or rheumatoid arthritis. The present sequence is used in the
CC exemplification of the invention.

XX
SQ Sequence 8 AA;

Query Match 52.1%; Score 25; DB 8; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TSLMIWTM 8
|| : ||:
Db 1 TSQLTWTV 8

Search completed: November 14, 2004, 14:03:53
Job time : 158 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2004, 13:58:00 ; Search time 36 Seconds
(without alignments)
16.579 Million cell updates/sec

Title: US-09-831-253F-5
Perfect score: 48
Sequence: 1 TSLMIWTMM 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 95011

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	52.1	8	4 US-08-979-847B-170	Sequence 170, Appl
2	24	50.0	5	4 US-09-632-570-35	Sequence 35, Appl
3	24	50.0	6	1 US-08-032-848C-20	Sequence 20, Appl
4	24	50.0	6	4 US-09-632-570-38	Sequence 38, Appl
5	24	50.0	7	4 US-08-635-886C-170	Sequence 170, Appl
6	24	50.0	7	4 US-08-974-690C-170	Sequence 170, Appl
7	24	50.0	7	4 US-08-974-685-170	Sequence 170, Appl
8	24	50.0	7	4 US-08-974-685-180	Sequence 180, Appl
9	24	50.0	8	2 US-08-641-314C-7	Sequence 7, Appl
10	24	50.0	8	4 US-09-548-938A-17	Sequence 17, Appl
11	24	50.0	8	4 US-08-979-847B-169	Sequence 169, Appl
12	24	50.0	9	4 US-08-466-601A-160	Sequence 160, Appl
13	22	45.8	6	4 US-08-134-231C-40	Sequence 40, Appl
14	22	45.8	7	3 US-09-258-754-385	Sequence 385, Appl
15	22	45.8	7	3 US-09-042-107-385	Sequence 385, Appl
16	22	45.8	7	4 US-09-722-250D-385	Sequence 385, Appl
17	22	45.8	7	4 US-09-676-475A-385	Sequence 385, Appl
18	22	45.8	8	4 US-08-979-847B-171	Sequence 171, Appl
19	22	45.8	9	3 US-09-183-931-43	Sequence 43, Appl
20	22	45.8	9	3 US-09-183-931-44	Sequence 44, Appl
21	22	45.8	9	3 US-09-359-503-5	Sequence 5, Appl
22	22	45.8	9	3 US-09-359-503-6	Sequence 6, Appl
23	22	45.8	9	3 US-09-062-422-5	Sequence 5, Appl
24	22	45.8	9	3 US-09-062-422-6	Sequence 6, Appl
25	22	45.8	9	3 US-08-937-263B-5	Sequence 5, Appl
26	22	45.8	9	3 US-08-937-263B-6	Sequence 6, Appl
27	22	45.8	9	3 US-09-166-448-80	Sequence 80, Appl

28	22	45.8	9	3 US-09-166-448-81	Sequence 81, Appl
29	22	45.8	9	3 US-09-705-160-43	Sequence 43, Appl
30	22	45.8	9	3 US-09-705-160-44	Sequence 44, Appl
31	22	45.8	9	4 US-09-440-621-2	Sequence 2, Appl
32	22	45.8	9	4 US-09-440-621-3	Sequence 3, Appl
33	22	45.8	9	4 US-09-440-621-6	Sequence 6, Appl
34	22	45.8	9	4 US-09-440-621-7	Sequence 7, Appl
35	22	45.8	9	4 US-09-440-621-8	Sequence 8, Appl
36	22	45.8	9	4 US-09-440-621-10	Sequence 10, Appl
37	22	45.8	9	4 US-09-697-884-80	Sequence 80, Appl
38	22	45.8	9	4 US-09-697-884-81	Sequence 81, Appl
39	22	45.8	9	4 US-09-670-456A-1	Sequence 1, Appl
40	22	45.8	9	4 US-09-751-798-5	Sequence 5, Appl
41	22	45.8	9	4 US-09-751-798-6	Sequence 6, Appl
42	22	45.8	9	4 US-09-344-040C-122	Sequence 122, App
43	22	45.8	9	4 US-09-344-040C-131	Sequence 131, App
44	22	45.8	9	4 US-09-344-040C-132	Sequence 132, App
45	22	45.8	9	4 US-09-574-749B-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1

US-08-979-847B-170
; Sequence 170, Application US/08979847B
; Patent No. 6582703
; GENERAL INFORMATION:
; APPLICANT: PERRON, HERVE
; BESEME, FREDERIC
; BEDIN, FREDERIC
; PARANHOS-BACCALA, GLAUCIA
; KOMURIAN-PRADEL, FLORENCE
; JOLIVET-REYNAUD, COLETTE
; MANDRAND, BERNARD
; GARSON, JEREMY
; TUKE, PHILIP

TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYL
THERAPEUTIC PURPOSES

NUMBER OF SEQUENCES: 210
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
STATE: VA
COUNTRY: USA
ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,847B
FILING DATE: 26-NO. 6582703-1997
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 39046A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
TELEFAX: 703-836-2787

INFORMATION FOR SEQ ID NO: 170:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 170:
US-08-979-847B-170

```
Query Match      52.1%; Score 25; DB 4; Length 8;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 TSLMIWTM 8
   || : ||:
Db 1 TSQLTWTW 8

RESULT 2
US-09-632-570-35
; Sequence 35, Application US/09632570
; Patent No. 6623949
; GENERAL INFORMATION:
; APPLICANT: Gualfetti, Peter
; APPLICANT: Mitchinson, Colin
; APPLICANT: Phillips, Jay Ian
; TITLE OF INVENTION: No. 6623949el Variant EGIII-Like Cellulase
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: GC631
; CURRENT APPLICATION NUMBER: US/09/632,570
; CURRENT FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: BOX2
US-09-632-570-35

Query Match      50.0%; Score 24; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LMIW 6
   ||||
Db 2 LMIW 5

RESULT 3
US-08-032-848C-20
; Sequence 20, Application US/08032848C
; Patent No. 5475101
; GENERAL INFORMATION:
; APPLICANT: Ward, Michael
; APPLICANT: Clarkson, Kathleen A.
; APPLICANT: Weiss, Geoffrey L.
; APPLICANT: Larenas, Edward
; APPLICANT: Lorch, Jeffrey D.
; TITLE OF INVENTION: Purification and Molecular Cloning of
; TITLE OF INVENTION: EG III Cellulase
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International
; STREET: 180 Kimball Way
; CITY: South San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/032,848C
; FILING DATE: MAR 17 1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Horn, Margaret A.
```

```
; REGISTRATION NUMBER: 33,401
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415 742-7356
; TELEFAX: 415 742-7217
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-032-848C-20

Query Match      50.0%; Score 24; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LMIW 6
   ||||
Db 2 LMIW 5

RESULT 4
US-09-632-570-38
; Sequence 38, Application US/09632570
; Patent No. 6623949
; GENERAL INFORMATION:
; APPLICANT: Gualfetti, Peter
; APPLICANT: Mitchinson, Colin
; APPLICANT: Phillips, Jay Ian
; TITLE OF INVENTION: No. 6623949el Variant EGIII-Like Cellulase
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: GC631
; CURRENT APPLICATION NUMBER: US/09/632,570
; CURRENT FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: BOX2'
US-09-632-570-38

Query Match      50.0%; Score 24; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LMIW 6
   ||||
Db 3 LMIW 6

RESULT 5
US-08-635-886C-170
; Sequence 170, Application US/08635886C
; Patent No. 6555114
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; FILE REFERENCE: 2752-18
; CURRENT APPLICATION NUMBER: US/08/635,886C
; CURRENT FILING DATE: 1996-04-25
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
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US-08-974-685-180

Query Match 50.0%; Score 24; DB 4; Length 7;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 MIWTMM 9
| | | |
Db 2 MAWDMM 7

RESULT 9

US-08-641-314C-7
; Sequence 7, Application US/08641314C
; Patent No. 5977440
; GENERAL INFORMATION:
; APPLICANT: LUTHE, DAWN S.
; APPLICANT: WILLIAMS, W. P.
; APPLICANT: BINGHUA, JIANG
; APPLICANT: PECHAN, TIBOR
; TITLE OF INVENTION: DNA MOLECULE ENCODING A 33 KD CYSTEINE
; TITLE OF INVENTION: PROTEINASE AND ITS USE IN TRANSFORMING PLANTS TO PROVIDE
; TITLE OF INVENTION: INSECT RESISTANCE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/641,314C
; FILING DATE: 30-APR-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: KELBER, STEVEN B.
; REGISTRATION NUMBER: 30,073
; REFERENCE/DOCKET NUMBER: 2343-045-27
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-641-314C-7

Query Match 50.0%; Score 24; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 SLMIW 6
| : | | |
Db 1 SVMVW 5

RESULT 10

US-09-548-938A-17
; Sequence 17, Application US/09548938A
; Patent No. 6573086
; GENERAL INFORMATION:
; APPLICANT: EMALFARB, MARK AARON
; APPLICANT: BURLINGAME, RICHARD PAUL

; APPLICANT: OLSON, PHILIP TERRY
; APPLICANT: SINITSYN, ARKADY PANTELEIMONOVICK
; APPLICANT: PARRICHE, MARTINE
; APPLICANT: BOUSSON, JEAN CHRISTOPHE
; APPLICANT: PYNNONEN, CHRISTINE MARIE
; APPLICANT: PUNT, PETER JAN
; APPLICANT: VAN-ZEIJL, CORNELIA MARIA JOHANNA
; TITLE OF INVENTION: TRANSFORMATION SYSTEM IN THE FIELD OF FILAMENTOUS FUNGI
; FILE REFERENCE: 3123-4001
; CURRENT APPLICATION NUMBER: US/09/548,938A
; CURRENT FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Chrysosporium sp.
US-09-548-938A-17

Query Match 50.0%; Score 24; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LMIW 6
| | | |
Db 5 LMIW 8

RESULT 11

US-08-979-847B-169
; Sequence 169, Application US/08979847B
; Patent No. 6582703
; GENERAL INFORMATION:
; APPLICANT: PERRON, HERVE
; BESEME, FREDERIC
; BEDIN, FREDERIC
; PARANHOS-BACCALA, GLAUCIA
; KOMURIAN-PRADEL, FLORENCE
; JOLIVET-REYNAUD, COLETTE
; MANDRAND, BERNARD
; GARSON, JEREMY
; TUKER, PHILIP
; TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
; ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYL
; THERAPEUTIC PURPOSES

NUMBER OF SEQUENCES: 210
CORRESPONDENCE ADDRESS:

ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. BOX 19928
CITY: ALEXANDRIA
STATE: VA
COUNTRY: USA
ZIP: 22320

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/979,847B
FILING DATE: 26-NO. 6582703-1997
CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 39046A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6400
TELEFAX: 703-836-2787
INFORMATION FOR SEQ ID NO: 169:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 169:
US-08-979-847B-169
Query Match      50.0%; Score 24; DB 4; Length 8;
Best Local Similarity 57.1%; Pred. No. 3.8e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 TSLMIWT 7
DB      2 TSQLTWT 8

RESULT 12
US-08-466-601A-160
; Sequence 160, Application US/08466601A
; Patent No. 6572864
; GENERAL INFORMATION:
; APPLICANT: BURKH, J., MILLER, R.H. AND
; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
; TITLE OF INVENTION: OF 51 ISOLATES OF HEPATITIS C AND THE USE
; TITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES IN
; TITLE OF INVENTION: DIAGNOSTIC METHODS AND VACCINES
; NUMBER OF SEQUENCES: 160
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,601A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/086,428
; FILING DATE: 29-JUN-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RICHARD W. BORK
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4070US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 160:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
US-08-466-601A-160
Query Match      50.0%; Score 24; DB 4; Length 9;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4 MIWTMM 9
DB      4 MAWDM 9

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 169:
US-08-979-847B-169
Query Match      50.0%; Score 24; DB 4; Length 8;
Best Local Similarity 57.1%; Pred. No. 3.8e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 TSLMIWT 7
DB      2 TSQLTWT 8

RESULT 13
US-08-134-231C-40
; Sequence 40, Application US/08134231C
; Patent No. 6562596
; GENERAL INFORMATION:
; APPLICANT: Silbiger, Scott M.
; Koski, Raymond A.
; TITLE OF INVENTION: Tissue Inhibitor Metalloproteinase Type
; Three (TIMP-3) Composition and Methods
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/134,231C
; FILING DATE: 06-Oct-1993
; CLASSIFICATION: <Unknown>
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-08-134-231C-40
Query Match      45.8%; Score 22; DB 4; Length 6;
Best Local Similarity 80.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 IWTMM 9
DB      2 IWTDM 6

RESULT 14
US-09-258-754-385
; Sequence 385, Application US/09258754
; Patent No. 6174887
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 09/042,107
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 385
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-385
Query Match      45.8%; Score 22; DB 3; Length 7;
Best Local Similarity 60.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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QY 5 IWTTM 9
| | | : :
Db 1 IWTVV 5

RESULT 15
US-09-042-107-385
; Sequence 385, Application US/09042107
; Patent No. 6232287
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 2892
; CURRENT APPLICATION NUMBER: US/09/042,107
; CURRENT FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 436
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 385
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-042-107-385

Query Match 45.8%; Score 22; DB 3; Length 7;
Best Local Similarity 60.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 IWTTM 9
| | | : :
Db 1 IWTVV 5

Search completed: November 14, 2004, 14:08:30
Job time : 36 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:26 ; Search time 7.08511 Seconds
(without alignments)
84.242 Million cell updates/sec

Title: US-09-831-253F-5
Perfect score: 48
Sequence: 1 TSLMWTMM 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	28	58.3	12	1	US-08-241-054-50
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4	28	58.3	12	1	US-08-241-054-61
5	28	58.3	12	1	US-08-390-156A-22
6	28	58.3	12	1	US-08-390-156A-57
7	28	58.3	12	1	US-08-390-156A-61
8	28	58.3	12	1	US-08-439-817-30
9	28	58.3	12	1	US-08-439-817-33
10	28	58.3	12	1	US-08-439-817-41
11	28	58.3	12	1	US-08-485-508-50
12	28	58.3	12	1	US-08-485-508-53
13	28	58.3	12	1	US-08-485-508-61
14	27	56.2	21	3	US-08-905-223-20
15	27	56.2	21	3	US-08-247-155-20
16	27	56.2	21	4	US-09-663-600A-20
17	27	56.2	21	4	US-09-621-976-2
18	27	56.2	21	4	US-09-513-999C-2
19	26	54.2	20	1	US-08-241-054-81
20	26	54.2	20	1	US-08-390-156A-38
21	26	54.2	20	1	US-08-439-817-61
22	26	54.2	20	1	US-08-485-508-81
23	25	52.1	8	4	US-08-979-847B-170
24	25	52.1	12	1	US-08-241-054-55
25	25	52.1	12	1	US-08-241-054-95
26	25	52.1	12	1	US-08-241-054-98
27	25	52.1	12	1	US-08-390-156A-45

28	25	52.1	12	1	US-08-390-156A-58
29	25	52.1	12	1	US-08-390-156A-87
30	25	52.1	12	1	US-08-439-817-35
31	25	52.1	12	1	US-08-439-817-75
32	25	52.1	12	1	US-08-439-817-78
33	25	52.1	12	1	US-08-439-817-200
34	25	52.1	12	1	US-08-485-508-55
35	25	52.1	12	1	US-08-485-508-95
36	25	52.1	12	1	US-08-485-508-98
37	25	52.1	12	4	US-09-428-082B-151
38	25	52.1	12	4	US-09-419-381-21
39	25	52.1	16	3	US-09-180-100-25
40	25	52.1	20	3	US-08-826-964-3
41	25	52.1	22	4	US-09-205-258-896
42	24	50.0	5	4	US-09-632-570-35
43	24	50.0	6	1	US-08-032-848C-20
44	24	50.0	6	4	US-09-632-570-38
45	24	50.0	7	4	US-08-635-886C-170

ALIGNMENTS

RESULT 1

US-09-149-476-551
; Sequence 551, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23

[illegible]

1	EARLIER	FILING DATE:	1997-08-22
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3	EARLIER	FILING DATE:	1997-08-22
4	EARLIER	APPLICATION NUMBER:	60/056,911
5	EARLIER	FILING DATE:	1997-08-22
6	EARLIER	APPLICATION NUMBER:	60/056,636
7	EARLIER	FILING DATE:	1997-08-22
8	EARLIER	APPLICATION NUMBER:	60/056,874
9	EARLIER	FILING DATE:	1997-08-22
10	EARLIER	APPLICATION NUMBER:	60/056,910
11	EARLIER	FILING DATE:	1997-08-22
12	EARLIER	APPLICATION NUMBER:	60/056,864
13	EARLIER	FILING DATE:	1997-08-22
14	EARLIER	APPLICATION NUMBER:	60/056,631
15	EARLIER	FILING DATE:	1997-08-22
16	EARLIER	APPLICATION NUMBER:	60/056,845
17	EARLIER	FILING DATE:	1997-08-22
18	EARLIER	APPLICATION NUMBER:	60/056,892
19	EARLIER	FILING DATE:	1997-08-22
20	EARLIER	APPLICATION NUMBER:	60/057,761
21	EARLIER	FILING DATE:	1997-08-22
22	EARLIER	APPLICATION NUMBER:	60/047,595
23	EARLIER	FILING DATE:	1997-05-23
24	EARLIER	APPLICATION NUMBER:	60/047,599
25	EARLIER	FILING DATE:	1997-05-23
26	EARLIER	APPLICATION NUMBER:	60/047,588
27	EARLIER	FILING DATE:	1997-05-23
28	EARLIER	APPLICATION NUMBER:	60/047,585
29	EARLIER	FILING DATE:	1997-05-23
30	EARLIER	APPLICATION NUMBER:	60/047,586
31	EARLIER	FILING DATE:	1997-05-23
32	EARLIER	APPLICATION NUMBER:	60/047,590
33	EARLIER	FILING DATE:	1997-05-23
34	EARLIER	APPLICATION NUMBER:	60/047,594
35	EARLIER	FILING DATE:	1997-05-23
36	EARLIER	APPLICATION NUMBER:	60/047,589
37	EARLIER	FILING DATE:	1997-05-23
38	EARLIER	APPLICATION NUMBER:	60/047,593
39	EARLIER	FILING DATE:	1997-05-23
40	EARLIER	APPLICATION NUMBER:	60/047,614
41	EARLIER	FILING DATE:	1997-05-23
42	EARLIER	APPLICATION NUMBER:	60/043,578
43	EARLIER	FILING DATE:	1997-04-11
44	EARLIER	APPLICATION NUMBER:	60/043,576
45	EARLIER	FILING DATE:	1997-04-11
46	EARLIER	APPLICATION NUMBER:	60/047,501
47	EARLIER	FILING DATE:	1997-05-23
48	EARLIER	APPLICATION NUMBER:	60/043,670
49	EARLIER	FILING DATE:	1997-04-11
50	EARLIER	APPLICATION NUMBER:	60/056,632
51	EARLIER	FILING DATE:	1997-08-22
52	EARLIER	APPLICATION NUMBER:	60/056,664
53	EARLIER	FILING DATE:	1997-08-22
54	EARLIER	APPLICATION NUMBER:	60/056,876
55	EARLIER	FILING DATE:	1997-08-22
56	EARLIER	APPLICATION NUMBER:	60/056,881
57	EARLIER	FILING DATE:	1997-08-22
58	EARLIER	APPLICATION NUMBER:	60/056,909
59	EARLIER	FILING DATE:	1997-08-22
60	EARLIER	APPLICATION NUMBER:	60/056,875
61	EARLIER	FILING DATE:	1997-08-22
62	EARLIER	APPLICATION NUMBER:	60/056,862
63	EARLIER	FILING DATE:	1997-08-22
64	EARLIER	APPLICATION NUMBER:	60/056,887
65	EARLIER	FILING DATE:	1997-08-22
66	EARLIER	APPLICATION NUMBER:	60/056,908
67	EARLIER	FILING DATE:	1997-08-22
68	EARLIER	APPLICATION NUMBER:	60/048,964
69	EARLIER	FILING DATE:	1997-06-06
70	EARLIER	APPLICATION NUMBER:	60/057,650
71	EARLIER	FILING DATE:	1997-09-05
72	EARLIER	APPLICATION NUMBER:	60/056,884
73	EARLIER	FILING DATE:	1997-08-22

EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02

Query Match 58.3%; Score 28; DB 4; Length 11;
Best Local Similarity 42.9%; Pred. No. 66;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 LMIWTMM 9
|:|:|:|:
Db 1 LLLWTL 7

RESULT 2

US-08-241-054-50
; Sequence 50, Application US/08241054
; Patent No. 5643873
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Cwiria, Steven E.
; APPLICANT: Dower, William J.
; APPLICANT: Koller, Kerry J.
; APPLICANT: Lee, Jung
; APPLICANT: Martens, Christine L.
; APPLICANT: Ruhland-Fritsch, Beatrice
; TITLE OF INVENTION: Peptides and Compounds That Bind
; TITLE OF INVENTION: Selectins Including Endothelium Leukocyte Adhesion
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/241,054
; FILING DATE: 11-MAY-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,295
; FILING DATE: 05-MAY-1993

; APPLICATION NUMBER: US 07/881,395
; FILING DATE: 06-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Gerald F. Swiss
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 000324-002
; TELEPHONE: 415-854-7400
; TELEFAX: 415-854-8275
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-241-054-50

Query Match 58.3%; Score 28; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 72;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 MIWTMM 9
|:|:|:|:
Db 6 MLWNMM 11

RESULT 3

US-08-241-054-53
; Sequence 53, Application US/08241054
; Patent No. 5643873
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Cwiria, Steven E.
; APPLICANT: Dower, William J.
; APPLICANT: Koller, Kerry J.
; APPLICANT: Lee, Jung
; APPLICANT: Martens, Christine L.
; APPLICANT: Ruhland-Fritsch, Beatrice
; TITLE OF INVENTION: Peptides and Compounds That Bind
; TITLE OF INVENTION: Selectins Including Endothelium Leukocyte Adhesion
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/241,054
; FILING DATE: 11-MAY-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,295
; FILING DATE: 05-MAY-1993
; APPLICATION NUMBER: US 07/881,395
; FILING DATE: 06-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Gerald F. Swiss
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 000324-002
; TELEPHONE: 415-854-7400
; TELEFAX: 415-854-8275
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-241-054-53

Query Match 58.3%; Score 28; DB 1; Length 12;
Best Local Similarity 80.0%; Pred. No. 72;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 IWTMM 9
|:|:|:|:
Db 7 LWTMM 11

RESULT 4

US-08-241-054-61
; Sequence 61, Application US/08241054
; Patent No. 5643873

GENERAL INFORMATION:
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Dower, William J.
APPLICANT: Koller, Kerry J.
APPLICANT: Lee, Jung
APPLICANT: Martens, Christine L.
APPLICANT: Ruhland-Fritsch, Beatrice
TITLE OF INVENTION: Peptides and Compounds That Bind
TITLE OF INVENTION: Selectins Including Endothelium Leukocyte Adhesion
TITLE OF INVENTION: Molecule 1
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22313
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/241,054
FILING DATE: 11-MAY-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,295
FILING DATE: 05-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/881,395
FILING DATE: 06-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gerald F. Swiss
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 000324-002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
TELEFAX: 415-854-8275
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-241-054-61

Query Match 58.3%; Score 28; DB 1; Length 12;
Best Local Similarity 80.0%; Pred. No. 72;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 IWTMM 9
DB 7 LWTMM 11

RESULT 5
US-08-390-156A-22
Sequence 22, Application US/08390156A
Patent No. 5648458
GENERAL INFORMATION:
APPLICANT: Cwirla, Steven E.
APPLICANT: Barrett, Ronald W.
APPLICANT: Dower, William J.
APPLICANT: Martens, Christine L.
TITLE OF INVENTION: Peptides and Compounds That Bind to
TITLE OF INVENTION: ELAM-1
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Affymax Technologies, N.V.

STREET: 4001 Miranda Ave.
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,156A
FILING DATE: 16-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,295
FILING DATE: 05-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/881,395
FILING DATE: 06-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Swiss, Gerald F.
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 1023.1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-496-2300
TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-390-156A-22

Query Match 58.3%; Score 28; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 72;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 MIWTMM 9
DB 6 MLWNMM 11

RESULT 6
US-08-390-156A-57
Sequence 57, Application US/08390156A
Patent No. 5648458
GENERAL INFORMATION:
APPLICANT: Cwirla, Steven E.
APPLICANT: Barrett, Ronald W.
APPLICANT: Dower, William J.
APPLICANT: Martens, Christine L.
TITLE OF INVENTION: Peptides and Compounds That Bind to
TITLE OF INVENTION: ELAM-1
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Affymax Technologies, N.V.
STREET: 4001 Miranda Ave.
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,156A
FILING DATE: 16-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,295

; FILING DATE: 05-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/881,395
; FILING DATE: 06-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Swiss, Gerald F.
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 1023.1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-390-156A-57

Query Match 58.3%; Score 28; DB 1; Length 12;
Best Local Similarity 80.0%; Pred. No. 72;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 IWTMM 9
Db 7 LWTMM 11

RESULT 7
US-08-390-156A-61
; Sequence 61, Application US/08390156A
; Patent No. 5648458
; GENERAL INFORMATION:
; APPLICANT: Cwirla, Steven E.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Dower, William J.
; APPLICANT: Martens, Christine L.
; TITLE OF INVENTION: Peptides and Compounds That Bind to
; TITLE OF INVENTION: ELAM-1
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies, N.V.
; STREET: 4001 Miranda Ave.
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,156A
; FILING DATE: 16-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,295
; FILING DATE: 05-MAY-1993

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/881,395
; FILING DATE: 06-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Swiss, Gerald F.
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 1023.1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832

; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-390-156A-61

Query Match 58.3%; Score 28; DB 1; Length 12;
Best Local Similarity 80.0%; Pred. No. 72;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 IWTMM 9
Db 7 LWTMM 11

RESULT 8
US-08-439-817-30
; Sequence 30, Application US/08439817
; Patent No. 5728802
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Cwirla, Steven E.
; APPLICANT: Dower, William J.
; APPLICANT: Koller, Kerry J.
; APPLICANT: Lee, Jung
; APPLICANT: Martens, Christine L.
; APPLICANT: Ruhland-Fritsch, Beatrice
; TITLE OF INVENTION: Peptides and Compounds That Bind
; TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion
; TITLE OF INVENTION: Molecule 1 (ELAM-1)
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies, NV
; STREET: 4001 Miranda Ave.
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/439,817
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/241,054
; FILING DATE: 11-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,295
; FILING DATE: 05-MAY-1993

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/881,395
; FILING DATE: 06-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 000324-046/1056.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-439-817-30

Query Match 58.3%; Score 28; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 72;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 MIWTMM 9
|:|:|
Db 6 MLWNMM 11

RESULT 9

US-08-439-817-33
; Sequence 33, Application US/08439817
; Patent No. 5728802
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Cwirla, Steven E.
; APPLICANT: Dower, William J.
; APPLICANT: Koller, Kerry J.
; APPLICANT: Lee, Jung
; APPLICANT: Martens, Christine L.
; APPLICANT: Ruhland-Fritsch, Beatrice
; TITLE OF INVENTION: Peptides and Compounds That Bind
; TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion
; TITLE OF INVENTION: Molecule I (ELAM-1)
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies, NV
; STREET: 4001 Miranda Ave.
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/439,817
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/241,054
; FILING DATE: 11-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,295
; FILING DATE: 05-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/881,395
; FILING DATE: 06-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 000324-046/1056.1
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-439-817-33

Query Match 58.3%; Score 28; DB 1; Length 12;
Best Local Similarity 80.0%; Pred. No. 72;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 IWTMM 9
|:|:|
Db 7 LWTMM 11

RESULT 10

US-08-439-817-41
; Sequence 41, Application US/08439817
; Patent No. 5728802
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Cwirla, Steven E.
; APPLICANT: Dower, William J.
; APPLICANT: Koller, Kerry J.
; APPLICANT: Lee, Jung
; APPLICANT: Martens, Christine L.
; APPLICANT: Ruhland-Fritsch, Beatrice
; TITLE OF INVENTION: Peptides and Compounds That Bind
; TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion
; TITLE OF INVENTION: Molecule I (ELAM-1)
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies, NV
; STREET: 4001 Miranda Ave.
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/439,817
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/241,054
; FILING DATE: 11-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,295
; FILING DATE: 05-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/881,395
; FILING DATE: 06-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 000324-046/1056.1
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-439-817-41

Query Match 58.3%; Score 28; DB 1; Length 12;
Best Local Similarity 80.0%; Pred. No. 72;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 IWTMM 9
|:|:|
Db 7 LWTMM 11

RESULT 11

US-08-485-508-50
; Sequence 50, Application US/08485508
; Patent No. 5786322
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Cwirla, Steven E.

APPLICANT: Dower, William J.
APPLICANT: Koller, Kerry J.
APPLICANT: Lee, Jung
APPLICANT: Martens, Christine L.
APPLICANT: Ruhland-Fritsch, Beatrice
TITLE OF INVENTION: Peptides and Compounds That Bind
TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion
TITLE OF INVENTION: Molecule I
NUMBER OF SEQUENCES: 162
CORRESPONDENCE ADDRESS:
ADDRESSEE: Affymax Technologies, NV
STREET: 4001 Miranda Ave.
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,508
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/241,054
FILING DATE: 11-MAY-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,295
FILING DATE: 05-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/881,395
FILING DATE: 06-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Stevens, Lauren L.
REGISTRATION NUMBER: 36,691
REFERENCE/DOCKET NUMBER: 000324-002/1056
TELEPHONE: 415-496-2300
TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-485-508-50

Query Match 58.3%; Score 28; DB 1; Length 12;
Best Local Similarity 56.7%; Pred. No. 72;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 MIWTMM 9
Db 6 MLNNMM 11

RESULT 12
US-08-485-508-53
Sequence 53, Application US/08485508
Patent No. 5786322

GENERAL INFORMATION:
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Dower, William J.
APPLICANT: Koller, Kerry J.
APPLICANT: Lee, Jung
APPLICANT: Martens, Christine L.
APPLICANT: Ruhland-Fritsch, Beatrice
TITLE OF INVENTION: Peptides and Compounds That Bind

TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion
TITLE OF INVENTION: Molecule I
NUMBER OF SEQUENCES: 162
CORRESPONDENCE ADDRESS:
ADDRESSEE: Affymax Technologies, NV
STREET: 4001 Miranda Ave.
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,508
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/241,054
FILING DATE: 11-MAY-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,295
FILING DATE: 05-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/881,395
FILING DATE: 06-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Stevens, Lauren L.
REGISTRATION NUMBER: 36,691
REFERENCE/DOCKET NUMBER: 000324-002/1056
TELEPHONE: 415-496-2300
TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-485-508-53

Query Match 58.3%; Score 28; DB 1; Length 12;
Best Local Similarity 80.0%; Pred. No. 72;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 IWTMM 9
Db 7 LWTMM 11

RESULT 13
US-08-485-508-61
Sequence 61, Application US/08485508
Patent No. 5786322

GENERAL INFORMATION:
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Dower, William J.
APPLICANT: Koller, Kerry J.
APPLICANT: Lee, Jung
APPLICANT: Martens, Christine L.
APPLICANT: Ruhland-Fritsch, Beatrice
TITLE OF INVENTION: Peptides and Compounds That Bind
TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion
TITLE OF INVENTION: Molecule I
NUMBER OF SEQUENCES: 162
CORRESPONDENCE ADDRESS:
ADDRESSEE: Affymax Technologies, NV
STREET: 4001 Miranda Ave.

```
;
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,508
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/241,054
; FILING DATE: 11-MAY-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,295
; FILING DATE: 05-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/881,395
; FILING DATE: 06-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 000324-002/1056
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-485-508-61

Query Match 58.3%; Score 28; DB 1; Length 12;
Best Local Similarity 80.0%; Pred. No. 72;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 INTMM 9
Db 7 LWTMM 11

RESULT 14
US-08-905-223-20
; Sequence 20, Application US/08905223
; Patent No. 6222029
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste D.
; APPLICANT: Duclert, Aymeric
; APPLICANT: Lacroix, Bruno
; TITLE OF INVENTION: 5' ESTE FOR SECRETED PROTEINS
; NUMBER OF SEQUENCES: 503
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 501 West Broadway
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-3505
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; OPERATING SYSTEM: Win95
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,223
; FILING DATE:
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;
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1..21
; IDENTIFICATION METHOD: Von Heijne matrix
; OTHER INFORMATION: score 5.5
; OTHER INFORMATION: seq SFLPSALVIWTS/AF
; US-08-905-223-20

Query Match 56.2%; Score 27; DB 3; Length 21;
Best Local Similarity 57.1%; Pred. No. 1.8e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSLMIWT 7
Db 13 SALVIWT 19

RESULT 15
US-09-247-155-20
; Sequence 20, Application US/09247155A
; Patent No. 6312922
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: Complementary DNAs
; FILE REFERENCE: GENSET.021A
; CURRENT APPLICATION NUMBER: US/09/247,155A
; CURRENT FILING DATE: 1999-02-09
; EARLIER APPLICATION NUMBER: 60/074,121
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/081,563
; EARLIER FILING DATE: 1998-04-13
; EARLIER APPLICATION NUMBER: 60/096,116
; EARLIER FILING DATE: 1998-08-10
; EARLIER APPLICATION NUMBER: 60/099,273
; EARLIER FILING DATE: 1998-10-04
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patent.pm
; SEQ ID NO 20
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: 1..21
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 5.5
; OTHER INFORMATION: seq SFLPSALVIWTS/AF
; US-09-247-155-20

Query Match 56.2%; Score 27; DB 3; Length 21;
Best Local Similarity 57.1%; Pred. No. 1.8e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSLMIWT 7
Db 13 SALVIWT 19
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Db 13 SALVWT 19

Search completed: November 14, 2004, 12:08:48
Job time : 8.08511 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:25 ; Search time 26.0426 Seconds
(without alignments)
123.973 Million cell updates/sec

Title: US-09-831-253F-5
Perfect score: 48
Sequence: 1 TSLMIWTMM 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 718658

Minimum DB seq length: 0
Maximum DB seq length: 23

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	9	3 AAY93096	Aay93096 Transform
2	48	100.0	9	3 AAY92949	Aay92949 Transform
3	36.5	76.0	12	3 AAY92947	Aay92947 Transform
4	36.5	76.0	12	3 AAY93008	Aay93008 Transform
5	35	72.9	11	3 AAY93094	Aay93094 Transform
6	35	72.9	12	3 AAY93009	Aay93009 Transform
7	35	72.9	12	3 AAY93010	Aay93010 Transform
8	31	64.6	18	4 AAB89123	Aab89123 HIV gp120
9	31	64.6	18	4 AAB89121	Aab89121 HIV gp120
10	31	64.6	18	4 AAB89122	Aab89122 HIV gp120
11	28	58.3	9	8 ADK08459	Adk08459 Human pap
12	28	58.3	9	8 ADK08095	Adk08095 Human pap
13	28	58.3	10	8 ADG94446	Adg94446 Human JAM
14	28	58.3	10	8 ADI46844	Adi46844 Permeabil
15	28	58.3	10	8 ADP87021	Adp87021 Junctiona
16	28	58.3	11	2 AAW74952	Aaw74952 Human sec
17	28	58.3	11	5 ABG95411	Abg95411 Human nov
18	28	58.3	11	6 ABO34605	Ab034605 Region of
19	28	58.3	11	8 ADI23266	Adi23266 Novel hum
20	28	58.3	11	7 ADH74268	Adh74268 Human sec
21	28	58.3	12	2 AAR86068	Aar86068 Anti-ELAM
22	28	58.3	12	2 AAR86065	Aar86065 Anti-ELAM
23	28	58.3	12	2 AAW26904	Aaw26904 ELAM-1 bi
24	28	58.3	12	2 AAW26900	Aaw26900 ELAM-1 bi
25	28	58.3	12	2 AAW26865	Aaw26865 ELAM-1 bi

26	28	58.3	12	2 AAW63875	Aaw63875 ELAM-1 pe
27	28	58.3	12	2 AAW63886	Aaw63886 ELAM-1 pe
28	28	58.3	12	2 AAW63878	Aaw63878 ELAM-1 pe
29	28	58.3	20	2 AAY17756	Aay17756 Target si
30	28	58.3	20	6 ABU93298	Abu93298 Single ch
31	28	58.3	21	4 ABB41629	Abb41629 Peptide #
32	28	58.3	21	4 AAM35422	Aam35422 Peptide #
33	28	58.3	21	4 AAM75309	Aam75309 Human bon
34	28	58.3	21	4 AAM62500	Aam62500 Human bra
35	27.5	57.3	14	3 AAY93098	Aay93098 Transform
36	27.5	57.3	14	3 AAY92950	Aay92950 Transform
37	27	56.2	9	6 ABU64837	Abu64837 Human NY-
38	27	56.2	10	8 ADK08116	Adk08116 Human pap
39	27	56.2	10	8 ADK08482	Adk08482 Human pap
40	27	56.2	20	4 AAM13980	Aam13980 Peptide #
41	27	56.2	20	4 ABB32925	Abb32925 Peptide #
42	27	56.2	20	4 AAM26386	Aam26386 Peptide #
43	27	56.2	20	4 ABB27754	Abb27754 Human pep
44	27	56.2	20	4 ABB18404	Abb18404 Protein #
45	27	56.2	20	4 AAM66109	Aam66109 Human bon

ALIGNMENTS

RESULT 1
AAY93096
ID AAY93096 standard; peptide; 9 AA.
XX AC AAY93096;
XX AC
DT 08-NOV-2000 (first entry)
XX
DE Transforming growth factor inhibitory peptide P142.
XX
KW Hepatotrophic; antagonist; transforming growth factor betal; TGF-b1;
KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX KW
OS Homo sapiens.
XX
PN WO200031135-A1.
XX
PD 02-JUN-2000.
XX
PF 23-NOV-1999; 99WO-ES000375.
XX
PR 24-NOV-1998; 98ES-00002465.
XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
XX
PI Exquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
PI Borrás Cuesta F;
XX WPI; 2000-411935/35.
PT Peptides that antagonize binding of transforming growth factor betal,
PT useful for treatment of liver disease, especially cirrhosis, are partial
XX sequences of the factor or its receptors.
XX Disclosure; Page 31; 86pp; Spanish.
CC The invention relates to synthetic peptides that antagonise the binding
CC of transforming growth (TGF) factor betal (TGF-b1) to its receptor in
CC vivo which have partial amino acid sequences identical, or similar, with
CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
CC examples of the peptides of the invention. The peptides act by
CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
CC they are inhibitors of stimulation of collagen synthesis in liver cells
CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
CC expression systems) encoding the peptides are used for treatment of liver
CC disease, specifically cirrhosis

```

XX
SQ Sequence 9 AA;
  Query Match      100.0%; Score 48; DB 3; Length 9;
  Best Local Similarity 100.0%; Pred. No. 1.7e+06;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLMIWTMM 9
  |||||
Db 1 TSLMIWTMM 9

RESULT 2
AAY92949
ID AAY92949 standard; peptide; 9 AA.
XX
AC AAY92949;
XX
DT 08-NOV-2000 (first entry)
XX
XX Transforming growth factor inhibitory peptide #5.
XX Hepatotropic; antagonist; transforming growth factor betal; TGF-b1;
XX competitive inhibition; collagen synthesis stimulation inhibitor; liver;
XX extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX Homo sapiens.
XX WO200031135-A1.
XX
PD 02-JUN-2000.
XX
PF 23-NOV-1999; 99WO-ES000375.
XX
PR 24-NOV-1998; 98ES-00002465.
XX
PA (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
XX Borrás Cuesta F;
XX Homo sapiens.
XX WO200031135-A1.
XX
PD 02-JUN-2000.
XX
PF 23-NOV-1999; 99WO-ES000375.
XX
PR 24-NOV-1998; 98ES-00002465.
XX
XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
XX Borrás Cuesta F;
XX WPI; 2000-411935/35.
XX Peptides that antagonize binding of transforming growth factor betal,
XX useful for treatment of liver disease, especially cirrhosis, are partial
XX sequences of the factor or its receptors.
XX Claim 6; Page 81; 86pp; Spanish.
XX
CC The invention relates to synthetic peptides that antagonise the binding
CC of transforming growth (TGF) factor betal (TGF-b1) to its receptor in
CC vivo which have partial amino acid sequences identical, or similar, with
CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
CC examples of the peptides of the invention. The peptides act by
CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
CC they are inhibitors of stimulation of collagen synthesis in liver cells
CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
CC expression systems) encoding the peptides are used for treatment of liver
CC disease, specifically cirrhosis
XX
SQ Sequence 9 AA;
  Query Match      100.0%; Score 48; DB 3; Length 9;
  Best Local Similarity 100.0%; Pred. No. 1.7e+06;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLMIWTMM 9
  |||||
Db 1 TSLMIWTMM 9

RESULT 3
AAY92949
ID AAY92949 standard; peptide; 9 AA.
XX
AC AAY92949;
XX
DT 08-NOV-2000 (first entry)
XX
XX Transforming growth factor inhibitory peptide #5.
XX Hepatotropic; antagonist; transforming growth factor betal; TGF-b1;
XX competitive inhibition; collagen synthesis stimulation inhibitor; liver;
XX extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX Homo sapiens.
XX WO200031135-A1.
XX
PD 02-JUN-2000.
XX
PF 23-NOV-1999; 99WO-ES000375.
XX
PR 24-NOV-1998; 98ES-00002465.
XX
XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
XX Borrás Cuesta F;
XX WPI; 2000-411935/35.
XX Peptides that antagonize binding of transforming growth factor betal,
XX useful for treatment of liver disease, especially cirrhosis, are partial
XX sequences of the factor or its receptors.
XX Claim 6; Page 81; 86pp; Spanish.
XX
CC The invention relates to synthetic peptides that antagonise the binding
CC of transforming growth (TGF) factor betal (TGF-b1) to its receptor in
CC vivo which have partial amino acid sequences identical, or similar, with
CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
CC examples of the peptides of the invention. The peptides act by
CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
CC they are inhibitors of stimulation of collagen synthesis in liver cells
CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
CC expression systems) encoding the peptides are used for treatment of liver
CC disease, specifically cirrhosis
XX
SQ Sequence 9 AA;
  Query Match      100.0%; Score 48; DB 3; Length 9;
  Best Local Similarity 100.0%; Pred. No. 1.7e+06;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLMIWTMM 9
  |||||
Db 1 TSLMIWTMM 9

RESULT 4
AAY93008
ID AAY93008 standard; peptide; 12 AA.
XX
AC AAY93008;
XX
DT 08-NOV-2000 (first entry)
XX
XX Transforming growth factor inhibitory peptide P54.
XX Hepatotropic; antagonist; transforming growth factor betal; TGF-b1;
XX competitive inhibition; collagen synthesis stimulation inhibitor; liver;
XX extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX

```

OS Rattus sp.
 XX WO200031135-A1.
 XX
 XX 02-JUN-2000.
 XX
 XX 23-NOV-1999; 99WO-ES000375.
 XX
 XX 24-NOV-1998; 98ES-00002465.
 XX
 XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
 XX
 XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
 PI Borras Cuesta F;
 XX WPI; 2000-411935/35.
 XX
 XX Peptides that antagonize binding of transforming growth factor betal,
 PT useful for treatment of liver disease, especially cirrhosis, are partial
 PT sequences of the factor or its receptors.
 XX
 XX Disclosure; Page 27; 86pp; Spanish.
 XX
 XX The invention relates to synthetic peptides that antagonise the binding
 CC of transforming growth (TGF) factor betal (TGF-b1) to its receptor in
 CC vivo which have partial amino acid sequences identical, or similar, with
 CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
 CC examples of the peptides of the invention. The peptides act by
 CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
 CC they are inhibitors of stimulation of collagen synthesis in liver cells
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
 CC expression systems) encoding the peptides are used for treatment of liver
 CC disease, specifically cirrhosis
 XX
 XX Sequence 12 AA;
 SQ

Query Match 76.0%; Score 36.5; DB 3; Length 12;
 Best Local Similarity 75.0%; Pred. No. 3.9;
 Matches 9; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
 QY 1 TSL---MIWTMM 9
 DB 1 TSLDATMIWTMM 12
 ||| |||||
 ||| |||||

RESULT 5
 AAY93094
 ID AAY93094 standard; peptide; 11 AA.
 XX
 XX AAY93094;
 AC
 XX 08-NOV-2000 (first entry)
 DT
 XX Transforming growth factor inhibitory peptide P140.
 DE
 XX Hepatotropic; antagonist; transforming growth factor betal; TGF-b1;
 KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
 KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
 XX
 XX Homo sapiens.
 OS
 XX WO200031135-A1.
 XX
 XX 02-JUN-2000.
 XX
 XX 23-NOV-1999; 99WO-ES000375.
 XX
 XX 24-NOV-1998; 98ES-00002465.
 XX
 XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
 XX
 XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
 PI

PI Borras Cuesta F;
 XX
 XX WPI; 2000-411935/35.
 XX
 XX Peptides that antagonize binding of transforming growth factor betal,
 PT useful for treatment of liver disease, especially cirrhosis, are partial
 PT sequences of the factor or its receptors.
 XX
 XX Disclosure; Page 31; 86pp; Spanish.
 XX
 XX The invention relates to synthetic peptides that antagonise the binding
 CC of transforming growth (TGF) factor betal (TGF-b1) to its receptor in
 CC vivo which have partial amino acid sequences identical, or similar, with
 CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
 CC examples of the peptides of the invention. The peptides act by
 CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
 CC they are inhibitors of stimulation of collagen synthesis in liver cells
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
 CC expression systems) encoding the peptides are used for treatment of liver
 CC disease, specifically cirrhosis
 XX
 XX Sequence 11 AA;
 SQ

Query Match 72.9%; Score 35; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.7;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 MIWTMM 9
 DB 6 MIWTMM 11
 |||||
 |||||

RESULT 6
 AAY93009
 ID AAY93009 standard; peptide; 12 AA.
 XX
 XX AAY93009;
 AC
 XX 08-NOV-2000 (first entry)
 DT
 XX Transforming growth factor inhibitory peptide P55.
 DE
 XX Hepatotropic; antagonist; transforming growth factor betal; TGF-b1;
 KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
 KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
 XX
 XX Rattus sp.
 OS
 XX WO200031135-A1.
 XX
 XX 02-JUN-2000.
 XX
 XX 23-NOV-1999; 99WO-ES000375.
 XX
 XX 24-NOV-1998; 98ES-00002465.
 XX
 XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
 XX
 XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
 PI Borras Cuesta F;
 XX WPI; 2000-411935/35.
 XX
 XX Peptides that antagonize binding of transforming growth factor betal,
 PT useful for treatment of liver disease, especially cirrhosis, are partial
 PT sequences of the factor or its receptors.
 XX
 XX Disclosure; Page 27; 86pp; Spanish.
 XX
 XX The invention relates to synthetic peptides that antagonise the binding
 CC of transforming growth (TGF) factor betal (TGF-b1) to its receptor in
 CC vivo which have partial amino acid sequences identical, or similar, with
 CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
 CC examples of the peptides of the invention. The peptides act by
 CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
 CC they are inhibitors of stimulation of collagen synthesis in liver cells
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
 CC expression systems) encoding the peptides are used for treatment of liver
 CC disease, specifically cirrhosis
 XX
 XX Sequence 11 AA;
 SQ

CC those of TGF- β 1 and/or its receptors. Peptides AAY92945-Y93133 represent
 CC examples of the peptides of the invention. The peptides act by
 CC competitive inhibition of the binding of TGF- β 1 to its receptors, e.g.
 CC they are inhibitors of stimulation of collagen synthesis in liver cells
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
 CC expression systems) encoding the peptides are used for treatment of liver
 CC disease, specifically cirrhosis
 XX
 SQ Sequence 12 AA;

Query Match 72.9%; Score 35; DB 3; Length 12;
 Best Local Similarity 100.0%; Pred. No. 7.3;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MIWTMM 9
 Db 6 MIWTMM 11
 |||||

RESULT 7
 AAY93010
 ID AAY93010 standard; peptide; 12 AA.

XX AAY93010;

XX 08-NOV-2000 (first entry)

XX Transforming growth factor inhibitory peptide P56.

XX Hepatotropic; antagonist; transforming growth factor β 1; TGF- β 1;
 KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
 KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.

XX Rattus sp.

XX WO200031135-A1.

XX 02-JUN-2000.

XX 23-NOV-1999; 99WO-ES000375.

XX 24-NOV-1998; 98ES-00002465.

XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.

XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
 PI Borras Cuesta F;

XX WPI; 2000-411935/35.

XX Peptides that antagonize binding of transforming growth factor β 1,
 PT useful for treatment of liver disease, especially cirrhosis, are partial
 PT sequences of the factor or its receptors.

XX Disclosure; Page 27; 86pp; Spanish.

XX The invention relates to synthetic peptides that antagonise the binding
 CC of transforming growth (TGF) factor β 1 (TGF- β 1) to its receptor in
 CC vivo which have partial amino acid sequences identical, or similar, with
 CC those of TGF- β 1 and/or its receptors. Peptides AAY92945-Y93133 represent
 CC examples of the peptides of the invention. The peptides act by
 CC competitive inhibition of the binding of TGF- β 1 to its receptors, e.g.
 CC they are inhibitors of stimulation of collagen synthesis in liver cells
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
 CC expression systems) encoding the peptides are used for treatment of liver
 CC disease, specifically cirrhosis

XX Sequence 12 AA;

Query Match 72.9%; Score 35; DB 3; Length 12;
 Best Local Similarity 100.0%; Pred. No. 7.3;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 MIWTMM 9
 Db 1 MIWTMM 6
 |||||

RESULT 8
 AAB89123
 ID AAB89123 standard; peptide; 18 AA.

XX AAB89123;

XX 23-MAY-2001 (first entry)

XX HIV gp120 protein binding peptide #216.

XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
 KW replication; CCR5; CXCR4; CD4; STRL33.

XX Homo sapiens.

XX WO200116182-A2.

XX 08-MAR-2001.

XX 25-AUG-2000; 2000WO-US023505.

XX 27-AUG-1999; 99US-0151270P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Saxinger C;

XX WPI; 2001-244398/25.

XX Novel polypeptides useful for treating HIV infection, have homology to
 PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
 PT and binds to HIV gp120 under physiological conditions.

XX Example 3; Page 43; 114pp; English.

XX The present invention describes a number of peptides which are able to
 CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
 CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
 CC useful in the treatment of HIV, as they prevent replication of the virus.
 CC The present sequence is an example of a peptide of the invention

XX Sequence 18 AA;

Query Match 64.6%; Score 31; DB 4; Length 18;
 Best Local Similarity 62.5%; Pred. No. 60;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 TSLMIWTM 8
 Db 3 TSLLIWVI 10
 |||||

RESULT 9
 AAB89121
 ID AAB89121 standard; peptide; 18 AA.

XX AAB89121;

XX 23-MAY-2001 (first entry)

XX HIV gp120 protein binding peptide #214.

XX Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
 KW replication; CCR5; CXCR4; CD4; STRL33.

XX Homo sapiens.

```

XX PN WO200116182-A2.
XX XX
XX PD 08-MAR-2001.
XX XX
XX PF 25-AUG-2000; 2000WO-US0233505.
XX XX
XX PR 27-AUG-1999; 99US-0151270P.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX XX
XX PI Saxinger C;
XX XX
XX DR WPI; 2001-244398/25.
XX XX
XX PT Novel polypeptides useful for treating HIV infection, have homology to
XX PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
XX PT and binds to HIV gp120 under physiological conditions.
XX PS
XX PS Example 3; Page 42; 114pp; English.
XX XX
XX CC The present invention describes a number of peptides which are able to
XX CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
XX CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
XX CC useful in the treatment of HIV, as they prevent replication of the virus.
XX CC The present sequence is an example of a peptide of the invention
XX XX
XX SQ Sequence 18 AA;
XX XX
XX Query Match 64.6%; Score 31; DB 4; Length 18;
XX XX Best Local Similarity 62.5%; Pred. No. 60;
XX XX Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
XX XX
XX QY 1 TSLMIWTM 8
XX DB |||:| :
XX 7 TSLLIWVI 14
XX
XX RESULT 11
XX ADK08459
XX ID ADK08459 standard; peptide; 9 AA.
XX XX
XX AC ADK08459;
XX XX
XX DT 06-MAY-2004 (first entry)
XX XX
XX DE Human papillomavirus peptide #514.
XX XX
XX KW pathogenic virus; alternative reading frame; antigenic determinant;
XX KW virucide; vaccine; therapeutic agent; infection; HPV.
XX OS Human papillomavirus.
XX XX
XX PN WO2004011650-A2.
XX XX
XX PD 05-FEB-2004.
XX XX
XX PF 24-JUL-2003; 2003WO-EP008112.
XX XX
XX PR 24-JUL-2002; 2002AT-00001124.
XX PR 11-JUL-2003; 2003EP-00450171.
XX XX
XX PA (INTB-) INTERCELL AG.
XX XX
XX PI Mattner F, Schmidt W, Habel A;
XX XX
XX DR WPI; 2004-169243/16.
XX XX
XX PT New polypeptide encoded by an alternative reading frame of a pathogenic
XX PT virus comprising an antigenic determinant, useful for treating or
XX PT preventing an infection with the pathogenic virus.
XX XX
XX PS Claim 18; Page 179; 220pp; English.
XX XX
XX CC This invention relates to a novel polypeptide encoded by an alternative
XX CC reading frame of a pathogenic virus, where the polypeptide starts with a
XX CC methionine amino acid residue, which comprises an antigenic determinant
XX CC and more than 7 amino acid residues. The invention may be useful for the
XX CC production of compounds with a virucide activity or the development of a
XX CC vaccine. The polypeptide or its fragments may be useful as a therapeutic
XX CC agent. It is also useful for the manufacture of a medicament for treating
XX CC or preventing an infection with the pathogenic virus. The present
XX CC sequence is that of a human papillomavirus (HPV) epitope peptide of the
XX CC invention.
XX XX
XX SQ Sequence 9 AA;
XX XX
XX Query Match 58.3%; Score 28; DB 8; Length 9;
XX XX Best Local Similarity 37.5%; Pred. No. 1.7e+06;
XX XX Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
XX XX
XX QY 2 SLMIWTM 9
XX DB |||:| :
XX 2 ALVLTLL 9
XX
XX RESULT 10
XX AAB89122
XX ID AAB89122 standard; peptide; 18 AA.
XX XX
XX AC AAB89122;
XX XX
XX DT 23-MAY-2001 (first entry)
XX XX
XX DE HIV gp120 protein binding peptide #215.
XX XX
XX KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX KW replication; CCR5; CXCR4; CD4; STRL33.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO200116182-A2.
XX XX
XX PD 08-MAR-2001.
XX XX
XX PF 25-AUG-2000; 2000WO-US0233505.
XX XX
XX PR 27-AUG-1999; 99US-0151270P.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX XX
XX PI Saxinger C;
XX XX
XX DR WPI; 2001-244398/25.
XX XX
XX PT Novel polypeptides useful for treating HIV infection, have homology to
XX PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
XX PT and binds to HIV gp120 under physiological conditions.
XX PS
XX PS Example 3; Page 42; 114pp; English.
XX XX

```

RESULT 12
ADK08095
ID ADK08095 standard; peptide; 9 AA.
XX
AC ADK08095;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human papillomavirus peptide #150.
XX
KW pathogenic virus; alternative reading frame; antigenic determinant;
KW virucide; vaccine; therapeutic agent; infection; HPV.
OS
OS Human papillomavirus.
XX
XX WO2004011650-A2.
XX
PD 05-FEB-2004.
XX
XX 24-JUL-2003; 2003WO-EP008112.
XX
PR 24-JUL-2002; 2002AT-00001124.
PR 11-JUL-2003; 2003EP-00450171.
XX
PA (INTE-) INTERCELL AG.
XX
PI Mattner F, Schmidt W, Habel A;
XX
XX WPI; 2004-169243/16.
XX
XX New polypeptide encoded by an alternative reading frame of a pathogenic
PT virus comprising an antigenic determinant, useful for treating or
PT preventing an infection with the pathogenic virus.
XX
PS Claim 18; Page 175; 220pp; English.
XX
XX This invention relates to a novel polypeptide encoded by an alternative
CC reading frame of a pathogenic virus, where the polypeptide starts with a
CC methionine amino acid residue, which comprises an antigenic determinant
CC and more than 7 amino acid residues. The invention may be useful for the
CC production of compounds with a virucide activity or the development of a
CC vaccine. The polypeptide or its fragments may be useful as a therapeutic
CC agent. It is also useful for the manufacture of a medicament for treating
CC or preventing an infection with the pathogenic virus. The present
CC sequence is that of a human papillomavirus (HPV) epitope peptide of the
CC invention.
XX
SQ Sequence 9 AA;
Query Match 58.3%; Score 28; DB 8; Length 9;
Best Local Similarity 37.5%; Pred. NO. 1.7e+06;
Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 2 SLMIWTMM 9
DB :||:|:|:
2 ALVLWTLL 9
RESULT 13
ADG94446
ID ADG94446 standard; peptide; 10 AA.
XX
AC ADG94446;
XX
XX 25-MAR-2004 (first entry)
DT
DE Human JAM-1 permeabilising peptide SEQ ID NO:425.
XX
XX human; permeabilising; interferon-beta; IFN-beta; mucosal delivery;
KW immunosuppressive; virucide; autoimmune disease; viral disease;
KW multiple sclerosis; chronic hepatitis B; condyloma acuminata;
KW

KW papilloma virus; childhood viral encephalitis; wart.
XX
OS Homo sapiens.
XX
PN WO2004002404-A2.
XX
PD 08-JAN-2004.
XX
PF 18-JUN-2003; 2003WO-US019261.
XX
PR 28-JUN-2002; 2002US-0393066P.
XX
PA (NAST-) NASTECH PHARM CO INC.
XX
PI Quay SC, Gupta M, De Meireles JC, Abd El- Shafy M;
XX
XX WPI; 2004-122360/12.
XX
PT Stable pharmaceutical composition comprising interferon compound(s)
PT formulated for mucosal delivery to mammalian subjects in combination with
PT mucosal delivery-enhancing agent(s).
XX
PS Disclosure; SEQ ID NO 425; 353pp; English.
XX
XX The invention relates to a novel stable pharmaceutical composition
CC comprising one or more interferon (IFN) beta compound(s) formulated for
CC mucosal delivery to a mammalian subject in combination with one or more
CC mucosal delivery-enhancing agent(s), where the composition following
CC mucosal administration to the subject yields enhanced mucosal delivery of
CC the one or more IFN-beta compound(s). A composition of the invention has
CC immunosuppressive and virucide activity. The composition is useful for
CC treating autoimmune diseases, viral disease, for alleviating one or more
CC symptom(s) of multiple sclerosis (MS), chronic hepatitis B, condyloma
CC acuminata, papilloma virus warts of the larynx or skin or childhood viral
CC encephalitis in the subject without unacceptable adverse side effects.
CC The composition can be delivered intranasally which reduces or eliminates
CC compliance problems and side effects that attend delivery by injection.
CC The sequences shown in ADG94022-ADG94810 represent permeabilising
CC peptides used in a composition of the invention.
XX
SQ Sequence 10 AA;
Query Match 58.3%; Score 28; DB 8; Length 10;
Best Local Similarity 62.5%; Pred. NO. 1.1e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 TSLMIWTM 8
DB |||||:
3 TSLKIWNV 10
RESULT 14
ADI46844
ID ADI46844 standard; peptide; 10 AA.
XX
AC ADI46844;
XX
XX 06-MAY-2004 (first entry)
DT
XX
DE Permeabilising peptide of human JAM-2 SeqID553.
XX
KW mucosal delivery; permeabilising peptide;
KW mucosal epithelial paracellular transport; epithelial junction;
KW epithelial membrane adhesive protein; junctional adhesion molecule; JAM;
KW occludin; claudin; sexual dysfunction; male erectile sexual dysfunction;
KW female sexual dysfunction; human.
XX
OS Homo sapiens.
XX
PN WO2004003145-A2.
XX
PD 08-JAN-2004.
XX

PF 24-JUN-2003; 2003WO-US019994.
 XX
 PR
 XX 28-JUN-2002; 2002US-0392512P.
 XX
 PA (NAST-) NASTECH PHARM CO INC.
 XX
 XX
 PI Quay SC;
 XX
 DR WPI; 2004-091087/09.
 XX
 XX
 PT Composition comprising biologically active agent and permeabilizing
 PT peptide that reversibly enhances mucosal epithelial paracellular
 PT transport by modulating epithelial junctional structure and/or physiology
 PT in mammal.
 XX
 XX Disclosure; SEQ ID NO 553; 426pp; English.
 XX
 CC This invention relates to a novel composition comprising a biologically
 CC active agent and mucosal delivery-enhancing effective amount of
 CC permeabilizing peptide that reversibly enhances mucosal epithelial
 CC paracellular transport by modulating epithelial junctional structure
 CC and/or physiology in a mammal. The agent of the invention inhibits
 CC homotypic binding of epithelial membrane adhesive protein chosen
 CC junctional adhesion molecule (JAM), occludin and claudin. The
 CC biologically active agent is effective for treatment of sexual
 CC dysfunction, for example male erectile sexual dysfunction or female
 CC sexual dysfunction. The present sequence is that of a permeabilizing
 CC peptide of human JAM-2 which may be used during the production of the
 CC composition of the invention.
 XX
 SQ Sequence 10 AA;
 Query Match 58.3%; Score 28; DB 8; Length 10;
 Best Local Similarity 62.5%; Pred. No. 1.1e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 TSLMIWTM 8
 ||| || :
 Db 3 TSLKIWNV 10

RESULT 15
 ADP87021
 ID ADP87021 standard; peptide; 10 AA.
 XX
 AC ADP87021;
 XX
 DT 09-SEP-2004 (first entry)
 XX
 XX Junctional adhesion molecule 2 (JAM-2) peptide seqid 426.
 DE
 DE anorectic; cytostatic; eating disorder; neuroprotective; nootropic;
 KW cachexia; intranasal composition; peptide YY; obesity; cancer;
 KW malnutrition; wasting; Alzheimer's disease; colon adenocarcinoma;
 KW pancreatic adenocarcinoma; breast carcinoma; cachexia; cancer cachexia;
 KW junctional adhesion molecule 2; JAM-2; epithelial junction; human.
 XX
 OS Homo sapiens.
 XX
 XX US2004115135-A1.
 PN
 XX 17-JUN-2004.
 XX
 XX 17-DEC-2002; 2002US-00322266.
 PF
 XX 17-DEC-2002; 2002US-00322266.
 PR
 XX (QUAY/) QUAY S C.
 PA
 XX Quay SC;
 PI
 XX WPI; 2004-478989/45.
 DR
 XX

PT Intranasal compositions for treating obesity, cancer, or malnutrition or
 PT wasting related to cancer, comprises peptide compound(s) formulated for
 PT mucosal delivery to mammalian subject.
 XX
 XX Disclosure; SEQ ID NO 426; 86pp; English.
 XX
 CC The invention describes an intranasal composition comprising peptide YY
 CC compound(s) formulated for mucosal delivery to a mammalian subject. Also
 CC described is a kit for treatment of a mammalian subject comprising the
 CC intranasal composition of peptide compound(s). The composition is used
 CC for treating obesity, cancer, or malnutrition or wasting related to
 CC cancer in the subject. It is used to alleviate Alzheimer's disease, colon
 CC adenocarcinoma, pancreatic adenocarcinoma, breast carcinoma, treatment
 CC and prevention of malnutrition resulting from iatrogenic causes or
 CC cachexia associated with advanced disease, or cancer cachexia in the
 CC subject. The composition alleviates the symptoms without unacceptable
 CC adverse side effects. This is the amino acid sequence of a human
 CC junctional adhesion molecule 2 (JAM-2) that may be used in a composition
 CC of the invention to modulate epithelial junction structure and/or
 CC physiology.
 XX
 SQ Sequence 10 AA;
 Query Match 58.3%; Score 28; DB 8; Length 10;
 Best Local Similarity 62.5%; Pred. No. 1.1e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 TSLMIWTM 8
 ||| || :
 Db 3 TSLKIWNV 10

Search completed: November 14, 2004, 12:02:11
 Job time : 28.0426 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2004, 12:03:21 ; Search time 21.2553 Seconds
(without alignments)
149.815 Million cell updates/sec

Title: US-09-831-253F-5

Perfect score: 48

Sequence: 1 TSLMIWTMM 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1568699 seqs, 353819137 residues

Total number of hits satisfying chosen parameters: 294451

Minimum DB seq length: 0

Maximum DB seq length: 23

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	64.6	18	14 US-10-084-813-236	Sequence 236, App
2	31	64.6	18	14 US-10-084-813-237	Sequence 237, App
3	31	64.6	18	14 US-10-084-813-238	Sequence 238, App
4	28	58.3	10	15 US-10-462-452-425	Sequence 425, App
5	28	58.3	10	15 US-10-601-953-553	Sequence 553, App
6	28	58.3	10	16 US-10-322-266-426	Sequence 426, App
7	28	58.3	11	10 US-09-809-391-551	Sequence 551, App
8	28	58.3	11	10 US-09-882-171-551	Sequence 551, App
9	28	58.3	11	14 US-10-164-861-551	Sequence 551, App
10	28	58.3	20	10 US-09-939-769-2	Sequence 2, Appl
11	28	58.3	21	9 US-09-864-761-45075	Sequence 45075, A
12	27	56.2	20	9 US-09-864-761-33702	Sequence 33702, A
13	27	56.2	21	10 US-09-903-190-20	Sequence 20, Appl

14	27	56.2	21	14	US-10-319-763-20	Sequence 20, Appl
15	27	56.2	23	9	US-09-864-761-45706	Sequence 45706, A
16	26	54.2	9	9	US-09-796-744-10	Sequence 10, Appl
17	26	54.2	9	14	US-10-231-452-7	Sequence 7, Appl
18	26	54.2	13	10	US-09-953-354-126	Sequence 126, Appl
19	26	54.2	13	10	US-10-092-750-17	Sequence 17, Appl
20	26	54.2	23	9	US-09-864-761-36057	Sequence 36057, A
21	25	52.1	8	8	US-08-979-847-170	Sequence 170, App
22	25	52.1	8	14	US-10-114-104-170	Sequence 170, App
23	25	52.1	9	15	US-10-182-252A-632	Sequence 632, App
24	25	52.1	9	15	US-10-182-252A-657	Sequence 657, App
25	25	52.1	10	14	US-10-200-708-79	Sequence 79, Appl
26	25	52.1	10	14	US-10-200-708-501	Sequence 501, Appl
27	25	52.1	10	15	US-10-430-685-173	Sequence 173, Appl
28	25	52.1	12	9	US-09-840-277-69	Sequence 69, Appl
29	25	52.1	12	15	US-10-609-217-151	Sequence 151, App
30	25	52.1	12	15	US-10-632-388-151	Sequence 151, App
31	25	52.1	12	15	US-10-651-723-151	Sequence 151, App
32	25	52.1	12	15	US-10-645-761-151	Sequence 151, App
33	25	52.1	12	15	US-10-666-696-151	Sequence 151, App
34	25	52.1	12	15	US-10-653-048-151	Sequence 151, App
35	25	52.1	12	16	US-10-692-151-21	Sequence 21, Appl
36	25	52.1	14	9	US-09-995-494-86	Sequence 86, Appl
37	25	52.1	16	9	US-09-949-713-25	Sequence 25, Appl
38	25	52.1	16	15	US-10-449-831A-39	Sequence 39, Appl
39	25	52.1	18	14	US-10-144-929-202	Sequence 202, App
40	25	52.1	18	15	US-10-144-929-202	Sequence 202, App
41	25	52.1	20	14	US-10-280-066-332	Sequence 332, App
42	25	52.1	20	14	US-10-029-386-30555	Sequence 30555, A
43	25	52.1	22	10	US-09-974-879-593	Sequence 593, App
44	25	52.1	22	10	US-09-305-736-594	Sequence 594, App
45	25	52.1	22	10	US-09-933-767-896	Sequence 896, App

ALIGNMENTS

RESULT 1

US-10-084-813-236
; Sequence 236, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 236
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-236

Query Match 64.6%; Score 31; DB 14; Length 18;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 TSLMIWTM 8

DB 11 TSLLIWVI 18

RESULT 2

US-10-084-813-237

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; Sequence 237, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 237
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-237

Query Match      64.6%; Score 31; DB 14; Length 18;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 TSLMIWTM 8
DB 7 TSLLIWVI 14

RESULT 3
US-10-084-813-238
; Sequence 238, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 238
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-238

Query Match      64.6%; Score 31; DB 14; Length 18;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 TSLMIWTM 8
DB 3 TSLLIWVI 10

RESULT 4
US-10-462-452-425
; Sequence 425, Application US/10462452
; Publication No. US20040037809A1
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven
; APPLICANT: El Shafy, Mohammed Abd

```

```

; APPLICANT: Gupta, Malini
; APPLICANT: de Meireles, Jorge
; TITLE OF INVENTION: Compositions and Methods for Enhanced
; TITLE OF INVENTION: Mucosal-Delivery of Interferon Beta
; FILE REFERENCE: 02-02US
; CURRENT APPLICATION NUMBER: US/10/462,452
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/393,066
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 790
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 425
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-462-452-425

Query Match      58.3%; Score 28; DB 15; Length 10;
Best Local Similarity 62.5%; Pred. No. 2.2e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TSLMIWTM 8
DB 3 TSLKIWNV 10

RESULT 5
US-10-601-953-553
; Sequence 553, Application US/10601953
; Publication No. US20040077540A1
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven C.
; TITLE OF INVENTION: Compositions and Methods For Modulating Physiology Of Epithelial
; TITLE OF INVENTION: Junctional Adhesion Molecules For Enhanced Mucosal Delivery Of
; FILE REFERENCE: 02-03US
; CURRENT APPLICATION NUMBER: US/10/601,953
; CURRENT FILING DATE: 2003-06-24
; PRIOR APPLICATION NUMBER: 60/392,512
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 900
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 553
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-601-953-553

Query Match      58.3%; Score 28; DB 15; Length 10;
Best Local Similarity 62.5%; Pred. No. 2.2e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TSLMIWTM 8
DB 3 TSLKIWNV 10

RESULT 6
US-10-322-266-426
; Sequence 426, Application US/10322266
; Publication No. US20040115135A1
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven C.
; TITLE OF INVENTION: Compositions And Methods For Enhanced Mucosal Delivery Of Peptid
; FILE REFERENCE: NPCI0567
; CURRENT APPLICATION NUMBER: US/10/322,266
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 797
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 426

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; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-322-266-426

Query Match      58.3%; Score 28; DB 16; Length 10;
Best Local Similarity 62.5%; Pred. No. 2.2e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 TSLMIWTM 8
      ||||| :
Db       3 TSLKIMNV 10

RESULT 7
US-09-809-391-551
; Sequence 551, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 551
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (9)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (11)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-809-391-551

Query Match      58.3%; Score 28; DB 10; Length 11;
Best Local Similarity 42.9%; Pred. No. 2.4e+02;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      3 LMIWTMM 9
      |::||::
Db       1 LLLWTLL 7

RESULT 8
US-09-882-171-551
; Sequence 551, Application US/09882171
; Publication No. US20030175859A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/882,171
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/043,672
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; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,315
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/048,974
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/056,886
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,877
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,889
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,893
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,630
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,878
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,662
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; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,879
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,880
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,894
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,911
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,636
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,874
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,910
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,864
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,631
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,845
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,892
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/057,761
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/047,595
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,599
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,588
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,585
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,586
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,590
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,594
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,589
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,593
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,614
; PRIOR FILING DATE: 1997-05-23

; PRIOR APPLICATION NUMBER: 60/043,578
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,576
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/047,501
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,670
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/056,632
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,664
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,876
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,881
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,909
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,875
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,862
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,887
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,908
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/048,964
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/057,650
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/056,884
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/057,669
; PRIOR FILING DATE: 1997-09-05

Query Match 58.3%; Score 28; DB 10; Length 11;
Best Local Similarity 42.9%; Pred No. 2.4e+02;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 LMIWTMM 9
Db 1 LLLWTL 7

RESULT 9

US-10-164-861-551
; Sequence 551, Application US/10164861
; Publication No. US20030225248A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/10/164,861
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US/09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 757
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 551
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (9)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (11)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-164-861-551

Query Match 58.3%; Score 28; DB 14; Length 11;
 Best Local Similarity 42.9%; Pred. No. 2.4e+02;
 Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 LMIWTMM 9
 DB 1 LLLWTL 7

RESULT 10

US-09-939-769-2
 ; Sequence 2, Application US/09939769
 ; Publication No. US20030017149A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HOEFFLER, MARIJANE
 ; APPLICANT: RUSSELL, MARIJANE
 ; TITLE OF INVENTION: SINGLE CHAIN ANTIBODY FUSION REAGENTS THAT REGULATE
 ; TITLE OF INVENTION: TRANSCRIPTION IN VIVO
 ; FILE REFERENCE: 039322/0226
 ; CURRENT APPLICATION NUMBER: US/09/939,769
 ; CURRENT FILING DATE: 2001-08-28
 ; PRIOR APPLICATION NUMBER: 08/728,890
 ; PRIOR FILING DATE: 1996-10-10
 ; NUMBER OF SEQ ID NOS: 96
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: illustrative
 ; OTHER INFORMATION: mitochondrial target signal
 US-09-939-769-2

Query Match 58.3%; Score 28; DB 10; Length 20;
 Best Local Similarity 33.3%; Pred. No. 4.3e+02;
 Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 TSLMIWTMM 9
 DB 3 TDLWLWLL 11

RESULT 11

US-09-864-761-45075
 ; Sequence 45075, Application US/09864761
 ; Patent No. US20020048763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharron G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ; APPLICANT: Chen, Wensheng
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 ; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
 ; FILE REFERENCE: Aecmica-X-1
 ; CURRENT APPLICATION NUMBER: US/09/864,761
 ; CURRENT FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: US 60/180,312
 ; PRIOR FILING DATE: 2000-02-04
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 09/632,366
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: GB 24263.6
 ; PRIOR FILING DATE: 2000-10-04
 ; PRIOR APPLICATION NUMBER: US 60/236,359
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00663
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00662
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00661
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00670
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: US 60/234,687
 ; PRIOR FILING DATE: 2000-09-21
 ; PRIOR APPLICATION NUMBER: US 09/608,408
 ; PRIOR FILING DATE: 2000-06-30
 ; PRIOR APPLICATION NUMBER: US 09/774,203
 ; PRIOR FILING DATE: 2001-01-29
 ; NUMBER OF SEQ ID NOS: 49117
 ; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
 ; SEQ ID NO 45075
 ; LENGTH: 21
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: MAP TO AC013751.3
 ; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.47
 ; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.53
 ; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.47
 ; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.46
 ; OTHER INFORMATION: EST_HUMAN HIT: AW026680.1, EVALUATE 9.00e-06
 US-09-864-761-45075

Query Match 58.3%; Score 28; DB 9; Length 21;
 Best Local Similarity 75.0%; Pred. No. 4.5e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 SLMITMM 9
 DB 2 SVMITMM 9

RESULT 12

US-09-864-761-33702
 ; Sequence 33702, Application US/09864761
 ; Patent No. US20020048763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharron G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ; APPLICANT: Chen, Wensheng
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 ; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
 ; FILE REFERENCE: Aecmica-X-1
 ; CURRENT APPLICATION NUMBER: US/09/864,761
 ; CURRENT FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: US 60/180,312
 ; PRIOR FILING DATE: 2000-02-04
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 09/632,366
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: GB 24263.6
 ; PRIOR FILING DATE: 2000-10-04
 ; PRIOR APPLICATION NUMBER: US 60/236,359
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667
 ; PRIOR FILING DATE: 2001-01-30

;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00662
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00661
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 33702
;; LENGTH: 20
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AC007683.2
;; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.77
;; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.92
;; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.89
;; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 0.74
;; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3
;; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.89
;; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
;; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.7
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
;; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.1
US-09-864-761-33702

Query Match 56.2%; Score 27; DB 9; Length 20;
Best Local Similarity 57.1%; Pred. No. 6.3e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 TSLMIWT 7
:::||||
Db 8 TTMWT 14

RESULT 13
US-09-903-190-20
;; Sequence 20, Application US/09903190
;; Publication No. US20030162176A1
;; GENERAL INFORMATION:
;; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
;; APPLICANT: Duclert, Aymeric
;; APPLICANT: Bougueleret, Lydie
;; TITLE OF INVENTION: Complementary DNAs
;; FILE REFERENCE: GENSET 021A
;; CURRENT APPLICATION NUMBER: US/09/903,190
;; CURRENT FILING DATE: 2001-07-11
;; PRIOR APPLICATION NUMBER: US/09/247,155A
;; PRIOR FILING DATE: 1999-02-09
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/074,121
;; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/081,563
;; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-13
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/096,116
;; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-10
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/099,273
;; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-04

;; NUMBER OF SEQ ID NOS: 182
;; SOFTWARE: Patent.pm
;; SEQ ID NO 20
;; LENGTH: 21
;; TYPE: PRT
;; ORGANISM: Homo Sapiens
;; FEATURE:
;; NAME/KEY: SIGNAL
;; LOCATION: 1..21
;; OTHER INFORMATION: Von Heijne matrix
;; OTHER INFORMATION: score 5.5
;; OTHER INFORMATION: seq SFLPSALVIWTS/AF
US-09-903-190-20

Query Match 56.2%; Score 27; DB 10; Length 21;
Best Local Similarity 57.1%; Pred. No. 6.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLMIWT 7
:::||||
Db 13 SALVIWT 19

RESULT 14
US-10-319-763-20
;; Sequence 20, Application US/10319763
;; Publication No. US2003014490A1
;; GENERAL INFORMATION:
;; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
;; APPLICANT: Bougueleret, Lydie
;; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
;; FILE REFERENCE: G-031.US04.DIV
;; CURRENT APPLICATION NUMBER: US/10/319,763
;; CURRENT FILING DATE: 2002-12-10
;; PRIOR APPLICATION NUMBER: 60/066,677
;; PRIOR FILING DATE: 1997-11-13
;; PRIOR APPLICATION NUMBER: 60/069,957
;; PRIOR FILING DATE: 1997-12-17
;; PRIOR APPLICATION NUMBER: 60/074,121
;; PRIOR FILING DATE: 1998-02-09
;; PRIOR APPLICATION NUMBER: 60/081,563
;; PRIOR FILING DATE: 1998-04-13
;; PRIOR APPLICATION NUMBER: 60/096,116
;; PRIOR FILING DATE: 1998-08-10
;; PRIOR APPLICATION NUMBER: 60/099,273
;; PRIOR FILING DATE: 1998-09-04
;; NUMBER OF SEQ ID NOS: 229
;; SOFTWARE: Patent.pm
;; SEQ ID NO 20
;; LENGTH: 21
;; TYPE: PRT
;; ORGANISM: Homo Sapiens
;; FEATURE:
;; NAME/KEY: SIGNAL
;; LOCATION: 1..21
;; OTHER INFORMATION: Von Heijne matrix
;; OTHER INFORMATION: score 5.5
;; OTHER INFORMATION: seq SFLPSALVIWTS/AF
US-10-319-763-20

Query Match 56.2%; Score 27; DB 14; Length 21;
Best Local Similarity 57.1%; Pred. No. 6.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLMIWT 7
:::||||
Db 13 SALVIWT 19

RESULT 15
US-09-864-761-45706
;; Sequence 45706, Application US/09864761

Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,697
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
SEQ ID NO 45706
LENGTH: 23
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC025539.2
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.63
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.6
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.5
US-09-864-761-45706

Query Match 56.2%; Score 27; DB 9; Length 23;
Best Local Similarity 55.6%; Pred. No. 7.2e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 1 TSLMIWTMM 9
Db 10 TRLEIWNMI 18

Search completed: November 14, 2004, 12:26:59
Job time : 21.2553 secs

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OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:26 ; Search time 24.0319 Seconds
(without alignments)
215.479 Million cell updates/sec

Title: US-09-831-253F-5
Perfect score: 48
Sequence: 1 TSLMIWTMM 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 17482

Minimum DB seq length: 0
Maximum DB seq length: 23

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_02:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	54.2	21	Q95N72	Q95N72 equus caball
2	25	52.1	11	Q9UELO	Q9ue10 homo sapien
3	25	52.1	17	O6LXL9	O6ldl9 rattus norv
4	25	52.1	17	AA41680	AA41680 rattus no
5	24	50.0	17	O6LEA8	O6lea8 xenopus lae
6	24	50.0	17	AAA49911	AAA49911 xenopus l.
7	24	50.0	19	O8W128	O8w128 scaevola pr
8	23	47.9	15	O8R5G1	O8r5g1 spermophilu
9	23	47.9	17	O8IVK5	O8ivk5 homo sapien
10	21	43.8	10	Q9ESU5	Q9eus5 mus musculu
11	21	43.8	17	Q7S3Q9	Q7s3q9 neurospora
12	21	43.8	17	O69074	O69074 human herpe
13	21	43.8	19	DCAM ACACA	P34039 acanthamoeb
14	21	43.8	21	O6LER5	O6ler5 homo sapien
15	21	43.8	21	BAA00902	Baa00902 homo sapi
16	21	43.8	22	O38287	O38287 lactococcus
17	21	43.8	22	O33R63	Q33r63 yersinia pe
18	21	43.8	23	O9NZ61	O9nz61 homo sapien
19	20	41.7	10	LABA JATMU	P13270 jatropha mu
20	20	41.7	12	O8SHF6	O8shf6 chamaeleo m
21	20	41.7	10	O6WRB2	O6wrb2 eudromia el
22	20	41.7	12	AAQ23391	AAq23391 eudromia
23	20	41.7	14	Q9NFK8	Q9nfk8 drugia paha
24	20	41.7	17	O6QLL7	O6ql17 influenza a
25	20	41.7	17	O6QLL9	O6ql19 influenza a
26	20	41.7	17	O6QLM0	O6qlm0 influenza a
27	20	41.7	17	O6QLM1	O6qlm1 influenza a
28	20	41.7	17	AAS57878	Aas57878 influenza
29	20	41.7	17	AAS57879	Aas57879 influenza
30	20	41.7	17	AAS57880	Aas57880 influenza
31	20	41.7	17	AAS57882	Aas57882 influenza

32	20	41.7	18	2	Q9ZYV8	Q9zyv8 aspilota sp
33	20	41.7	18	2	Q9ZYX7	Q9zyx7 periga conde
34	20	41.7	19	2	O6QLM2	O6qlm2 influenza a
35	20	41.7	19	2	AAS57877	Aas57877 influenza
36	20	41.7	20	2	P92689	P92689 podospora a
37	20	41.7	20	2	Q93TW0	Q93tw0 neisseria m
38	20	41.7	21	2	Q9R4X8	Q9r4x8 myxococcus
39	20	41.7	22	2	O19454	O19454 mus musculu
40	20	41.7	22	2	O25012	O25012 helicobacte
41	20	41.7	23	2	Q9NZ62	Q9nz62 homo sapien
42	19	39.6	8	2	O85406	O85406 coxiella bu
43	19	39.6	9	2	O8NHL3	O8nhl3 homo sapien
44	19	39.6	10	2	Q7RPE0	Q7rpe0 plasmodium
45	19	39.6	11	2	O77896	O77896 oreochromis

ALIGNMENTS

RESULT 1

Q95N72 PRELIMINARY; PRT; 21 AA.
AC Q95N72;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE NRAMP1 (Fragment).
GN Name=NRAMP1;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Matiasovic J., Horin P.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF354453; AAK43589.1; -.
FT NON TER 1 1
FT NON TER 21 21
SQ SEQUENCE 21 AA; 2259 MW; A064CFFD5F9A71E4 CRC64;

Query Match 54.2%; Score 26; DB 2; Length 21;
Best Local Similarity 42.9%; Pred. No. 8.1e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TSLMIWT 7
Db 7 TTYLVWT 13
| : : : |
| : : : |

RESULT 2

Q9UELO PRELIMINARY; PRT; 11 AA.
AC Q9UELO;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Fas antigen (CD95 antigen) (Fragment).
GN Name=CD95;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=95355401; PubMed=7543095;
RA Wada N., Matsumura M., Ohba Y., Kobayashi N., Takizawa T.,
RA Nakanishi Y.;
RT "Transcription Stimulation of the Fas-encoding gene by nuclear factor
for interleukin-6 expression upon influenza virus infection.";
RL J. Biol. Chem. 270:18007-18012(1995).
RN [2]

RP SEQUENCE FROM N.A.
RA Muschen M., Re D., Brauning A., Wolf J., Hansmann M.L., Diehl V.,
RA Kuppers R., Rajewsky K.; to the EMBL/GenBank/DBJ databases.
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Muschen M., Re D., Jungnickel B., Diehl V., Rajewsky K., Kuppers R.;
RA Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22404279; PubMed=12516573;
RA Kurth J., Pernio A., Schmitz R., Iking-Konert C., Chiorazzi N.,
RA Thompson K.M., Winkler T., Rajewsky K., Kuppers R.;
RT "Lack of deleterious somatic mutations in the CD95 gene of
RT plasmablasts from systemic lupus erythematosus patients and
RT autointerferon-producing cell lines.";
RL Eur. J. Immunol. 32:3785-3792(2002).
DR EMBL; D31968; BAA20850.1; -;
DR EMBL; AJ279011; CAC35539.1; -;
DR EMBL; AJ279012; CAC35540.1; -;
DR EMBL; AJ279013; CAC35541.1; -;
DR EMBL; AJ509179; CAD48929.1; -;
DR EMBL; AJ509180; CAD48930.1; -;
FT NON_TER 11
SQ SEQUENCE 11 AA; 1256 MW; 0802145E2731B370 CRC64;

Query Match 52.1%; Score 25; DB 2; Length 11;
Best Local Similarity 57.1%; Pred. No. 6.7e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 LMIWTM 9
| : : : :
Db 2 LGIWTLL 8

RESULT 3
Q6LDL9 PRELIMINARY; PRT; 17 AA.
ID Q6LDL9 PRELIMINARY; PRT; 17 AA.
AC Q6LDL9;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Neural cell adhesion molecule (Fragment).
GN Name=NCAM-C;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=90287121; PubMed=1694009;
RA Chen A., Reyes A., Akesson R.A.;
RT "Transcription initiation sites and structural organization of the
RT extreme 5' region of the rat neural cell adhesion molecule gene.";
RL Mol. Cell. Biol. 10:3314-3324(1990).
DR EMBL; M32612; AAA41680.1; -;
FT NON_TER 1
SQ SEQUENCE 17 AA; 2026 MW; AEA1EB5F252E84F5 CRC64;

Query Match 52.1%; Score 25; DB 2; Length 17;
Best Local Similarity 50.0%; Pred. No. 1e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 TSLMIWTM 8
| : : : :
Db 4 TKDLIWTLL 11

RESULT 4
AAA41680 PRELIMINARY; PRT; 17 AA.
ID AAA41680
AC AAA41680;

DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE Neural cell adhesion molecule (Fragment).
GN NCAM-C.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=90287121; PubMed=1694009;
RA Chen A., Reyes A., Akesson R.A.;
RT "Transcription initiation sites and structural organization of the
RT extreme 5' region of the rat neural cell adhesion molecule gene.";
RL Mol. Cell. Biol. 10:3314-3324(1990).
DR EMBL; M32612; AAA41680.1; -;
FT NON_TER 17
SQ SEQUENCE 17 AA; 2026 MW; AEA1EB5F252E84F5 CRC64;

Query Match 52.1%; Score 25; DB 2; Length 17;
Best Local Similarity 50.0%; Pred. No. 1e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 TSLMIWTM 8
| : : : :
Db 4 TKDLIWTLL 11

RESULT 5
Q6LEA8 PRELIMINARY; PRT; 17 AA.
ID Q6LEA8 PRELIMINARY; PRT; 17 AA.
AC Q6LEA8;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Neural cell adhesion molecule (Fragment).
GN Name=NCAM;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Johnson A.D., Ovsenek N., Tonissen K.F., Krieg P.A.;
RL Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; L26396; AAA49911.1; -;
FT NON_TER 17
SQ SEQUENCE 17 AA; 2005 MW; AEBD9B5855262107 CRC64;

Query Match 50.0%; Score 24; DB 2; Length 17;
Best Local Similarity 60.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 MIWTM 8
| : : : :
Db 7 LIWTLL 11

RESULT 6
AAA49911 PRELIMINARY; PRT; 17 AA.
ID AAA49911 PRELIMINARY; PRT; 17 AA.
AC AAA49911;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE Neural cell adhesion molecule (Fragment).
GN NCAM.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;

OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX PubMed=14583598;
 RA Johnson A.D., Ovsenek N., Tonissen K.F., Krieg P.A.;
 RT "The Xenopus NCM promoter: Appropriate expression in response to
 RT neural inducing signals and identification of a conserved sequence
 RT element.";
 RL Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.
 DR EMBL; L26396; AAA49911.1; --
 FT NON_TER 17 17
 SQ SEQUENCE 17 AA; 2005 MW; AEBD9B5855262107 CRC64;
 Query Match 50.0%; Score 24; DB 2; Length 17;
 Best Local Similarity 60.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 4 MIWTM 8
 Db 7 LIWTL 11
 RESULT 7
 Q8W128 ID Q8W128 PRELIMINARY; PRT; 19 AA.
 AC Q8W128;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Nitrate reductase (Fragment).
 GN Name=NIA;
 OS Scaevola procera.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC campanulids; Asterales; Goodeniaceae; Scaevola.
 OX NCBI_TaxID=184417;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22096038; PubMed=12099803;
 RA Howard D.G., Baum D.A.;
 RT "Phylogenetic utility of a nuclear intron from nitrate reductase for
 RT the study of closely related plant species.";
 RL Mol. Phylogenet. Evol. 23:525-528 (2002).
 DR EMBL; AF460205; AAL66737.1; --
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR InterPro; IPR005066; No-co dimer.
 DR Pfam; PF03404; No-co_dimer; 1.
 FT NON_TER 1 1
 FT NON_TER 19 19
 SQ SEQUENCE 19 AA; 2357 MW; 5C0582771535B26A CRC64;
 Query Match 50.0%; Score 24; DB 2; Length 19;
 Best Local Similarity 50.0%; Pred. No. 1.7e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 4 MIWTM 9
 Db 6 LIWNL 11
 RESULT 8
 Q8R5G1 ID Q8R5G1 PRELIMINARY; PRT; 15 AA.
 AC Q8R5G1;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Pancreatic triacylglycerol lipase (Fragment).
 GN Name=PTL;
 OS Spermophilus tridecemlineatus (Thirteen-lined ground squirrel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Scuridae; Sciurinae;
 OC Spermophilus.

OX NCBI_TaxID=43179;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX PubMed=14583598;
 RA Squire T.L., Andrews M.T.;
 RT "Pancreatic triacylglycerol lipase in a hibernating mammal. I. Novel
 RT genomic organization.";
 RL Physiol. Genomics (Online) 16:119-130 (2003).
 DR EMBL; AY071823; AAL73074.1; --
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1570 MW; C6F85151A7050414 CRC64;
 Query Match 47.9%; Score 23; DB 2; Length 15;
 Best Local Similarity 33.3%; Pred. No. 2.1e+03;
 Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 3 LMIWTM 8
 Db 2 LLVWSL 7
 RESULT 9
 Q8IVK5 ID Q8IVK5 PRELIMINARY; PRT; 17 AA.
 AC Q8IVK5;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Steerin2 protein (Fragment).
 GN Name=STEERIN2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Peeters P.J., Verhasselt P., Moechars D.W., Luyten W.H.M.L.,
 RA Geysen J.J.G.H.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ488206; CAD32559.1; --
 FT NON_TER 17 17
 SQ SEQUENCE 17 AA; 2169 MW; 1F508A5824873F9E CRC64;
 Query Match 47.9%; Score 23; DB 2; Length 17;
 Best Local Similarity 60.0%; Pred. No. 2.3e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 2 SLMIW 6
 Db 2 SYMLW 6
 RESULT 10
 Q9ESU5 ID Q9ESU5 PRELIMINARY; PRT; 10 AA.
 AC Q9ESU5;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Fas death receptor (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C3H/He;
 RX MEDLINE=20127858; PubMed=10660538;
 RA Munsch D., Watanabe-Fukunaga R., Bourdon J.C., Nagata S., May E.,
 RA Yonish-Rouach E., Reisdlorff P.;
 RT "Human and mouse Fas (APO-1/CD95) death receptor genes each contain a
 RT p53-responsive element that is activated by p53 mutants unable to

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RT induce apoptosis.";
RL J. Biol. Chem. 275:3867-3872(2000).
DR EMBL; AF282865; AAG02410.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1242 MW; 22145E32CDC37043 CRC64;

Query Match 43.8%; Score 21; DB 2; Length 10;
Best Local Similarity 42.9%; Pred. No. 3.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 LMIWTM 9
DB 2 LMIWAVL 8

RESULT 11
ID Q7S3Q9 PRELIMINARY; PRT; 17 AA.
AC Q7S3Q9;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Predicted protein.
GN Name-NCU04958.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]_TaxID=5141;
RP SEQUENCE FROM N.A.
RC STRAIN=OK74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehm B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamysysselis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA Krystofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catheide D., Li W., Pratt R.J., Osmari S.A.,
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Siller S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABX01000407; EAA30170.1; -.
SQ SEQUENCE 17 AA; 2044 MW; 33C34BDEBAF0F3A2 CRC64;

Query Match 43.8%; Score 21; DB 2; Length 17;
Best Local Similarity 40.8%; Pred. No. 5.4e+03;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 LMIWT 7
DB 1 LMIWT 5

RESULT 12
Q69074
ID Q69074 PRELIMINARY; PRT; 17 AA.
AC Q69074;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HSV-1 glycoprotein C (Fragment).
QS Human herpesvirus 1 (HHV-1) (Human herpes simplex virus 1).

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OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10298;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87089706; PubMed=3025606;
RA Homa F.L., Otal T.M., Glorioso J.C., Levine M.;
RT "Transcriptional control signals of a herpes simplex virus type 1 late
RT (gamma-2) gene lie within bases -34 to +124 relative to the 5'
RT terminus of the mRNA.";
RL Mol. Cell. Biol. 6:3652-3666(1986).
DR EMBL; M14128; AAA45784.1; -.
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1868 MW; B4ED3CE6ABAE92 CRC64;

Query Match 43.8%; Score 21; DB 2; Length 17;
Best Local Similarity 12.5%; Pred. No. 5.4e+03;
Matches 1; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 2 SLMWTM 9
DB 9 AVWLMSLL 16

RESULT 13
DCAM_ACACA
ID DCAM_ACACA STANDARD; PRT; 19 AA.
AC P34039;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE S-adenosylmethionine decarboxylase alpha subunit (EC 4.1.1.50)
DE (AdoMetDC) (SAMDC) (Fragment).
OS Acanthamoeba castellanii (Amoeba).
OC Eukaryota; Acanthamoebidae; Acanthamoeba.
OX NCBI_TaxID=5755;
RN [1]_TaxID=5755;
RP SEQUENCE, AND CHARACTERIZATION.
RX MEDLINE=94029912; PubMed=8216217;
RA Hugo B.R., Byers T.J.;
RT "S-adenosyl-L-methionine decarboxylase of Acanthamoeba castellanii
RT (Neff): purification and properties.";
RL Biochem. J. 295:203-209(1993).
CC -!- FUNCTION: S-adenosylmethionine decarboxylase is essential for the
CC biosynthesis of spermine and spermidine. The alpha subunit
CC contains the active site.
CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (S)-deoxy-5-
CC adenosyl(3-aminopropyl) methylsulfonium salt + CO(2).
CC -!- COFACTOR: Pyruvoyl group.
CC -!- PATHWAY: Decarboxylation of S-adenosylmethionine provides the
CC aminopropyl moiety required for spermidine and spermine
CC biosynthesis from putrescine.
CC -!- SUBUNIT: Heterotetramer of two alpha and two beta chains.
CC -!- DEVELOPMENTAL STAGE: Expressed only during exponential growth.
CC -!- INDUCTION: Stimulated by putrescine. Inhibited by aromatic
CC diamidines berenil, pentamidine, propamidine, hydroxyethylaminidine,
CC by ethidium bromide and methylglyoxal.
CC -!- SIMILARITY: Belongs to the eukaryotic AdoMetDC family.
DR PIR; S38763; S38763.
DR InterPro; IPR001985; SAM decarbox.
DR Pfam; PF01536; SAM decarbox; 1.
DR PROSITE; PS01336; ADOMETDC; PARTIAL.
KW Decarboxylase; Direct protein sequencing; Lyase; Pyruvate;
KW Spermidine biosynthesis.
FT MOD_RES 1 1 Pyruvic acid (Ser).
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 2153 MW; 88B18AD9B6142AEF CRC64;

Query Match 43.8%; Score 21; DB 1; Length 19;
Best Local Similarity 33.3%; Pred. No. 6e+03;
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 TSLMIW 6

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Db 1 SSMFVW 6

RESULT 14

Q6LERS PRELIMINARY; PRT; 21 AA.
AC Q6LERS;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome P4501IE1 (Fragment).
GN Name=CYP2E1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89166510; PubMed=3233219;
RA Umeno M., McBride W.O., Yang C.S., Gelboin H.V., Gonzalez F.J.;
RT "Human ethanol-ineudible P4501IE1: complete gene sequence, promoter
RT characterization chromosome mapping, and cDNA-directed expression.";
RL Biochemistry 27:9006-9013(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92138659; PubMed=1778977;
RA Hayaashi S.;
RT "Genetic polymorphisms in the 5'-flanking region change transcriptional
RT regulation of the Human cytochrome P4501IE1 gene.";
RL J. Biochem. 110:559-565(1991).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=95122459; PubMed=7529759;
RA Watanabe J., Hayaashi S., Kawajiri K.;
RT "Different regulation and expression of the human CYP2E1 gene due to
RT the RsaI polymorphism in the 5'-flanking region.";
RL J. Biochem. 116:321-326(1994).
DR EMBL; D10014; BAA00902.1; -.
FT NON TER 21
SQ SEQUENCE 21 AA; 2175 MW; 60A85A2B034F339B CRC64;

Query Match 43.8%; Score 21; DB 2; Length 21;
Best Local Similarity 40.0%; Pred. No. 6.6e+03;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 SLMIW 6
Db 9 ALLVW 13

RESULT 15

BAA00902 PRELIMINARY; PRT; 21 AA.
ID BAA00902;
AC BAA00902;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome P4501IE1 (Fragment).
GN CYP2E1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92138659; PubMed=1778977;
RA Hayaashi S.;
RT "Genetic polymorphisms in the 5'-flanking region change transcriptional
RT regulation of the Human cytochrome P4501IE1 gene.";
RL J. Biochem. 110:559-565(1991).
RN [2]
RP SEQUENCE FROM N.A.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:25 ; Search time 5.55319 Seconds
(without alignments)
155.938 Million cell updates/sec

Title: US-09-831-253F-5

Perfect score: 48

Sequence: 1 TSLMIWTMM 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 4495

Minimum DB seq length: 0

Maximum DB seq length: 23

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	56.2	16	2 PH1638	Ig H chain V-D-J r
2	25	52.1	7	2 PX0008	glucuronosyltransf
3	25	52.1	16	2 PH1637	Ig H chain V-D-J r
4	24	50.0	13	2 PH1636	Ig H chain V-D-J r
5	23	47.9	13	2 PH1620	Ig H chain V-D-J r
6	23	47.9	14	2 PH1625	Ig H chain V-D-J r
7	23	47.9	14	2 PH1627	Ig H chain V-D-J r
8	23	47.9	15	2 PH1613	Ig H chain V-D-J r
9	23	47.9	15	2 PH1612	Ig H chain V-D-J r
10	23	47.9	17	2 PH1630	Ig H chain V-D-J r
11	23	47.9	20	2 PH1358	Ig heavy chain DJ
12	22	45.8	14	2 A35105	hypothetical prote
13	21	43.8	14	2 PH1327	Ig heavy chain DJ
14	21	43.8	15	2 PH1590	Ig H chain V-D-J r
15	21	43.8	20	2 PL0192	Ig lambda 2 chain
16	21	43.8	20	2 S38763	S-adenosyl-L-methi
17	20	41.7	14	2 PH1626	Ig H chain V-D-J r
18	20	41.7	22	2 I58038	MHC class I transp
19	20	41.7	22	2 A64548	hypothetical prote
20	19	39.6	12	2 I58273	thyroglobulin - ra
21	19	39.6	15	2 PH0782	T-cell receptor al
22	19	39.6	17	2 PH1331	Ig heavy chain DJ
23	19	39.6	18	2 I59649	human leukocyte an
24	19	39.6	19	2 A28702	cytochrome P450-C-
25	19	39.6	19	2 I45957	protein kinase (EC
26	19	39.6	19	2 I53673	amyloid protein -
27	19	39.6	19	2 PH1352	Ig heavy chain DJ
28	19	39.6	19	2 PH1315	Ig heavy chain DJ
29	19	39.6	19	2 I40063	shikimate 5-dehydr

ALIGNMENTS

RESULT 1

PH1638

Ig H chain V-D-J region (clone B-less 228) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999

C;Accession: PH1638

R;Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mic

A;Reference number: PH1580; MUID:93301609; PMID:8315387

A;Accession: PH1638

A;Molecule type: DNA

A;Residues: 1-16 <LSV>

A;Experimental source: bone marrow pre-B lymphocyte

C;Keywords: immunoglobulin

Query Match 56.2%; Score 27; DB 2; Length 16;
Best Local Similarity 57.1%; Pred. No. 58;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 TSLMIWT 7

Db 10 TTSMLWT 16

RESULT 2

PX0008

glucuronosyltransferase (EC 2.4.1.17), hepatic - rat (fragment)

N;Alternate names: UDP-glucuronyltransferase

C;Species: Rattus norvegicus (Norway rat)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 07-Feb-1997

C;Accession: PX0008

R;Yokota, H.; Yuasa, A.; Sato, R.

J. Biochem. 104, 531-536, 1988

A;Title: Purification and properties of a form of UDP-glucuronyltransferase from liver

A;Reference number: PX0008; MUID:89197852; PMID:3149280

A;Accession: PX0008

A;Molecule type: protein

A;Residues: 1-7 <YOK>

C;Keywords: glycosyltransferase; hexosyltransferase; liver

Query Match 52.1%; Score 25; DB 2; Length 7;

Best Local Similarity 50.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 TSLMIW 6

Db 1 TKLLVW 6

RESULT 3

PH1637

RESULT 4
 PH1636
 Ig H chain V-D-J region (clone B-less 224) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
 C:Accession: PH1637
 R:Levinson, D.A.; Campos-Torres, J.; Leder, P.
 J. Exp. Med. 178, 317-329, 1993
 A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
 A:Reference number: PH1580; MUID:93301609; PMID:8315387
 A:Accession: PH1637
 A:Molecule type: DNA
 A:Residues: 1-16 <LEV>
 A:Experimental source: bone marrow pre-B lymphocyte
 C:Keywords: immunoglobulin

Query Match 52.1%; Score 25; DB 2; Length 16;
 Best Local Similarity 57.1%; Pred. No. 1.3e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 TSLMIWT 7
 Db 10 TLTMLWT 16
 | : | |

RESULT 5
 PH1620
 Ig H chain V-D-J region (clone B-less 40) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
 C:Accession: PH1620
 R:Levinson, D.A.; Campos-Torres, J.; Leder, P.
 J. Exp. Med. 178, 317-329, 1993
 A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
 A:Reference number: PH1580; MUID:93301609; PMID:8315387
 A:Accession: PH1620
 A:Molecule type: DNA
 A:Residues: 1-13 <LEV>
 A:Experimental source: bone marrow pre-B lymphocyte
 C:Keywords: immunoglobulin

Query Match 50.0%; Score 24; DB 2; Length 13;
 Best Local Similarity 75.0%; Pred. No. 1.7e+02;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 4 MIWT 7
 Db 10 MVWT 13
 | : | |

RESULT 6
 PH1625
 Ig H chain V-D-J region (clone B-less 109) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
 C:Accession: PH1625
 R:Levinson, D.A.; Campos-Torres, J.; Leder, P.
 J. Exp. Med. 178, 317-329, 1993
 A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
 A:Reference number: PH1580; MUID:93301609; PMID:8315387
 A:Accession: PH1625
 A:Molecule type: DNA
 A:Residues: 1-14 <LEV>
 A:Experimental source: bone marrow pre-B lymphocyte
 C:Keywords: immunoglobulin

Query Match 47.9%; Score 23; DB 2; Length 13;
 Best Local Similarity 75.0%; Pred. No. 2.5e+02;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 4 MIWT 7
 Db 10 MLWT 13
 | : | |

RESULT 7
 PH1627
 Ig H chain V-D-J region (clone B-less 120) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
 C:Accession: PH1627
 R:Levinson, D.A.; Campos-Torres, J.; Leder, P.
 J. Exp. Med. 178, 317-329, 1993
 A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
 A:Reference number: PH1580; MUID:93301609; PMID:8315387
 A:Accession: PH1627
 A:Molecule type: DNA
 A:Residues: 1-14 <LEV>
 A:Experimental source: bone marrow pre-B lymphocyte
 C:Keywords: immunoglobulin

Query Match 47.9%; Score 23; DB 2; Length 14;
 Best Local Similarity 75.0%; Pred. No. 2.7e+02;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 4 MIWT 7
 Db 11 MLWT 14
 | : | |

RESULT 8
 PH1613
 Ig H chain V-D-J region (clone B-less 17) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
 C:Accession: PH1613
 R:Levinson, D.A.; Campos-Torres, J.; Leder, P.
 J. Exp. Med. 178, 317-329, 1993
 A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
 A:Reference number: PH1580; MUID:93301609; PMID:8315387
 A:Accession: PH1613
 A:Molecule type: DNA
 A:Residues: 1-14 <LEV>
 A:Experimental source: bone marrow pre-B lymphocyte
 C:Keywords: immunoglobulin

Query Match 47.9%; Score 23; DB 2; Length 14;
 Best Local Similarity 75.0%; Pred. No. 2.7e+02;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 4 MIWT 7
 Db 11 MLWT 14
 | : | |

RESULT 9
 PH1620
 Ig H chain V-D-J region (clone B-less 40) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
 C:Accession: PH1620
 R:Levinson, D.A.; Campos-Torres, J.; Leder, P.
 J. Exp. Med. 178, 317-329, 1993
 A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
 A:Reference number: PH1580; MUID:93301609; PMID:8315387
 A:Accession: PH1620
 A:Molecule type: DNA
 A:Residues: 1-13 <LEV>
 A:Experimental source: bone marrow pre-B lymphocyte
 C:Keywords: immunoglobulin

Query Match 47.9%; Score 23; DB 2; Length 15;
 Best Local Similarity 75.0%; Pred. No. 2.9e+02;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 4 MIWT 7
 Db 12 MLWT 15
 | : | |

Db

8 TTTTWT 14

RESULT 9

PH1612
Ig H chain V-D-J region (wild-type clone 344) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PH1612
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A;Reference number: PH1580; MUID:93301609; PMID:8315387
A;Accession: PH1612
A;Molecule type: DNA
A;Residues: 1-15 <LEV>
A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin

Query Match 47.9%; Score 23; DB 2; Length 15;
Best Local Similarity 75.0%; Pred. No. 2.9e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 MIWT 7
|:|
Db 12 MLWT 15

RESULT 10

PH1630
Ig H chain V-D-J region (clone B-less 156) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PH1630
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A;Reference number: PH1580; MUID:93301609; PMID:8315387
A;Accession: PH1630
A;Molecule type: DNA
A;Residues: 1-17 <LEV>
A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin

Query Match 47.9%; Score 23; DB 2; Length 17;
Best Local Similarity 75.0%; Pred. No. 3.3e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 MIWT 7
|:|
Db 14 MLWT 17

RESULT 11

PH1358
Ig heavy chain DJ region (clone C178-117) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PH1358
R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A;Title: Predominance of fetal type DJH joining in young children with B precursor lymphoma
A;Reference number: PH1302; MUID:93094761; PMID:1460419
A;Accession: PH1358
A;Molecule type: DNA
A;Residues: 1-20 <WAS>
C;Keywords: heterotetramer; immunoglobulin

Query Match 47.9%; Score 23; DB 2; Length 20;
Best Local Similarity 42.9%; Pred. No. 3.9e+02;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 TSLMIWT 7
|:|

RESULT 12

A35105
Hypothetical protein - Neurospora crassa mitochondrion (fragment)
C;Species: Neurospora crassa
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 07-Dec-1999
C;Accession: A35105
R;Saville, B.J.; Collins, R.A.
Cell 61, 685-696, 1990
A;Title: A site-specific self-cleavage reaction performed by a novel RNA in neurospora
A;Reference number: A35105; MUID:90263093; PMID:2160856
A;Accession: A35105
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-14 <SAV>
C;Genetics:
A;Genome: mitochondrion
A;Genetic code: SGC3
C;Keywords: mitochondrion

Query Match 45.8%; Score 22; DB 2; Length 14;
Best Local Similarity 40.0%; Pred. No. 4.1e+02;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 5 IWTMM 9
:|:|
Db 4 LWTLL 8

RESULT 13

PH1327
Ig heavy chain DJ region (clone C113-105) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PH1327
R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A;Title: Predominance of fetal type DJH joining in young children with B precursor lymphoma
A;Reference number: PH1302; MUID:93094761; PMID:1460419
A;Accession: PH1327
A;Molecule type: DNA
A;Residues: 1-14 <WAS>
C;Keywords: heterotetramer; immunoglobulin

Query Match 43.8%; Score 21; DB 2; Length 14;
Best Local Similarity 75.0%; Pred. No. 6.3e+02;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 WTMM 9
|||
Db 2 WVTMM 5

RESULT 14

PH1590
Ig H chain V-D-J region (wild-type clone 141) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PH1590
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A;Reference number: PH1580; MUID:93301609; PMID:8315387
A;Accession: PH1590
A;Molecule type: DNA
A;Residues: 1-15 <LEV>
A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin

Query Match 43.8%; Score 21; DB 2; Length 15;
Best Local Similarity 60.0%; Pred. No. 6.8e+02;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 LMIWT 7
| :||
Db 11 LYLWT 15

RESULT 15

PL0192
Ig lambda 2 chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
C;Accession: PL0192
R;Alonso, A.; Chang, L.A.; Murialdo, H.
Mol. Immunol. 27, 115-127, 1990
A;Title: Analysis of the expression of murine lambda genes transfected into immunocompetent cells
A;Reference number: PL0192; MUID:90205873; PMID:2108323
A;Accession: PL0192
A;Molecule type: DNA
A;Residues: 1-20 <ALO>
C;Genetics:
A;Introns: 16/2
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 43.8%; Score 21; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 9e+02; Indels 0; Gaps 0;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 MIWTMM 9
| :||
Db 1 MAWTSL 6

Search completed: November 14, 2004, 12:03:12
Job time : 6.55319 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2004, 12:56:07 ; Search time 100 Seconds
(without alignments)
86.306 Million cell updates/sec

Title: US-09-831-253F-4

Perfect score: 75

Sequence: 1 SNPSAFQVDIIVDI 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 7754

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	28	37.3	9	2 Q7RA82	Q7RA82 plasmodium
2	26	34.7	12	2 Q9S550	Q9S550 streptococ
3	25	33.3	10	2 Q76NM5	Q76NM5 eurypharynx
4	25	33.3	10	2 BAB87140	BAB87140 euryphary
5	25	33.3	11	2 Q7M154	Q7M154 bacillus th
6	25	33.3	12	2 Q7XB05	Q7XB05 zea mays (m
7	25	33.3	13	2 Q7X761	Q7X761 zea mays (m
8	25	33.3	13	2 Q79A22	Q79A22 borrelia bu
9	25	33.3	14	2 P81801	P81801 streptomyc
10	24	32.0	8	2 Q91U19	Q91U19 influenza a
11	24	32.0	8	2 Q91U21	Q91U21 influenza a
12	23	30.7	10	2 Q76MK9	Q76MK9 eurypharynx
13	23	30.7	10	2 BAB87148	BAB87148 euryphary
14	23	30.7	10	2 BAB87156	BAB87156 euryphary
15	23	30.7	10	2 BAB87164	BAB87164 euryphary
16	23	30.7	14	2 Q7S366	Q7S366 neurospora
17	23	30.7	15	2 Q9F8B2	Q9F8B2 silene aega
18	22	29.3	8	1 ALL3_CYDPO	P82154 cydia pomon
19	22	29.3	11	2 P83128	P83128 bos indicus
20	22	29.3	12	1 VESP_VESMA	Q7M3T3 vespa manda
21	22	29.3	14	2 Q7S366	Q7S366 neurospora
22	22	29.3	15	1 ALL3_MANSE	P42559 manduca sex
23	22	29.3	15	1 IRBP_CRISP	P12665 cricetidae
24	22	29.3	15	2 Q9TWE9	Q9TWE9 galliera me
25	21	28.0	7	1 ALL5_CARMA	P81808 carcinus ma
26	21	28.0	13	2 Q7M014	Q7M014 bacillus ce
27	21	28.0	14	1 CATA_ACICA	P83715 acinetobact
28	21	28.0	15	1 LEC3_AXIPO	P28588 axinella po
29	21	28.0	15	2 Q7M4Y2	Q7M4Y2 fusarium sp
30	21	28.0	15	2 Q9UCC4	Q9UCC4 homo sapien
31	20	26.7	9	2 Q7M2M7	Q7M2M7 bos taurus

32 20 26.7 9 2 Q6EKR5
33 20 26.7 10 2 Q84140
34 20 26.7 11 2 P83168
35 20 26.7 12 2 Q89243
36 20 26.7 14 2 Q71GT6
37 20 26.7 14 2 Q71GW6
38 20 26.7 14 2 Q71GZ0
39 20 26.7 14 2 Q71H06
40 20 26.7 14 2 Q71H14
41 20 26.7 14 2 Q71H34
42 20 26.7 14 2 AAQ07615
43 20 26.7 14 2 AAQ07635
44 20 26.7 14 2 AAQ07643
45 20 26.7 14 2 AAQ07659

ALIGNMENTS

RESULT 1
Q7RA82 PRELIMINARY; PRT; 9 AA.
AC Q7RA82;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DE Hypothetical protein (Fragment)...
GN Name=PY06620;
OS Plasmodium yoelii yoelii;
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=12368865;
RA Carlson J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M., Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L., Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L., Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V., Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M., Florens L., Yates P.R., Raine J.D., Sinden R.E., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J., Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria parasite Plasmodium yoelii yoelii";
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.
CC EMBL: AABL01002263; EAA18865.1; -.
DR Hypothetical protein.
KW NON TER
SQ SEQUENCE 9 AA; 1001 MW; 4687A5AB476455B7 CRC64;

Query Match 37.3%; Score 28; DB 2; Length 9;

Best Local Similarity 100.0%; Pred.No.1.8e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNPS 5

Db 3 SNPS 7

RESULT 2

ID Q9S550 PRELIMINARY; PRT; 12 AA.

AC Q9S550;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DE 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)

DE DexB (Fragment).

GN Name=dexB;
 OS Streptococcus pneumoniae.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1313;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=D39;
 RX MEDLINE=99214122; PubMed=10198036;
 RA Iannelli F., Pearce B.J., Pozzi G.;
 RT "The type 2 capsule locus of Streptococcus pneumoniae.";
 RL J. Bacteriol. 181:2652-2654(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=D39;
 RA Pearce B.J., Iannelli F., Pozzi G.;
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF026471; AAD10169.1; -;
 FT NON TER 1
 SQ SEQUENCE 12 AA; 1405 MW; 90A979D2B2B9CDDA CRC64;

Query Match 34.7%; Score 26; DB 2; Length 12;
 Best Local Similarity 40.0%; Pred. No. 1.2e+03;
 Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 PYSAFOVDII 12

Db ||| ||| |||

3 PWDAPCVELL 12

RESULT 3

Q76MWS ID Q76MWS PRELIMINARY; PRT; 10 AA.

AC Q76MWS;
 DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
 DE NADH dehydrogenase subunit 2 (Fragment).
 GN Name=ND2;
 OS Eurypharynx pelecyanoides (pelican eel).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes;
 OC Eurypharyngidae; Eurypharynx.
 OX NCBI_TaxID=55117;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=22967687; PubMed=12949142;
 RA Inoue J.G., Miya M., Tsukamoto K., Nishida M.;
 RT "Evolution of the deep-sea gulper eel mitochondrial genomes: large-scale gene rearrangements originated within the eels.";
 RL Mol. Biol. Evol. 20:1917-1924(2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB046477; BAB87140.1; -;
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON TER 10
 SQ SEQUENCE 10 AA; 1261 MW; 357BFE29C682DB47 CRC64;

Query Match 33.3%; Score 25; DB 2; Length 10;
 Best Local Similarity 62.5%; Pred. No. 1.5e+03;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 NPYSAFQV 9

Db ||| ||| |||

2 NPYVMFLV 9

RESULT 4

BAB87140

ID BAB87140 PRELIMINARY; PRT; 10 AA.
 AC BAB87140;
 DT 02-MAR-2004 (TRENBLrel. 27, Created)
 DT 02-MAR-2004 (TRENBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TRENBLrel. 27, Last annotation update)
 DE NADH dehydrogenase subunit 2 (Fragment).
 GN ND2.
 OS Eurypharynx pelecyanoides (pelican eel).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes;
 OC Eurypharyngidae; Eurypharynx.
 OX NCBI_TaxID=55117;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A;
 RA Inoue J.G., Miya M., Tsukamoto K., Nishida M.;
 RT "Evolution of the Deep-Sea Gulper Eel Mitochondrial Genomes: Large-Scale Gene Rearrangements Originated Within the Eels.";
 RL Mol. Biol. Evol. 20:1917-1924(2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A;
 RA Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB046477; BAB87140.1; -;
 KW Mitochondrion.
 FT NON TER 10
 SQ SEQUENCE 10 AA; 1261 MW; 357BFE29C682DB47 CRC64;

Query Match 33.3%; Score 25; DB 2; Length 10;
 Best Local Similarity 62.5%; Pred. No. 1.5e+03;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 NPYSAFQV 9

Db ||| ||| |||

2 NPYVMFLV 9

RESULT 5

Q7M154 ID Q7M154 PRELIMINARY; PRT; 11 AA.

AC Q7M154;
 DT 01-MAR-2004 (TRENBLrel. 26, Created)
 DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Parasporal crystal protein, wax moth-specific (fragment).
 OS Bacillus thuringiensis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1428;
 RN [1]
 RP SEQUENCE.
 RA Chestukhina G.G., Kostina L.I., Zalunin I.A., Khodova O.M.,
 RA Stepanov V.M.;
 RT "Bacillus thuringiensis ssp. galleriae simultaneously produces two
 RT delta-endotoxins differing strongly in primary structure and
 RT entomocidal activity.";
 RL FEBS Lett. 232:249-251(1988).
 DR PIR; S00616; S00616.
 FT NON TER 1
 FT NON TER 11
 SQ SEQUENCE 11 AA; 1237 MW; C6FF9BD64764444D CRC64;

Query Match 33.3%; Score 25; DB 2; Length 11;
 Best Local Similarity 80.0%; Pred. No. 1.7e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNPYS 5

Db :||| |||

5 NNPYS 9

RESULT 6

Q7XB05
ID Q7XB05 PRELIMINARY; PRT; 12 AA.
AC Q7XB05;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Phytoene synthase 2 (Fragment).
GN Name=psy2;
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Y-14;
RX MEDLINE=22779048; PubMed=12897253;
RA Palaisa K.A., Morgante M., Williams M., Rafalski A.;
RT "Contrasting effects of selection on sequence diversity and linkage
RT disequilibrium at two phytoene synthase loci.";
RL Plant Cell 15:1795-1806(2003).
DR EMBL; AY300568; AAP55307.1; -.
FT NON_TER 1
FT NON_TER 12
SQ SEQUENCE 12 AA; 1335 MW; 9B1E0AA00869C325 CRC64;
Query Match 33.3%; Score 25; DB 2; Length 12;
Best Local Similarity 54.5%; Pred. No. 1.8e+03;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 SNPYSAFOVDI 11
| : | | | |
DB 1 SDTVSKFPVDI 11

RESULT 7
Q7X761
ID Q7X761 PRELIMINARY; PRT; 13 AA.
AC Q7X761;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Phytoene synthase 2 (Fragment).
GN Name=psy2;
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=W-17 and W-50;
RX MEDLINE=22779048; PubMed=12897253;
RA Palaisa K.A., Morgante M., Williams M., Rafalski A.;
RT "Contrasting effects of selection on sequence diversity and linkage
RT disequilibrium at two phytoene synthase loci.";
RL Plant Cell 15:1795-1806(2003).
DR EMBL; AY300592; AAP55331.1; -.
DR EMBL; AY300599; AAP55338.1; -.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1449 MW; 9B1E0AA05615C325 CRC64;
Query Match 33.3%; Score 25; DB 2; Length 13;
Best Local Similarity 54.5%; Pred. No. 2e+03;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 SNPYSAFOVDI 11
| : | | | |
DB 2 SDTVSKFPVDI 12

RESULT 8

Q79A22
ID Q79A22 PRELIMINARY; PRT; 13 AA.
AC Q79A22;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MoxR protein (Fragment).
GN Name=moxR;
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=212;
RX Old I.G.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; X95668; CAA64970.1; -.
FT NON_TER 13
FT NON_TER 13
SQ SEQUENCE 13 AA; 1484 MW; C7C2DF4CFD83A046 CRC64;
Query Match 33.3%; Score 25; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 2e+03;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 SAFQVDIIVD 14
| : | | | |
DB 3 SGFQIDSEVE 12

RESULT 9
P81801
ID P81801 PRELIMINARY; PRT; 14 AA.
AC P81801;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Puromycin-hydrolyzing enzyme (EC 3.-.-.-) (Fragment).
OS Streptomyces morookaensis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1970;
RN [1]
RP SEQUENCE.
RC STRAIN=JCM4673 / KCC S-0673;
RX PubMed=9538199;
RA Nishimura M., Matsuo H., Nakamura A., Sugiyama M.;
RT "Purification and characterization of a puromycin-hydrolyzing enzyme
RT from blastocidin S-producing Streptomyces morookaensis.";
RL J. Biochem. 123:247-252(1998).
RN [2]
RP CHARACTERIZATION, AND FUNCTION.
RA Nishimura M., Matsuo H., Sugiyama M.;
RT "Blastocidin S-producing Streptomyces morookaensis possesses an enzyme
RT activity with hydrolyzes puromycin.";
RL FEMS Microbiol. Lett. 132:95-100(1995).
CC -1- FUNCTION: INACTIVATES PUROMYCIN BY CATALYZING THE HYDROLYSIS OF
CC THE AMIDE LINKAGE BETWEEN ITS AMINONUCLEOSIDE AND O-METHYL-L-
CC TYROSINE MOIETIES. THE OPTIMUM PH IS 8.0 AND THE OPTIMAL
CC TEMPERATURE IS 45 DEGREES CELSIUS.
CC -1- FUNCTION: MAY HAVE AMINOPEPTIDASE ACTIVITY.
CC -1- ENZYME REGULATION: STIMULATED BY DTT. STRONGLY INHIBITED BY ZINC
CC ION, FERROUS ION, CUPRIC ION, MERCURY ION, N-BROMOSUCCINIMIDE AND
CC N-ETHYLMALIMIDE. PARTIALLY INHIBITED BY COBALT ION.
CC -1- SUBUNIT: MONOMER.
CC -1- MISCELLANEOUS: HAS AN ISOELECTRIC POINT OF 6.4.
DR GO; GO:0004177; F:aminopeptidase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
KW Aminopeptidase; Hydrolase.
FT NON_TER 14
FT NON_TER 14
SQ SEQUENCE 14 AA; 1492 MW; 3F980730E45BF3D8 CRC64;
Query Match 33.3%; Score 25; DB 2; Length 14;
Best Local Similarity 55.6%; Pred. No. 2.1e+03;

Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 PYSAFQVDI 11
 ||| ||| |
 Db 5 PYGAWSQSI 13

RESULT 10

Q91U19 PRELIMINARY; PRT; 8 AA.

ID Q91U19
 AC Q91U19;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Nuclear export protein NS2 (Fragment).
 OS Influenza A virus (A/Hong Kong/503/97(H5N1)).
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 OC Influenzavirus A; H5N1 subtype.
 OX NCBI_TaxID=155224;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A/Hong Kong/503/97;
 RA Shaw M.W., Cooper L.A., Xu X., Thompson W.W., Kraus S.L., Guan Y.,
 RA Zhou N.N., Klimov A., Cox N.J., Webster R.G., Lim W., Shortridge K.F.,
 RA Subbarao K.;
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF256192; AAK49326.1; -;
 FT NON_TER 1 1
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA; 869 MW; D9D9D5A5A2D1A455 CRC64;

Query Match 32.0%; Score 24; DB 2; Length 8;

Best Local Similarity 62.5%; Pred. NO. 1.8e+06;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SNPYSAFQ 8

||| ||| |

Db 1 SNTVSSSQ 8

RESULT 11

Q91U21 PRELIMINARY; PRT; 8 AA.

ID Q91U21
 AC Q91U21;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Nuclear export protein NS2 (Fragment).
 OS Influenza A virus (A/Hong Kong/491/97(H5N1)).
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 OC Influenzavirus A; H5N1 subtype.
 OX NCBI_TaxID=155223;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A/Hong Kong/491/97;
 RA Shaw M.W., Cooper L.A., Xu X., Thompson W.W., Kraus S.L., Guan Y.,
 RA Zhou N.N., Klimov A., Cox N.J., Webster R.G., Lim W., Shortridge K.F.,
 RA Subbarao K.;
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF256191; AAK49324.1; -;
 FT NON_TER 1 1
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA; 869 MW; D9D9D5A5A2D1A455 CRC64;

Query Match 32.0%; Score 24; DB 2; Length 8;

Best Local Similarity 62.5%; Pred. NO. 1.8e+06;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SNPYSAFQ 8

||| ||| |

Db 1 SNTVSSSQ 8

RESULT 12

Q76MK9 PRELIMINARY; PRT; 10 AA.

ID Q76MK9
 AC Q76MK9;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE NADH dehydrogenase subunit 2 (Fragment).
 GN Name=ND2;
 OS Eurypharynx pelecanoides (pelican eel).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes;
 OC Eurypharyngidae; Eurypharynx.
 OX NCBI_TaxID=55117;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22967687; PubMed=12949142;
 RA Inoue J.G., Miya M., Tsukamoto K., Nishida M.;
 RT "Evolution of the deep-sea gulper eel mitochondrial genomes: large-
 RT scale gene rearrangements originated within the eels.";
 RL Mol. Biol. Evol. 20:1917-1924(2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB046485; BAB87156.1; -;
 DR EMBL; AB046489; BAB87164.1; -;
 DR EMBL; AB046481; BAB87148.1; -;
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1293 MW; 356FAE29C682DB47 CRC64;

Query Match 30.7%; Score 23; DB 2; Length 10;

Best Local Similarity 66.7%; Pred. NO. 3.5e+03;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NPYSAF 7

||| |

Db 2 NEYVMF 7

RESULT 13

BAB87148 PRELIMINARY; PRT; 10 AA.

ID BAB87148
 AC BAB87148;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE NADH dehydrogenase subunit 2 (Fragment).
 GN ND2.
 OS Eurypharynx pelecanoides (pelican eel).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes;
 OC Eurypharyngidae; Eurypharynx.
 OX NCBI_TaxID=55117;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B;
 RA Inoue J.G., Miya M., Tsukamoto K., Nishida M.;
 RT "Evolution of the Deep-Sea Gulper Eel Mitochondrial Genomes: Large-
 RT Scale Gene Rearrangements Originated Within the Eels.";
 RL Mol. Biol. Evol. 20:1917-1924(2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB046481; BAB87148.1; -;
 KW Mitochondrion.
 FT NON_TER 10 10

SQ SEQUENCE 10 AA; 1293 MW; 356FAE29C682DB47 CRC64;
 Query Match 30.7%; Score 23; DB 2; Length 10;
 Best Local Similarity 66.7%; Pred. No. 3.5e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NPYSAP 7
 |||||
 Db 2 NPYVMF 7

RESULT 14

BAB87156 ID BAB87156 PRELIMINARY; PRT; 10 AA.
 AC BAB87156;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE NADH dehydrogenase subunit 2 (Fragment).
 GN ND2.
 OS Eurypharynx pelecanoides (pelican eel).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes;
 OC Eurypharyngidae; Eurypharynx.
 OX NCBI_TaxID=55117;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C;
 RA Inoue J.G., Miya M., Tsukamoto K., Nishida M.;
 RT "Evolution of the Deep-Sea Gulper Bel Mitochondrial Genomes: Large-
 RL Scale Gene Rearrangements Originated Within the Bels."; Mol. Biol. Evol. 20:1917-1924(2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C;
 RA Inoue J.G., Miya M., Tsukamoto K., Nishida M.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB046485; BAB87156.1; -.
 KW Mitochondrion.
 FT NON TER 10 10
 SQ SEQUENCE 10 AA; 1293 MW; 356FAE29C682DB47 CRC64;

Query Match 30.7%; Score 23; DB 2; Length 10;
 Best Local Similarity 66.7%; Pred. No. 3.5e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NPYSAP 7
 |||||
 Db 2 NPYVMF 7

RESULT 15

BAB87164 ID BAB87164 PRELIMINARY; PRT; 10 AA.
 AC BAB87164;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE NADH dehydrogenase subunit 2 (Fragment).
 GN ND2.
 OS Eurypharynx pelecanoides (pelican eel).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes;
 OC Eurypharyngidae; Eurypharynx.
 OX NCBI_TaxID=55117;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=D;
 RA Inoue J.G., Miya M., Tsukamoto K., Nishida M.;
 RT "Evolution of the Deep-Sea Gulper Bel Mitochondrial Genomes: Large-
 RL Scale Gene Rearrangements Originated Within the Bels."; Mol. Biol. Evol. 20:1917-1924(2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=D;
 RA Inoue J.G., Miya M., Tsukamoto K., Nishida M.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB046485; BAB87164.1; -.
 KW Mitochondrion.
 FT NON TER 10 10
 SQ SEQUENCE 10 AA; 1293 MW; 356FAE29C682DB47 CRC64;

RL Mol. Biol. Evol. 20:1917-1924(2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=D;
 RA Inoue J.G., Miya M., Tsukamoto K., Nishida M.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB046489; BAB87164.1; -.
 KW Mitochondrion.
 FT NON TER 10 10
 SQ SEQUENCE 10 AA; 1293 MW; 356FAE29C682DB47 CRC64;

Query Match 30.7%; Score 23; DB 2; Length 10;
 Best Local Similarity 66.7%; Pred. No. 3.5e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NPYSAP 7
 |||||
 Db 2 NPYVMF 7

Search completed: November 14, 2004, 13:16:22
 Job time : 101 secs

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OM protein - protein search, using sw model

Run on: November 14, 2004, 13:03:52 ; Search time 18.3333 Seconds
(without alignments)
78.723 Million cell updates/sec

Title: US-09-831-253F-4

Perfect score: 75

Sequence: 1 SNPYSAFQVDIIIVDI 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79: *
1: piri: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	33.3	11	2 S00616	parasporal crystal
2	23	30.7	13	2 A54326	glandular kallikre
3	23	30.7	14	2 B44854	L-2,4-diaminobuty
4	22	29.3	12	2 A61360	vespakinin M - hor
5	22	29.3	15	2 PS0185	27K protein A 3.4/
6	22	29.3	15	2 A61612	allatostatin - tob
7	22	29.3	15	2 G24417	interphotoreceptor
8	21	28.0	11	2 PT0229	Ig heavy chain CDR
9	21	28.0	12	2 S36899	ribosomal protein
10	21	28.0	13	2 PC2369	unidentified 85K p
11	21	28.0	15	2 PA0061	protein QF200039 -
12	21	28.0	15	2 S29174	D-galactose-bindin
13	20	26.7	9	2 S10784	enamelin i - bovin
14	20	26.7	14	2 A59018	MUC1 enhancer bind
15	20	26.7	15	2 S08209	hypothetical prote
16	20	26.7	15	2 PQ0778	NADH2 dehydrogenas
17	19	25.3	9	2 S36898	ribosomal protein
18	19	25.3	11	2 A40795	glycoprotein H-a -
19	19	25.3	13	2 S65612	tubulin alpha-chai
20	19	25.3	13	2 G22565	R-phycoerythrin ga
21	19	25.3	13	2 PQ0700	unidentified 6.3/4
22	19	25.3	14	2 A28018	very late antigen-
23	19	25.3	14	2 S07768	soluble hydrogenas
24	18	24.0	8	2 D47393	neuropeptide calla
25	18	24.0	11	2 PT0250	Ig heavy chain CRD
26	18	24.0	12	2 S70344	amine oxidase (cop
27	18	24.0	13	2 B20907	Ig kappa-1 chain J
28	18	24.0	14	2 S29209	avenin alpha-2 - o
29	18	24.0	14	2 T46634	acyl carrier prote

30	18	24.0	14	2 B56884	Pax-QNR, long form
31	18	24.0	15	2 PH1365	Ig heavy chain DJ
32	18	24.0	15	2 S62641	porphobilinogen sy
33	18	24.0	15	2 PT0090	alpha-glucosidase
34	18	24.0	15	4 I38335	hypothetical TEL/M
35	17	22.7	8	2 I49404	prealbumin - weste
36	17	22.7	9	2 JQ0914	MHC class I histoc
37	17	22.7	10	2 PA0050	protein QA100052 -
38	17	22.7	10	2 C39111	Ig heavy chain C x
39	17	22.7	10	2 B33710	ornithine decarbox
40	17	22.7	12	2 S63123	proton-translocati
41	17	22.7	12	2 PH0771	T-cell receptor be
42	17	22.7	12	2 I40663	bma protein - Clos
43	17	22.7	13	2 S47361	T-cell antigen rec
44	17	22.7	14	2 S21247	H+-transporting tw
45	17	22.7	14	2 PS0371	hypothetical prote

ALIGNMENTS

RESULT 1

S00616

parasporal crystal protein, wax moth-specific - Bacillus thuringiensis (strain galleria N; Alternate names: delta-endotoxin; parasporal crystal protein positive chain C; Species: Bacillus thuringiensis C; Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004 C; Accession: S00616 R; Chestukhina, G.G.; Kostina, L.I.; Zalunin, I.A.; Khodova, O.M.; Stepanov, V.M. FEBS Lett. 232, 249-251, 1988 A; Title: Bacillus thuringiensis ssp. galleriae simultaneously produces two delta-endotoxins A; Reference number: S00615 A; Accession: S00616 A; Molecule type: protein A; Residues: 1-11 <CHE> A; Cross-references: UNIPROT:Q7M154 C; Comment: This toxin is effective against the larvae of Galleria mellonella (greater wax moth); Superfamily: parasporal crystal protein C; Keywords: delta-endotoxin

Query Match 33.3%; Score 25; DB 2; Length 11;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	SNPYS	5
Db	5	NNPYS	9

RESULT 2

A54326

glandular kallikrein-1 - human (fragment) C; Species: Homo sapiens (man) C; Date: 29-Aug-1994 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995 C; Accession: A54326 R; Riegman, P.H.; Vlietstra, R.J.; van der Korput, H.A.; Romijn, J.C.; Trapman, J. Mol. Cell. Endocrinol. 76, 181-190, 1991 A; Title: Identification and androgen-regulated expression of two major human glandular A; Reference number: A54326; MUID:92324494; PMID:1726490 A; Accession: A54326 A; Status: preliminary; not compared with conceptual translation A; Molecule type: nucleic acid A; Residues: 1-13 <RIE> A; Experimental source: prostate A; Note: sequence extracted from NCBI backbone (NCBI:P108060)

Query Match 30.7%; Score 23; DB 2; Length 13;
Best Local Similarity 80.0%; Pred. No. 6.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	SNPYS	5
Db	2	SHPYS	6

RESULT 3
B44854
L-2,4-diaminobutyrate decarboxylase (EC 4.1.1.-) - *Vibrio alginolyticus* (fragment)
C:Species: *Vibrio alginolyticus*
C:Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: B44854, B41817
R:Yamamoto, S.; Tsunaka, Y.; Tougou, K.; Shinoda, S.
J. Gen. Microbiol. 138, 1461-1465, 1992
A:Title: Purification and characterization of L-2,4-diaminobutyrate decarboxylase from *V. alginolyticus*
A:Reference number: A44854; MUID:92381494; PMID:1512577
A:Accession: B44854
A:Molecule type: protein
A:Residues: 1-14 <YAM>
A:Cross-references: UNIPROT:Q9R518
A:Note: sequence extracted from NCBI backbone (NCBIP:112332)
C:Keywords: carbon-carbon lyase; carboxy-lyase

Query Match 30.7%; Score 23; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 7.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 SAFOVD 10
: : : :
Db 2 TAFEVD 7

RESULT 4
A61360
vespakinin M - hornet (*Vespa mandarinia*)
C:Species: *Vespa mandarinia*
C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
C:Accession: A61360
R:Kishimura, H.; Yasuhara, T.; Yoshida, H.; Nakajima, T.
Chem. Pharm. Bull. 24, 2896-2897, 1976
A:Title: Vespakinin-M, a novel bradykinin analogue containing hydroxyproline, in the venom of *Vespa mandarinia*
A:Reference number: A61360; MUID:77114342; PMID:1017116
A:Accession: A61360
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-12 <KIS>
A:Cross-references: UNIPROT:Q7M3T3
A:Superfamily: unassigned animal peptides
C:Keywords: hydroxyproline; venom
F:4/Modified site: 4-hydroxyproline (Pro) #status experimental

Query Match 29.3%; Score 22; DB 2; Length 12;
Best Local Similarity 42.9%; Pred. No. 9.4e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 YSAFQVD 10
: : : :
Db 6 FSPFRID 12

RESULT 5
PS0185
27K protein A 3.4/5 - rice (fragment)
C:Species: *Oryza sativa* (rice)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 24-Feb-1995
C:Accession: PS0185
R:Kamo, M.; Tsugita, A.
submitted to JIPID, June 1991
A:Reference number: PS0184
A:Accession: PS0185
A:Molecule type: protein
A:Residues: 1-15 <KAM>

Query Match 29.3%; Score 22; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

us-09-831-253f-4.closed.rpr

QY 8 QVDIIVDI 15
: : : :
Db 1 QXEYIVDV 8

RESULT 6
A61612
allatostatin - tobacco hornworm
C:Species: *Manduca sexta* (tobacco hornworm)
C:Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C:Accession: A61612
R:Kramer, S.J.; Toschi, A.; Miller, C.A.; Kataoka, H.; Quistad, G.B.; Li, J.P.; Carney, Proc. Natl. Acad. Sci. U.S.A. 88, 9458-9462, 1991
A:Title: Identification of an allatostatin from the tobacco hornworm *Manduca sexta*.
A:Reference number: A61612; MUID:92052112; PMID:1946359
A:Accession: A61612
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <KRA>
A:Cross-references: UNIPROT:P42559
A:Keywords: neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 29.3%; Score 22; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NPYSAP 7
: : : :
Db 10 NPISCF 15

RESULT 7
G24417
interphotoreceptor retinoid-binding protein - hamster (fragment)
N:Alternate names: interstitial retinol-binding protein
C:Species: *Cricetinae* gen. sp. (hamster)
C:Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 09-Jul-2004
C:Accession: G24417
R:Fong, S.L.; Cook, R.G.; Alvarez, R.A.; Liou, G.I.; Landers, R.A.; Bridges, C.D.B. FEBS Lett. 205, 309-312, 1986
A:Title: N-terminal sequence homologies in interstitial retinol-binding proteins from 10 species of *Cricetinae*
A:Reference number: A91365; MUID:86301171; PMID:3743780
A:Accession: G24417
A:Molecule type: protein
A:Residues: 1-15 <FON>
A:Cross-references: UNIPROT:P12665

Query Match 29.3%; Score 22; DB 2; Length 15;
Best Local Similarity 33.3%; Pred. No. 1.2e+03;
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 7 FQVDIIVDI 15
: : : :
Db 7 FQPSLVLDL 15

RESULT 8
PT0229
IG heavy chain CDR3 region (clone 1-115) - human (fragment)
C:Species: *Homo sapiens* (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0229
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G. J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0229
A:Molecule type: DNA
A:Residues: 1-11 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 28.0%; Score 21; DB 2; Length 11;
 Best Local Similarity 38.5%; Pred. No. 1.3e+03;
 Matches 5; Conservative 2; Mismatches 2; Indels 4; Gaps 1;

QY 2 NPYSAFQVDIIVD 14
 |||||
 Db 2 NPY-----YDILTE 10

RESULT 9

S36899
 ribosomal protein S6 - Mycobacterium bovis (fragment)

C;Species: Mycobacterium bovis
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Jan-1995
 C;Accession: S36899
 R;Ohara, N.; Kimura, M.; Higashi, Y.; Yamada, T.
 FEBS Lett. 331, 9-14, 1993
 A;Title: Isolation and amino acid sequence of the 30S ribosomal protein S19 from Mycobacterium bovis
 A;Reference number: S36887; MUID:94009653; PMID:8405418
 A;Accession: S36899
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-12 <OHA>
 C;Keywords: protein biosynthesis; ribosome

Query Match 28.0%; Score 21; DB 2; Length 12;
 Best Local Similarity 50.0%; Pred. No. 1.4e+03;
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 PYSAFQVD 10
 |||||
 Db 3 PYEIMVVD 10

RESULT 10

PC2369
 unidentified 85K protein [imported] - Bacillus cereus (strain ts-4) (fragment)
 C;Species: Bacillus cereus
 C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
 C;Accession: PC2369
 R;Matsuno, K.; Miyamoto, T.; Yamaguchi, K.; Sayed, M.A.; Kajiwara, T.; Hatanoto, S.
 Biosci. Biotechnol. Biochem. 59, 231-235, 1995
 A;Title: Identification of DNA-binding proteins changed after induction of sporulation in Bacillus cereus
 A;Reference number: PC2369; MUID:95218265; PMID:7766022
 A;Accession: PC2369
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-13 <MAS>
 A;Cross-references: UNIPROT:Q7MOL4

Query Match 28.0%; Score 21; DB 2; Length 13;
 Best Local Similarity 50.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAF 7
 |||||
 Db 8 NPWAKF 13

RESULT 11

PA0061
 protein OF200039 - fungus (Fusarium sporotrichioides) (fragment)
 C;Species: Fusarium sporotrichioides
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
 C;Accession: PA0061
 R;Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Taugita, A.
 submitted to JIPID, October 1994
 A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides
 A;Reference number: PA0061
 A;Accession: PA0061
 A;Molecule type: protein
 A;Residues: 1-15 <CHO>
 A;Cross-references: UNIPROT:Q7MAY2

Query Match 28.0%; Score 21; DB 2; Length 15;
 Best Local Similarity 50.0%; Pred. No. 1.8e+03;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 SAFQVDIIVD 14
 :|||
 Db 3 TAAQVAIVKD 12

RESULT 12

S29174
 D-galactose-binding lectin III - Axinella polypoides (fragment)
 C;Species: Axinella polypoides
 C;Date: 19-Mar-1997 #sequence_revision 14-Nov-1997 #text_change 09-Jul-2004
 C;Accession: S29174
 R;Buck, F.; Luth, C.; Strupat, K.; Bretting, H.
 Biochim. Biophys. Acta 1159, 1-8, 1992
 A;Title: Comparative investigations on the amino-acid sequences of different isolectins
 A;Reference number: S29172; MUID:93003351; PMID:1390906
 A;Accession: S29174
 A;Molecule type: protein
 A;Residues: 1-15 <BUC>
 A;Cross-references: UNIPROT:P28588

Query Match 28.0%; Score 21; DB 2; Length 15;
 Best Local Similarity 20.0%; Pred. No. 1.8e+03;
 Matches 3; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 SNPYSAFQVDIIVDI 15
 :|||
 Db 1 ASPXENYQXYIILN 15

RESULT 13

S10784
 enamelin i - bovine (fragment)
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
 C;Accession: S10784
 R;Strawich, E.; Glincher, M.J.
 Eur. J. Biochem. 191, 47-56, 1990
 A;Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is also
 A;Reference number: S10780; MUID:90336641; PMID:2379503
 A;Accession: S10784
 A;Molecule type: protein
 A;Residues: 1-9 <STR>
 A;Cross-references: UNIPROT:Q7M2M7
 C;Keywords: enamel; phosphoprotein

Query Match 26.7%; Score 20; DB 2; Length 9;
 Best Local Similarity 60.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 PYSAF 7
 |||||
 Db 2 PYDGF 6

RESULT 14

A59018
 MUC1 enhancer binding protein 70K chain MUC1EBP-70 - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 08-May-1998
 C;Accession: A59018
 R;Abe, M.; Smith, C.J.; Larson, C.J.
 submitted to the Protein Sequence Database, May 1998
 A;Description: Involvement of "Ku-like" proteins in the transcription of MUC1/DF3, a
 A;Reference number: A59018
 A;Accession: A59018
 A;Molecule type: protein
 A;Residues: 1-14 <ABE>
 A;Experimental source: breast cancer cell line MCF-7

A;Note: 3-Val was also found
C;Keywords: DNA binding, heterodimer

Query Match 26.7%; Score 20; DB 2; Length 14;
Best Local Similarity 33.3%; Pred. No. 2.5e+03;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 SNPYSAFQV 9
Db 2 SQIYGSYQI 10

RESULT 15

S08209
hypothetical protein 2 - garden pea
N;Alternate names: phytochrome
C;Species: Pisum sativum (garden pea)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Sep-1997
C;Accession: S08209
P;Sato, N.
Plant Mol. Biol. 11, 697-710, 1988
A;Title: Nucleotide sequence and expression of the phytochrome gene in Pisum sativum: di
A;Reference number: S06856
A;Accession: S08209
A;Molecule type: DNA
A;Residues: 1-15 <SAT>
A;Cross-references: EMBL:X14077; NID:g20836; PID:g20838
C;Genetics:
A;Gene: phy

Query Match 26.7%; Score 20; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NPY 4
Db 12 NPY 14

Search completed: November 14, 2004, 13:17:22
Job time : 18.3333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2004, 12:55:26 ; Search time 93.3333 Seconds
(without alignments)
57.653 Million cell updates/sec

Title: US-09-831-253F-4

Perfect score: 75

Sequence: 1 SNFYSAFQVDIIVIDI 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 605831

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Genesep_23Sep04:*

1: Genesep1990s:*

2: Genesep1990s:*

3: Genesep2000s:*

4: Genesep2001s:*

5: Genesep2002s:*

6: Genesep2003as:*

7: Genesep2003bs:*

8: Genesep2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	75	100.0	15	3 AAY92948	Aay92948 Transform
2	75	100.0	15	3 AAY93066	Aay93066 Transform
3	65	86.7	14	3 AAY92951	Aay92951 Transform
4	65	86.7	14	3 AAY93099	Aay93099 Transform
5	53	70.7	15	3 AAY93059	Aay93059 Transform
6	47	62.7	15	3 AAY93067	Aay93067 Transform
7	31	41.3	15	5 ABP55430	Abp55430 Human bre
8	31	41.3	15	6 ABR75594	Abp75594 Liver res
9	31	41.3	15	7 ADN07473	Adn07473 Liver res
10	30	40.0	15	8 ADL70819	Adl70819 PTP1B pho
11	30	40.0	15	8 ADL70905	Adl70905 PTP1B pho
12	30	40.0	15	8 ADL70907	Adl70907 PTP1B pho
13	30	40.0	15	8 ADL70906	Adl70906 PTP1B pho
14	30	40.0	15	8 ADL70908	Adl70908 PTP1B pho
15	29	38.7	15	4 AAG66403	Agag66403 Human vas
16	28	37.3	10	5 ABP47086	Abp47086 Human BLY
17	28	37.3	10	7 ADG97913	Adg97913 scFV VHCD
18	28	37.3	13	3 AAB10012	Aab10012 H. pylori
19	28	37.3	13	4 AAB86092	Aab86092 H. pylori
20	28	37.3	13	4 AAB86060	Aab86060 H. pylori
21	28	37.3	15	3 AAY93058	Aay93058 Transform
22	27	36.0	9	4 AAB98867	Aab98867 HIV gp120
23	27	36.0	9	4 AAB98868	Aab98868 HIV gp120
24	27	36.0	9	4 AAB98866	Aab98866 HIV gp120
25	27	36.0	10	7 ADH48572	Adh48572 ATP-depen

ALIGNMENTS

RESULT 1

AAV92948

ID AAY92948 standard; peptide; 15 AA.

XX AAY92948;

XX

DT 08-NOV-2000 (first entry)

XX

DE Transforming growth factor inhibitory peptide #4.

XX

KW Hepatotrophic; antagonist; transforming growth factor betai; TGF-b1; competitive inhibition; collagen synthesis stimulation inhibitor; liver; extracellular matrix degradation inhibitor; mimetope; cirrhosis.

XX Homo sapiens.

XX WO200031135-A1.

XX

PD 02-JUN-2000.

XX

XX 23-NOV-1999; 99WO-ES000375.

XX

XX 24-NOV-1998; 98ES-00002465.

XX

(CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.

XX Ezquerro Saenz JJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;

XX Borras Cuesta F;

XX WPI; 2000-411935/35.

XX

PT Peptides that antagonize binding of transforming growth factor betai, useful for treatment of liver disease, especially cirrhosis, are partial sequences of the factor or its receptors.

XX

PS Claim 5; Page 81; 86pp; Spanish.

XX

CC The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betai (TGF-b1) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-b1 and/or its receptors. Peptides AAY92948-Y9133 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-b1 to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetopes and/or DNA (or expression systems) encoding the peptides are used for treatment of liver disease, specifically cirrhosis

```

XX SQ Sequence 15 AA;
Query Match 100.0%; Score 75; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNPYSAFQVDIIIVDI 15
Db 1 SNPYSAFQVDIIIVDI 15

RESULT 2
AAY93066
ID AAY93066 standard; peptide; 15 AA.
XX AC AAY93066;
XX DT 08-NOV-2000 (first entry)
XX DE Transforming growth factor inhibitory peptide P106.
XX KW Hepatotrophic; antagonist; transforming growth factor betal; TGF-b1;
KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX OS Rattus sp.
XX PN WO200031135-A1.
XX PD 02-JUN-2000.
XX PF 23-NOV-1999; 99WO-ES000375.
XX PR 24-NOV-1998; 98ES-00002465.
XX PS Claim 8; Page 82; 86pp; Spanish.
XX PA (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
XX PI Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
PI Borrás Cuesta F;
XX DR WO200031135/35.
XX PT Peptides that antagonize binding of transforming growth factor betal,
PT useful for treatment of liver disease, especially cirrhosis, are partial
PT sequences of the factor or its receptors.
XX SQ Sequence 14 AA;
Query Match 86.7%; Score 65; DB 3; Length 14;
Best Local Similarity 85.7%; Pred. No. 2.8e-05;
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNPYSAFQVDIIIVD 14
Db 1 SNPYSAFQVDIIITD 14

RESULT 4
AAY93099
ID AAY93099 standard; peptide; 14 AA.
XX AC AAY93099;
XX DT 08-NOV-2000 (first entry)
XX DE Transforming growth factor inhibitory peptide P145.
XX KW Hepatotrophic; antagonist; transforming growth factor betal; TGF-b1;
KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.

```


OS Homo sapiens.
 PN WO2000031135-A1.
 XX
 PD 02-JUN-2000.
 XX
 XX 23-NOV-1999; 99WO-ES000375.
 XX
 XX 24-NOV-1998; 98ES-00002465.
 XX
 XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
 XX
 XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
 PI Borras Cuesta F;
 XX WPI; 2000-411935/35.
 XX
 XX Peptides that antagonize binding of transforming growth factor betal,
 PT useful for treatment of liver disease, especially cirrhosis, are partial
 PT sequences of the factor or its receptors.
 XX
 XX Disclosure; Page 31; 86pp; Spanish.
 XX
 XX The invention relates to synthetic peptides that antagonise the binding
 CC of transforming growth (TGF) factor betal (TGF-b1) to its receptor in
 CC vivo which have partial amino acid sequences identical, or similar, with
 CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
 CC examples of the peptides of the invention. The peptides act by
 CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
 CC they are inhibitors of stimulation of collagen synthesis in liver cells
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
 CC expression systems) encoding the peptides are used for treatment of liver
 CC disease, specifically cirrhosis
 XX
 XX Sequence 14 AA;
 SQ
 Query Match 86.7%; Score 65; DB 3; Length 14;
 Best Local Similarity 85.7%; Pred. No. 2.8e-05;
 Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 SNPYSAFQVDIIIVD 14
 Db 1 SNPYSAFQVDITD 14
 |||||
 RESULT 5
 AAY93059
 ID AAY93059 standard; peptide; 15 AA.
 XX
 AC AAY93059;
 XX
 DT 08-NOV-2000 (first entry)
 XX
 DE Transforming growth factor inhibitory peptide P105.
 XX
 KW Hepatotropic; antagonist; transforming growth factor betal; TGF-b1;
 KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
 KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
 XX
 OS Rattus sp.
 XX
 PN WO2000031135-A1.
 XX
 PD 02-JUN-2000.
 XX
 XX 23-NOV-1999; 99WO-ES000375.
 XX
 XX 24-NOV-1998; 98ES-00002465.
 XX
 XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
 XX
 XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
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 XX Disclosure; Page 31; 86pp; Spanish.
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 XX The invention relates to synthetic peptides that antagonise the binding
 CC of transforming growth (TGF) factor betal (TGF-b1) to its receptor in
 CC vivo which have partial amino acid sequences identical, or similar, with
 CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
 CC examples of the peptides of the invention. The peptides act by
 CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
 CC they are inhibitors of stimulation of collagen synthesis in liver cells
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
 CC expression systems) encoding the peptides are used for treatment of liver
 CC disease, specifically cirrhosis
 XX
 XX Sequence 14 AA;
 SQ
 Query Match 86.7%; Score 65; DB 3; Length 14;
 Best Local Similarity 85.7%; Pred. No. 2.8e-05;
 Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 SNPYSAFQVDIIIVD 14
 Db 1 SNPYSAFQVDITD 14
 |||||
 RESULT 5
 AAY93059
 ID AAY93059 standard; peptide; 15 AA.
 XX
 AC AAY93059;
 XX
 DT 08-NOV-2000 (first entry)
 XX
 DE Transforming growth factor inhibitory peptide P105.
 XX
 KW Hepatotropic; antagonist; transforming growth factor betal; TGF-b1;
 KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
 KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
 XX
 OS Rattus sp.
 XX
 PN WO2000031135-A1.
 XX
 PD 02-JUN-2000.
 XX
 XX 23-NOV-1999; 99WO-ES000375.
 XX
 XX 24-NOV-1998; 98ES-00002465.
 XX
 XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
 XX
 XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
 PI Borras Cuesta F;
 XX WPI; 2000-411935/35.
 XX
 XX Peptides that antagonize binding of transforming growth factor betal,
 PT useful for treatment of liver disease, especially cirrhosis, are partial
 PT sequences of the factor or its receptors.
 XX
 XX Disclosure; Page 31; 86pp; Spanish.
 XX
 XX The invention relates to synthetic peptides that antagonise the binding
 CC of transforming growth (TGF) factor betal (TGF-b1) to its receptor in
 CC vivo which have partial amino acid sequences identical, or similar, with
 CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
 CC examples of the peptides of the invention. The peptides act by
 CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
 CC they are inhibitors of stimulation of collagen synthesis in liver cells
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
 CC expression systems) encoding the peptides are used for treatment of liver
 CC disease, specifically cirrhosis
 XX
 XX Sequence 14 AA;
 SQ
 Query Match 86.7%; Score 65; DB 3; Length 14;
 Best Local Similarity 85.7%; Pred. No. 2.8e-05;
 Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 SNPYSAFQVDIIIVD 14
 Db 1 SNPYSAFQVDITD 14
 |||||

PI Borras Cuesta F;
 XX
 DR WPI; 2000-411935/35.
 XX
 XX Peptides that antagonize binding of transforming growth factor betal,
 PT useful for treatment of liver disease, especially cirrhosis, are partial
 PT sequences of the factor or its receptors.
 XX
 XX Disclosure; Page 28; 86pp; Spanish.
 XX
 XX The invention relates to synthetic peptides that antagonise the binding
 CC of transforming growth (TGF) factor betal (TGF-b1) to its receptor in
 CC vivo which have partial amino acid sequences identical, or similar, with
 CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
 CC examples of the peptides of the invention. The peptides act by
 CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
 CC they are inhibitors of stimulation of collagen synthesis in liver cells
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
 CC expression systems) encoding the peptides are used for treatment of liver
 CC disease, specifically cirrhosis
 XX
 XX Sequence 15 AA;
 SQ
 Query Match 70.7%; Score 53; DB 3; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.0057;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 SNPYSAFQVD 10
 Db 6 SNPYSAFQVD 15
 |||||
 RESULT 6
 AAY93067
 ID AAY93067 standard; peptide; 15 AA.
 XX
 AC AAY93067;
 XX
 DT 08-NOV-2000 (first entry)
 XX
 DE Transforming growth factor inhibitory peptide P107.
 XX
 KW Hepatotropic; antagonist; transforming growth factor betal; TGF-b1;
 KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
 KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
 XX
 OS Rattus sp.
 XX
 PN WO2000031135-A1.
 XX
 PD 02-JUN-2000.
 XX
 XX 23-NOV-1999; 99WO-ES000375.
 XX
 XX 24-NOV-1998; 98ES-00002465.
 XX
 XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
 XX
 XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
 PI Borras Cuesta F;
 XX WPI; 2000-411935/35.
 XX
 XX Peptides that antagonize binding of transforming growth factor betal,
 PT useful for treatment of liver disease, especially cirrhosis, are partial
 PT sequences of the factor or its receptors.
 XX
 XX Disclosure; Page 28; 86pp; Spanish.
 XX
 XX The invention relates to synthetic peptides that antagonise the binding
 CC of transforming growth (TGF) factor betal (TGF-b1) to its receptor in
 CC vivo which have partial amino acid sequences identical, or similar, with
 CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
 CC examples of the peptides of the invention. The peptides act by
 CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
 CC they are inhibitors of stimulation of collagen synthesis in liver cells
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
 CC expression systems) encoding the peptides are used for treatment of liver
 CC disease, specifically cirrhosis
 XX
 XX Sequence 15 AA;
 SQ
 Query Match 70.7%; Score 53; DB 3; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.0057;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 SNPYSAFQVD 10
 Db 6 SNPYSAFQVD 15
 |||||

CC those of TGF- β 1 and/or its receptors. Peptides AAY92945-Y93133 represent
 CC examples of the peptides of the invention. The peptides act by
 CC competitive inhibition of the binding of TGF- β 1 to its receptors, e.g.
 CC they are inhibitors of stimulation of collagen synthesis in liver cells
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
 CC expression systems) encoding the peptides are used for treatment of liver
 CC disease, specifically cirrhosis
 XX
 XX Sequence 15 AA;

Query Match 62.7%; Score 47; DB 3; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.078;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AFOVDIIVDI 15
 DB 1 AFOVDIIVDI 10
 |||||

RESULT 7
 ABP55430
 ID ABP55430 standard; peptide; 15 AA.
 XX AC
 XX ABP55430;

XX 04-FEB-2003 (first entry)

XX Human breast susceptible gene protein 10.45 N-terminal peptide SEQ:7.
 DE Human;
 XX Human; breast susceptible gene coded protein 10.45; tumour;
 KW embryonic development deformity.
 XX Homo sapiens.

OS

XX CN1342702-A.

XX 03-APR-2002.

XX 12-SEP-2000; 2000CN-00125173.

XX 12-SEP-2000; 2000CN-00125173.

XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.

PI Mao Y, Xie Y;

XX WPI; 2002-529778/57.

XX A novel human breast susceptible gene coded protein 10.45 polypeptide,
 PT and the polynucleotide encoding it, useful for treating several diseases
 PT e.g. embryonic development deformity and tumors.

XX Example 5; Page 20 (Disclosure); 34pp; Chinese.

XX The present invention describes human breast susceptible gene coded
 CC protein 10.45 (I). Also described is a process for preparing (I) using
 CC DNA recombination techniques. (I) can be used for treating several
 CC diseases e.g. embryonic development deformity and tumors. The present
 CC sequence represents the N-terminal peptide of (I), which is used in an
 CC example from the present invention
 XX

XX Sequence 15 AA;

Query Match 41.3%; Score 31; DB 5; Length 15;
 Best Local Similarity 45.5%; Pred. No. 84;
 Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 NPYSAFQVDII 12
 DB 5 SPYFRVNVII 15
 :||| |::|

RESULT 8

ABR75594

ID ABR75594 standard; peptide; 15 AA.

XX AC ABR75594;

XX 28-AUG-2003 (first entry)

XX DE Liver response-associated protein isoform (LRPI) peptide SEQ ID NO:332.

XX KW Biomarker; liver response; liver response-associated protein isoform;
 KW LRPI; liver response-associated feature; LRF.

XX OS Synthetic.

XX WO2003038444-A2.

XX 08-MAY-2003.

XX 31-OCT-2002; 2002WO-US034847.

XX 31-OCT-2001; 2001US-0335964P.

XX (PFIZ) PFIZER PROD INC.

XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX PI Amacher DE, Fasulo LM, Herath HWAC, Holt GD, Stiger TR;

XX WPI; 2003-430566/40.

XX Screening, diagnosing, staging or identifying subject at risk of
 PT developing, liver response, or monitoring effect of therapy on liver
 PT response, by detecting liver response-associated protein isoforms in
 PT subject sample.

XX Claim 1; Page 66; 256pp; English.

XX The present invention describes a method (M1) for screening or diagnosing
 CC a liver response in a subject, determining the stage or severity of a
 CC liver response in a subject, identifying a subject at risk of developing
 CC liver response, or monitoring the effect of therapy administered to a
 CC subject having liver response, involving detecting liver response-
 CC associated protein isoforms (LRPIs) (see the peptides given in ABR75395
 CC to ABR75806) in a test biological sample from the subject. Alternatively,
 CC screening or diagnosing a liver response in a subject, or monitoring the
 CC effect of a drug or therapy administered to a subject, involves
 CC contacting at least one oligonucleotide probe comprising 10 or more
 CC consecutive nucleotides complementary to a nucleotide sequence encoding
 CC an LRPI with RNA obtained from a biological sample from the subject or
 CC with cDNA copied from the RNA, where the contacting occurs under
 CC conditions that permit hybridisation of the probe to the nucleotide
 CC sequence if present, detecting hybridisation, if any, between the probe
 CC and the nucleotide sequence, and comparing the hybridisation, if any,
 CC detected in the above step, with the hybridisation detected in a control
 CC sample, or with a previously determined reference range. M1 is useful for
 CC screening or diagnosing a liver response in a subject, determining the
 CC stage or severity of a liver response in a subject, identifying a subject
 CC at risk of developing liver response, and monitoring the effect of
 CC therapy administered to a subject having liver response

XX Sequence 15 AA;

Query Match 41.3%; Score 31; DB 6; Length 15;
 Best Local Similarity 45.5%; Pred. No. 84;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 YSAFOVDIIVD 14
 DB 2 YFGSQDILID 12
 |::|

RESULT 9
 ADN07473

ID ADN07473 standard; peptide; 15 AA.
 XX AC ADN07473;
 XX DT 17-JUN-2004 (first entry)
 XX DE Liver response-associated feature LRF405 #3.
 XX KW liver response; liver response-associated protein isoform; LRPI;
 KW drug monitoring; therapy monitoring; liver response-associated feature;
 KW LRF.
 XX OS Homo sapiens.
 XX PN US2003228583-A1.
 XX PD 11-DEC-2003.
 XX PF 31-OCT-2002; 2002US-00285394.
 XX PR 31-OCT-2001; 2001US-0335964P.
 XX PA (AMAC/) AMACHER D E.
 PA (FASU/) FASULO L M.
 PA (HERA/) HERATH H M A C.
 PA (HOLT/) HOLT G D.
 PA (STIG/) STIGER T R.
 XX PI Amacher DE, Fasulo LM, Herath H MAC, Holt GD, Stiger TR;
 XX WPI; 2003-430566/40.
 XX Screening, diagnosing, staging or identifying subject at risk of
 PT developing, liver response, or monitoring effect of therapy on liver
 PT response, by detecting Liver Response-Associated Protein Isoforms in
 PT subject sample.
 XX Disclosure; SEQ ID NO 332; 75pp; English.
 CC The invention describes a method of screening (MI) or diagnosing a liver
 CC response in a subject, determining the stage or severity of a liver
 CC response in a subject, identifying a subject at risk of developing liver
 CC response, or monitoring the effect of therapy administered to a subject
 CC having liver response. The method involves detecting Liver Response-
 CC Associated Protein Isoforms (LRPIs) in a test biological sample from the
 CC subject, which has an activity or level indicative of a liver response.
 CC LRPIs are selected from any one of the compounds given in the
 CC specification e.g. LRPI-1.1, LRPI-2.1, LRPI-3.1 and LRPI-4.1.
 CC Alternatively, screening or diagnosing a liver response in a subject, or
 CC monitoring the effect of a drug or therapy administered to a subject,
 CC involves contacting at least one oligonucleotide probe comprising 10 or
 CC more consecutive nucleotides complementary to a nucleotide sequence
 CC encoding an LRPI with RNA obtained from a biological sample from the
 CC subject or with cDNA copied from the RNA, where the contacting occurs
 CC under conditions that permit hybridisation of the probe to the nucleotide
 CC sequence if present, detecting hybridisation, if any, between the probe
 CC and the nucleotide sequence, and comparing the hybridisation, if any,
 CC detected in the above step, with the hybridisation detected in a control
 CC sample, or with a previously determined reference range. The method is
 CC useful for screening or diagnosing a liver response in a subject,
 CC determining the stage or severity of a liver response in a subject,
 CC identifying a subject at risk of developing liver response, and
 CC monitoring the effect of therapy administered to a subject having liver
 CC response. This is the amino acid sequence of a liver response-associated
 CC feature (LRF) comprising one or more LRPI.
 XX SQ Sequence 15 AA;
 Query Match 41.3%; Score 31; DB 7; Length 15;
 Best Local Similarity 45.5%; Pred. No. 84;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 4 YSAFQVDIIVD 14

Db 2 YPGSQLDILID 12
 RESULT 10
 ADL70819
 ID ADL70819 standard; peptide; 15 AA.
 XX AC ADL70819;
 XX DT 03-JUN-2004 (first entry)
 XX DE PTP1B phosphopeptide, SEQ ID 17.
 XX KW Cytostatic; Antidiabetic; Anorectic; Antiinflammatory; Antimicrobial;
 KW Cardiant; Neuroprotective; Protein tyrosine phosphatase inhibitor;
 KW phosphopeptide; protein tyrosine phosphatase; cancer; diabetes; obesity;
 KW inflammation; multiple sclerosis; angiogenesis-dependent disease;
 KW infectious disease; appetite suppressor; congestive heart failure;
 KW neurodegenerative disease; ischaemia; demyelinating disease; PTP1B;
 KW protein tyrosine phosphatase 1B.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Modified-site 6
 FT /notes="Phosphotyrosine"
 XX PN WO2004020466-A1.
 XX PD 11-MAR-2004.
 XX PF 20-AUG-2003; 2003WO-BP050385.
 XX PR 29-AUG-2002; 2002EP-00019357.
 XX PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
 XX PI Hoofst Van Huijsduijn R, Walchli S, Arigoni F;
 XX WPI; 2004-269210/25.
 XX New phosphopeptides that inhibit protein tyrosine phosphatases, useful
 PT for manufacturing a medicament for preventing or treating e.g. cancer,
 PT diabetes, obesity, inflammation, multiple sclerosis or infectious
 PT diseases.
 XX Example 1; SEQ ID NO 17; 77pp; English.
 CC The present invention relates to phosphopeptides that inhibit protein
 CC tyrosine phosphatase. The phosphopeptides are useful as a medicament or
 CC for manufacturing a medicament for the treatment and/or prevention of
 CC cancer (i.e. stomach or intestinal cancer), diabetes and/or obesity,
 CC inflammation, multiple sclerosis, angiogenesis-dependent disease (e.g.
 CC solid cancer or metastatic cancer) or infectious disease (i.e.
 CC leishmaniasis), or as a suppressor of appetite. These may also be used
 CC for preventing or treating congestive heart failure, neurodegenerative
 CC diseases, ischaemic events of the brain or demyelinating diseases. The
 CC present sequence is one such phosphopeptide from protein tyrosine
 CC phosphatase 1B (PTP1B).
 XX SQ Sequence 15 AA;
 Query Match 40.0%; Score 30; DB 8; Length 15;
 Best Local Similarity 71.4%; Pred. No. 1.3e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 4 YSAFQVD 10
 Db 6 YNAYQVD 12
 RESULT 11

```

ADL70905
ID ADL70905 standard; peptide; 15 AA.
XX
AC ADL70905;
XX
DT 03-JUN-2004 (first entry)
XX
DE PTP1B phosphopeptide #19.
XX
XX Cytostatic; Antidiabetic; Anorectic; Antiinflammatory; Antimicrobial;
KW Cardiant; Neuroprotective; Protein tyrosine phosphatase inhibitor;
KW phosphopeptide; protein tyrosine phosphatase; cancer; diabetes; obesity;
KW inflammation; multiple sclerosis; angiogenesis-dependent disease;
KW infectious disease; appetite suppressor; congestive heart failure;
KW neurodegenerative disease; ischaemia; demyelinating disease; PTP1B;
KW protein tyrosine phosphatase 1B.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 12
XX /note= "Phosphotyrosine"
PN WO2004020466-A1.
XX
PD 11-MAR-2004.
XX
PF 20-AUG-2003; 2003WO-EP050385.
XX
PR 29-AUG-2002; 2002EP-00019357.
XX
PA (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
XX
PI Hooft Van Huijsduijn R, Walchli S, Arigoni F;
XX WPI; 2004-269210/25.
XX
XX New phosphopeptides that inhibit protein tyrosine phosphatases, useful
PT for manufacturing a medicament for preventing or treating e.g. cancer,
PT diabetes, obesity, inflammation, multiple sclerosis or infectious
PT diseases.
XX
PS Example 1; Fig 1; 77pp; English.
XX
CC The present invention relates to phosphopeptides that inhibit protein
CC tyrosine phosphatase. The phosphopeptides are useful as a medicament or
CC for manufacturing a medicament for the treatment and/or prevention of
CC cancer (i.e. stomach or intestinal cancer), diabetes and/or obesity,
CC inflammation, multiple sclerosis, angiogenesis-dependent disease (e.g.
CC solid cancer or metastatic cancer) or infectious disease (i.e.
CC leishmaniasis), or as a suppressor of appetite. These may also be used
CC for preventing or treating congestive heart failure, neurodegenerative
CC diseases, ischaemic events of the brain or demyelinating diseases. The
CC present sequence is one such phosphopeptide from protein tyrosine
CC phosphatase 1B (PTP1B).
XX
SQ Sequence 15 AA;
Query Match 40.0%; Score 30; DB 8; Length 15;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YSAFQVD 10
Db |:|:|
9 YNAYQVD 15

RESULT 13
ADL70906
ID ADL70906 standard; peptide; 15 AA.
XX
AC ADL70906;
XX
DT 03-JUN-2004 (first entry)
XX
DE PTP1B phosphopeptide #20.
XX
XX Cytostatic; Antidiabetic; Anorectic; Antiinflammatory; Antimicrobial;
KW Cardiant; Neuroprotective; Protein tyrosine phosphatase inhibitor;
KW phosphopeptide; protein tyrosine phosphatase; cancer; diabetes; obesity;
KW inflammation; multiple sclerosis; angiogenesis-dependent disease;
KW infectious disease; appetite suppressor; congestive heart failure;
KW neurodegenerative disease; ischaemia; demyelinating disease; PTP1B;
KW protein tyrosine phosphatase 1B.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 12
XX /note= "Phosphotyrosine"
PN WO2004020466-A1.
XX
PD 11-MAR-2004.
XX
PF 20-AUG-2003; 2003WO-EP050385.
XX
PR 29-AUG-2002; 2002EP-00019357.
XX
PA (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.
XX
PI Hooft Van Huijsduijn R, Walchli S, Arigoni F;
XX WPI; 2004-269210/25.
XX
XX New phosphopeptides that inhibit protein tyrosine phosphatases, useful
PT for manufacturing a medicament for preventing or treating e.g. cancer,
PT diabetes, obesity, inflammation, multiple sclerosis or infectious
PT diseases.
XX
PS Example 1; Fig 1; 77pp; English.
XX
CC The present invention relates to phosphopeptides that inhibit protein
CC tyrosine phosphatase. The phosphopeptides are useful as a medicament or
CC for manufacturing a medicament for the treatment and/or prevention of
CC cancer (i.e. stomach or intestinal cancer), diabetes and/or obesity,
CC inflammation, multiple sclerosis, angiogenesis-dependent disease (e.g.
CC solid cancer or metastatic cancer) or infectious disease (i.e.
CC leishmaniasis), or as a suppressor of appetite. These may also be used
CC for preventing or treating congestive heart failure, neurodegenerative
CC diseases, ischaemic events of the brain or demyelinating diseases. The
CC present sequence is one such phosphopeptide from protein tyrosine
CC phosphatase 1B (PTP1B).
XX
SQ Sequence 15 AA;
Query Match 40.0%; Score 30; DB 8; Length 15;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YSAFQVD 10
Db |:|:|
9 YNAYQVD 15

RESULT 12
ADL70907
ID ADL70907 standard; peptide; 15 AA.
XX
AC ADL70907;
XX
DT 03-JUN-2004 (first entry)
XX
DE PTP1B phosphopeptide #21.
XX

```

KW neurodegenerative disease; ischaemia; demyelinating disease; PTP1B;
 KW protein tyrosine phosphatase 1B.

OS Synthetic.

FH Key Location/Qualifiers
 FT Modified-site 9 /note= "Phosphotyrosine"
 FT Modified-site 12 /note= "Phosphotyrosine"

XX WO2004020466-A1.

XX 11-MAR-2004.

XX 20-AUG-2003; 2003WO-EP050385.

XX 29-AUG-2002; 2002EP-00019357.

XX (ISTP) ARS APPLIED RES SYSTEMS HOLDING NV.

XX Hoofst Van Huijsduijn R, Walchli S, Arigoni F;

XX WPI; 2004-269210/25.

XX New phosphopeptides that inhibit protein tyrosine phosphatases, useful
 PT for manufacturing a medicament for preventing or treating e.g. cancer,
 PT diabetes, obesity, inflammation, multiple sclerosis or infectious
 PT diseases.

XX Example 1; Fig 1; 77pp; English.

CC The present invention relates to phosphopeptides that inhibit protein
 CC tyrosine phosphatase. The phosphopeptides are useful as a medicament or
 CC for manufacturing a medicament for the treatment and/or prevention of
 CC cancer (i.e. stomach or intestinal cancer), diabetes and/or obesity,
 CC inflammation, multiple sclerosis, angiogenesis-dependent disease (e.g.
 CC solid cancer or metastatic cancer) or infectious disease (i.e.
 CC leishmaniasis), or as a suppressor of appetite. These may also be used
 CC for preventing or treating congestive heart failure, neurodegenerative
 CC diseases, ischaemic events of the brain or demyelinating diseases. The
 CC present sequence is one such phosphopeptide from protein tyrosine
 CC phosphatase 1B (PTP1B).

XX Sequence 15 AA;

Query Match 40.0%; Score 30; DB 8; Length 15;
 Best Local Similarity 71.4%; Pred. No. 1.3e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YSAFQVD 10

Db |.:|:|
 9 YNAYQVD 15

RESULT 14

ADL70908

ID ADL70908 standard; peptide; 15 AA.

XX ADL70908;

XX 03-JUN-2004 (first entry)

XX PTP1B phosphopeptide #22.

XX Cytostatic; Antidiabetic; Anorectic; Antiinflammatory; Antimicrobial;
 KW Cardiant; Neuroprotective; Protein tyrosine phosphatase inhibitor;
 KW phosphopeptide; protein tyrosine phosphatase; cancer; diabetes; obesity;
 KW inflammation; multiple sclerosis; angiogenesis-dependent disease;
 KW infectious disease; appetite suppressor; congestive heart failure;
 KW neurodegenerative disease; ischaemia; demyelinating disease; PTP1B;
 KW protein tyrosine phosphatase 1B.

XX Synthetic.

OS

FH Key Location/Qualifiers
 FT Modified-site 9 /note= "Phosphotyrosine"
 FT Modified-site 12 /note= "Phosphotyrosine"

XX WO2004020466-A1.

XX 11-MAR-2004.

XX 20-AUG-2003; 2003WO-EP050385.

XX 29-AUG-2002; 2002EP-00019357.

XX (ISTP) ARS APPLIED RES SYSTEMS HOLDING NV.

XX Hoofst Van Huijsduijn R, Walchli S, Arigoni F;

XX WPI; 2004-269210/25.

XX New phosphopeptides that inhibit protein tyrosine phosphatases, useful
 PT for manufacturing a medicament for preventing or treating e.g. cancer,
 PT diabetes, obesity, inflammation, multiple sclerosis or infectious
 PT diseases.

XX Example 1; Fig 1; 77pp; English.

CC The present invention relates to phosphopeptides that inhibit protein
 CC tyrosine phosphatase. The phosphopeptides are useful as a medicament or
 CC for manufacturing a medicament for the treatment and/or prevention of
 CC cancer (i.e. stomach or intestinal cancer), diabetes and/or obesity,
 CC inflammation, multiple sclerosis, angiogenesis-dependent disease (e.g.
 CC solid cancer or metastatic cancer) or infectious disease (i.e.
 CC leishmaniasis), or as a suppressor of appetite. These may also be used
 CC for preventing or treating congestive heart failure, neurodegenerative
 CC diseases, ischaemic events of the brain or demyelinating diseases. The
 CC present sequence is one such phosphopeptide from protein tyrosine
 CC phosphatase 1B (PTP1B).

XX Sequence 15 AA;

Query Match 40.0%; Score 30; DB 8; Length 15;
 Best Local Similarity 71.4%; Pred. No. 1.3e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YSAFQVD 10

Db |.:|:|
 9 YNAYQVD 15

RESULT 15

AAG66403

ID AAG66403 standard; peptide; 15 AA.

XX AAG66403;

XX 16-OCT-2001 (first entry)

XX Human vascular epithelium cadherin 54 peptide fragment.

XX Human; vascular epithelium cadherin 54; cancer; HIV infection; anti-HIV;
 KW cytotostatic.

XX Homo sapiens.

OS CN1296963-A.

PN 30-MAY-2001.

XX 22-NOV-1999; 99CN-00124058.

XX 22-NOV-1999; 99CN-00124058.

XX

PA (SHAN-) SHANGHAI BORONG GENE DEV CO LTD.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2001-483895/53.
XX
PT Human vascular epithelium cadherin 54 and polynucleotide for coding said
XX polypeptide.
PT
PS Example 6; Page 18 (Disclosure); 34pp; Chinese.
XX
CC The present invention relates to human vascular epithelium cadherin 54
CC and coding sequence (see AAH75794 and AAG66401). Vascular epithelium
CC cadherin 54 is useful for treating diseases e.g. cancer and HIV
CC infection. The present sequence is a peptide of vascular epithelium
CC cadherin 54, which was used in example from the present invention. Note:
CC the present sequence is the SEQ ID 7 shown on page 18 of the disclosure.
CC This sequence differs from the SEQ ID 7 shown in the sequence listing
CC (see AAG66402)
XX
SQ Sequence 15 AA;

Query Match 38.7%; Score 29; DB 4; Length 15;
Best Local Similarity 30.8%; Pred. NO. 2e+02;
Matches 4; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 SNPYSAFQVDIIV 13
| | : : : : :
Db 3 SVPYTEWELSVII 15

Search completed: November 14, 2004, 13:11:15
Job time : 94.3333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2004, 13:16:33 ; Search time 79.6667 Seconds
(without alignments)
66.619 Million cell updates/sec

Title: US-09-831-253F-4

Perfect score: 75

Sequence: 1 SNPSAFQVDIIVDI 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1568699 seqs, 353819137 residues

Total number of hits satisfying chosen parameters: 238011

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	41.3	15	14	US-10-285-394-332
2	28	37.3	10	10	US-09-880-748-3097
3	28	37.3	10	14	US-10-293-418-3097
4	28	37.3	13	11	US-09-842-776A-30
5	27	36.0	9	14	US-10-084-813-973
6	27	36.0	9	14	US-10-084-813-974
7	27	36.0	11	10	US-10-084-813-975
8	27	36.0	11	10	US-09-880-748-2839
9	27	36.0	11	14	US-10-293-418-2839
10	27	36.0	12	14	US-10-084-813-1019
11	27	36.0	12	14	US-10-084-813-1020
12	27	36.0	12	14	US-10-084-813-1021
13	27	36.0	12	14	US-10-084-813-1022

14	27	36.0	12	14	US-10-084-813-1023	Sequence 1023, Ap
15	27	36.0	12	14	US-10-084-813-1024	Sequence 1024, Ap
16	27	36.0	12	14	US-10-286-457-177	Sequence 177, Ap
17	27	36.0	12	16	US-10-128-520-34	Sequence 34, Appl
18	27	36.0	15	14	US-10-084-813-780	Sequence 780, Ap
19	27	36.0	15	14	US-10-084-813-781	Sequence 781, Ap
20	27	36.0	15	14	US-10-084-813-782	Sequence 782, Ap
21	27	36.0	15	14	US-10-084-813-783	Sequence 783, Ap
22	27	36.0	15	14	US-10-084-813-784	Sequence 784, Ap
23	27	36.0	15	14	US-10-084-813-785	Sequence 785, Ap
24	27	36.0	15	14	US-10-084-813-786	Sequence 786, Ap
25	27	36.0	15	14	US-10-084-813-787	Sequence 787, Ap
26	27	36.0	15	14	US-10-084-813-788	Sequence 788, Ap
27	27	36.0	15	14	US-10-354-240-95	Sequence 95, Appl
28	26.5	35.3	10	14	US-10-151-882-26	Sequence 26, Appl
29	26	34.7	7	9	US-09-927-180-3	Sequence 3, Appli
30	26	34.7	9	14	US-10-334-726-118	Sequence 118, Ap
31	26	34.7	9	14	US-10-334-726-220	Sequence 220, Ap
32	26	34.7	13	16	US-10-408-765A-3056	Sequence 3056, Ap
33	26	34.7	13	16	US-10-468-496-1532	Sequence 1532, Ap
34	26	34.7	14	15	US-10-403-847-59	Sequence 59, Appl
35	26	34.7	14	15	US-10-403-847-83	Sequence 83, Appl
36	25	33.3	7	14	US-10-400-991-50	Sequence 50, Appl
37	25	33.3	9	10	US-09-995-529-83	Sequence 83, Appl
38	25	33.3	9	11	US-09-995-529-83	Sequence 83, Appl
39	25	33.3	10	10	US-09-572-404B-2428	Sequence 2428, Ap
40	25	33.3	10	16	US-10-327-598-519	Sequence 519, Ap
41	25	33.3	10	16	US-10-327-598-705	Sequence 705, Ap
42	25	33.3	11	9	US-09-966-871-70	Sequence 70, Appl
43	25	33.3	11	13	US-10-039-645-70	Sequence 70, Appl
44	25	33.3	11	14	US-10-139-084-70	Sequence 70, Appl
45	25	33.3	11	14	US-10-239-313A-238	Sequence 238, Ap

ALIGNMENTS

RESULT 1

US-10-285-394-332
; Sequence 332, Application US/10285394
; Publication No. US20030228593A1
; GENERAL INFORMATION:
; APPLICANT: AMACHER, DAVID E.
; APPLICANT: FASULO, LISA M.
; APPLICANT: HERATH, HERATH MUDIYANSELAGE ATHULA CHANDRASIRI
; APPLICANT: HOLT, GORDON DUANE
; APPLICANT: STIGER, THOMAS R.
; TITLE OF INVENTION: BIOMARKERS OF LIVER RESPONSE
; FILE REFERENCE: POA-003.01
; CURRENT APPLICATION NUMBER: US/10/285,394
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: 60/335,964
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 412
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 332
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-285-394-332

Query Match 41.3%; Score 31; DB 14; Length 15;
Best Local Similarity 45.5%; Pred. No. 11e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 4 YSAFQVDIIVD 14
| | | | | | | | | | | | | | | |
Db 2 YPGSLDILID 12

RESULT 2

US-09-880-748-3097
; Sequence 3097, Application US/09880748

```
/ Publication No. US20030059937A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PF523
/ CURRENT APPLICATION NUMBER: US/09/880,748
/ CURRENT FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/212,210
/ PRIOR FILING DATE: 2000-06-15
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ NUMBER OF SEQ ID NOS: 3239
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 3097
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-880-748-3097

Query Match      37.3%; Score 28; DB 10; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 NPYSAFQV 9
Db      3 SPYDAFDI 10

RESULT 3
US-10-293-418-3097
/ Sequence 3097, Application US/10293418
/ Publication No. US20030223996A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PF523P2
/ CURRENT APPLICATION NUMBER: US/10/293,418
/ CURRENT FILING DATE: 2002-11-27
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ PRIOR APPLICATION NUMBER: 60/212,210
/ PRIOR FILING DATE: 2000-06-16
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 3097
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-10-293-418-3097

Query Match      37.3%; Score 28; DB 14; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 NPYSAFQV 9
Db      3 SPYDAFDI 10

RESULT 4
US-09-842-776A-30
/ Sequence 30, Application US/09842776A
/ Publication No. US20040023316A1
/ GENERAL INFORMATION:
/ APPLICANT: CONNEX GMBH
/ TITLE OF INVENTION: NEW METHOD FOR DETECTING ACID-RESISTANT MICROORGANISMS
/ FILE REFERENCE: 41735
/ CURRENT APPLICATION NUMBER: US/09/842,776A
/ CURRENT FILING DATE: 2002-08-15
/ PRIOR APPLICATION NUMBER: PCT/EP99/08212
/ PRIOR FILING DATE: 1999-10-29
/ NUMBER OF SEQ ID NOS: 64
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 30
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:
/ OTHER INFORMATION: Complementarity determining region (CDR3) of an
/ OTHER INFORMATION: antibody heavy chain directed to a beta-urease
/ OTHER INFORMATION: epitope (alternative sequence)
/ US-09-842-776A-30

Query Match      37.3%; Score 28; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SNPYS 5
Db      6 SNPYS 10

RESULT 5
US-10-084-813-973
/ Sequence 973, Application US/10084813
/ Publication No. US20030068615A1
/ GENERAL INFORMATION:
/ APPLICANT: SAXINGER, CARL
/ TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
/ FILE REFERENCE: 215875
/ CURRENT APPLICATION NUMBER: US/10/084,813
/ CURRENT FILING DATE: 2002-02-27
/ PRIOR APPLICATION NUMBER: PCT/US00/23505
/ PRIOR FILING DATE: 2000-08-25
/ PRIOR APPLICATION NUMBER: US 60/151,270
/ PRIOR FILING DATE: 1999-08-27
/ NUMBER OF SEQ ID NOS: 1242
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 973
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: binding peptide
/ US-10-084-813-973

Query Match      36.0%; Score 27; DB 14; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.4e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      7 FQVDIIV 13
Db      3 FKIDIV 9

RESULT 6
```



```
US-10-084-813-974
; Sequence 974, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 974
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-974
Query Match 36.0%; Score 27; DB 14; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.4e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 7 FOVDIV 13
DB 2 FKDIV 8
RESULT 7
US-10-084-813-975
; Sequence 975, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 975
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-975
Query Match 36.0%; Score 27; DB 14; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.4e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 7 FOVDIV 13
DB 1 FKDIV 7
RESULT 8
US-09-880-748-2839
; Sequence 2839, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
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; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2839
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2839
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Query Match 36.0%; Score 27; DB 10; Length 11;
Best Local Similarity 57.1%; Pred. No. 4.1e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 3 PYSAFOV 9
DB 5 PYDAFDI 11
```

```
RESULT 9
US-10-293-418-2839
; Sequence 2839, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2839
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2839
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Query Match 36.0%; Score 27; DB 14; Length 11;
Best Local Similarity 57.1%; Pred. No. 4.1e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 3 PYSAFOV 9
DB 5 PYDAFDI 11
```

```

RESULT 10
US-10-084-813-1019
; Sequence 1019, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1019
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1019

Query Match          36.0%; Score 27; DB 14; Length 12;
Best Local Similarity 57.1%; Pred. No. 4.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      7 FOVDIIV 13
        |::||:|
Db      6 FKIDIVV 12

RESULT 11
US-10-084-813-1020
; Sequence 1020, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1020
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1020

Query Match          36.0%; Score 27; DB 14; Length 12;
Best Local Similarity 57.1%; Pred. No. 4.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      7 FOVDIIV 13
        |::||:|
Db      5 FKIDIVV 11

RESULT 12
US-10-084-813-1021
; Sequence 1021, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1021
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1021

Query Match          36.0%; Score 27; DB 14; Length 12;
Best Local Similarity 57.1%; Pred. No. 4.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      7 FOVDIIV 13
        |::||:|
Db      3 FKIDIVV 9

RESULT 13
US-10-084-813-1022
; Sequence 1022, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1022
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1022

Query Match          36.0%; Score 27; DB 14; Length 12;
Best Local Similarity 57.1%; Pred. No. 4.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      7 FOVDIIV 13
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Db      4 FKIDIVV 10

RESULT 14
US-10-084-813-1023
; Sequence 1023, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813

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; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1023
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1023

Query Match      36.0%; Score 27; DB 14; Length 12;
Best Local Similarity 57.1%; Pred. No. 4.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      7 FQVDIIV 13
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Db      2 FKIDIV 8

RESULT 15
US-10-084-813-1024
; Sequence 1024, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GPI20 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1024
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1024

Query Match      36.0%; Score 27; DB 14; Length 12;
Best Local Similarity 57.1%; Pred. No. 4.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      7 FQVDIIV 13
      |::|||
Db      1 FKIDIV 7
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Search completed: November 14, 2004, 13:36:58
Job time : 79.6667 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 14, 2004, 13:04:13 ; Search time 23.3333 Seconds
(without alignments)
42.633 Million cell updates/sec

Title: US-09-831-253F-4

Perfect score: 75

Sequence: 1 SNFYSAFQVDIIVDI 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 157298

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:*
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 - 2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
 - 3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
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 - 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	27	36.0	14	2	US-08-934-222-110
2	27	36.0	14	2	US-08-933-402-110
3	27	36.0	14	2	US-09-207-621-110
4	27	36.0	14	2	US-08-532-818-110
5	27	36.0	14	3	US-09-231-797-110
6	27	36.0	14	3	US-08-934-224-110
7	27	36.0	14	3	US-08-933-843-110
8	27	36.0	14	3	US-08-934-223-110
9	27	36.0	14	3	US-09-413-492-110
10	27	36.0	15	4	US-09-142-524D-95
11	26	34.7	7	1	US-08-281-193-3
12	26	34.7	7	1	US-08-422-106-3
13	26	34.7	7	2	US-08-735-716-3
14	26	34.7	7	2	US-08-555-568B-3
15	26	34.7	7	3	US-09-519-223-3
16	26	34.7	7	4	US-09-927-180-3
17	26	34.7	7	5	PCT-US95-08069-3
18	25	33.3	8	3	US-08-444-818-304
19	25	33.3	8	3	US-08-444-818-305
20	25	33.3	12	3	US-08-819-286-22
21	24	32.0	14	2	US-08-811-949-25
22	24	32.0	15	5	PCT-US91-09422-27
23	23	30.7	7	1	US-07-688-352C-57
24	23	30.7	7	2	US-08-474-379C-57
25	23	30.7	7	3	US-09-146-249A-57
26	23	30.7	7	3	US-08-206-188B-57
27	23	30.7	7	5	PCT-US91-02714-55

28	23	30.7	9	3	US-09-187-859-2837	Sequence 2837, Ap
29	23	30.7	9	4	US-09-839-542B-2837	Sequence 2837, Ap
30	23	30.7	10	3	US-09-187-859-2840	Sequence 2840, Ap
31	23	30.7	10	4	US-09-839-542B-2840	Sequence 2840, Ap
32	23	30.7	10	6	5166058-8	Patent No. 5166058
33	23	30.7	11	2	US-08-621-803-99	Sequence 99, Appl
34	23	30.7	11	2	US-08-598-873-39	Sequence 39, Appl
35	23	30.7	11	3	US-08-605-430-39	Sequence 39, Appl
36	23	30.7	11	3	US-09-217-352-99	Sequence 99, Appl
37	23	30.7	11	4	US-09-717-054-39	Sequence 39, Appl
38	23	30.7	12	1	US-08-212-433A-10	Sequence 10, Appl
39	23	30.7	12	3	US-08-716-256-10	Sequence 10, Appl
40	23	30.7	12	3	US-08-329-799-21	Sequence 21, Appl
41	23	30.7	12	5	PCT-US95-03239-10	Sequence 10, Appl
42	23	30.7	14	2	US-08-348-353-36	Sequence 36, Appl
43	23	30.7	14	2	US-08-465-965-36	Sequence 36, Appl
44	23	30.7	14	3	US-08-465-966-36	Sequence 36, Appl
45	23	30.7	15	1	US-08-213-452-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1

US-08-934-222-110
; Sequence 110, Application US/08934222
; Patent No. 5928896
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
; TITLE OF INVENTION: Site
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,222
; FILING DATE: 19-SEPT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isaacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-934-222-110

Query Match 36.0%; Score 27; DB 2; Length 14;
Best Local Similarity 57.1%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8
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Db 1 NPWTVFQ 7

RESULT 2

US-08-933-402-110
; Sequence 110, Application US/08933402
; Patent No. 5948887
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
; TITLE OF INVENTION: Site
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/933,402
; FILING DATE: 19-SEPT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; NAME: Isaacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-933-402-110

Query Match 36.0%; Score 27; DB 2; Length 14;
Best Local Similarity 57.1%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8
||: ||
Db 1 NPWTVFQ 7

RESULT 3

US-09-207-621-110
; Sequence 110, Application US/09207621
; Patent No. 5952465
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
; TITLE OF INVENTION: Site
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW

; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/207,621
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
; APPLICATION NUMBER: PCT/US94/04294
; FILING DATE: 21-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isaacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-09-207-621-110

Query Match 36.0%; Score 27; DB 2; Length 14;
Best Local Similarity 57.1%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8
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Db 1 NPWTVFQ 7

RESULT 4

US-08-532-818-110
; Sequence 110, Application US/08532818
; Patent No. 5965698
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
; TITLE OF INVENTION: Site
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/532,818
; FILING DATE: 03-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/04294
; FILING DATE: 21-APR-1994
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isaacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-532-818-110

Query Match 36.0%; Score 27; DB 2; Length 14;
Best Local Similarity 57.1%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8
DB 1 NPWTVFQ 7

RESULT 5
US-09-231-797-110
Sequence 110, Application US/09231797
Patent No. 6084066
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
TITLE OF INVENTION: Polypeptides That Include Conformation-
CONSTRAINING GROUPS WHICH FLANK A PROTEIN-PROTEIN INTERACTION
TITLE OF INVENTION: Polypeptides That Include Conformation-
CONSTRAINING GROUPS WHICH FLANK A PROTEIN-PROTEIN INTERACTION
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/231.797
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isaacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-231-797-110

Query Match 36.0%; Score 27; DB 3; Length 14;

Best Local Similarity 57.1%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2 NPYSAFQ 8
DB 1 NPWTVFQ 7

RESULT 6
US-08-934-224-110
Sequence 110, Application US/08934224
Patent No. 6100044
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
TITLE OF INVENTION: Polypeptides That Include Conformation-
CONSTRAINING GROUPS WHICH FLANK A PROTEIN-PROTEIN INTERACTION
TITLE OF INVENTION: Polypeptides That Include Conformation-
CONSTRAINING GROUPS WHICH FLANK A PROTEIN-PROTEIN INTERACTION
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,224
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isaacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-934-224-110

Query Match 36.0%; Score 27; DB 3; Length 14;
Best Local Similarity 57.1%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8
DB 1 NPWTVFQ 7

RESULT 7
US-08-933-843-110
Sequence 110, Application US/08933843
Patent No. 6111069
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
TITLE OF INVENTION: Polypeptides That Include Conformation-
CONSTRAINING GROUPS WHICH FLANK A PROTEIN-PROTEIN INTERACTION
TITLE OF INVENTION: Polypeptides That Include Conformation-
CONSTRAINING GROUPS WHICH FLANK A PROTEIN-PROTEIN INTERACTION

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; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
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; TITLE OF INVENTION: Site
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
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; FILING DATE: 03-MAY-1996
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Isaacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
;
; INFORMATION FOR SEQ ID NO: 110:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
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; US-08-933-843-110
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; Query Match 36.0%; Score 27; DB 3; Length 14;
; Best Local Similarity 57.1%; Pred. No. 1.3e+02;
; Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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; QY 2 NPYSAFQ 8
; DB 1 NPWTVFQ 7
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; RESULT 8
; US-08-934-223-110
; Sequence 110, Application US/08934223
; Patent No. 6147189
;
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; constraining Groups Which Flank A Protein-Protein Interaction
;
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,223
; FILING DATE:
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; TITLE OF INVENTION: Site
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; constraining Groups Which Flank A Protein-Protein Interaction
;
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,223
; FILING DATE:
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/532,818
; FILING DATE: 03-MAY-1996
; APPLICATION NUMBER: PCT/US94/04294
; FILING DATE: 21-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isaacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
;
; INFORMATION FOR SEQ ID NO: 110:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
; US-08-934-223-110
;
; Query Match 36.0%; Score 27; DB 3; Length 14;
; Best Local Similarity 57.1%; Pred. No. 1.3e+02;
; Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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; QY 2 NPYSAFQ 8
; DB 1 NPWTVFQ 7
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; RESULT 9
; US-09-413-492-110
; Sequence 110, Application US/09413492
; Patent No. 6258550
;
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; constraining Groups Which Flank A Protein-Protein Interaction
;
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/413,492
; FILING DATE:
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
; APPLICATION NUMBER: PCT/US94/04294
; FILING DATE: 21-APR-1994
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isaacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
;
; INFORMATION FOR SEQ ID NO: 110:
```


; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-09-413-492-110

Query Match 36.0%; Score 27; DB 3; Length 14;
Best Local Similarity 57.1%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8
|:|:|:
Db 1 NPWTVFQ 7

RESULT 10

US-09-142-524D-95
; Sequence 95, Application US/09142524D
; Patent No. 6719976
; GENERAL INFORMATION:
; APPLICANT: Sone, Toshio
; APPLICANT: Kume, Akinori
; APPLICANT: Dairiki, Kazuo
; APPLICANT: Iwama, Akiko
; APPLICANT: Kino, Kohsuke
; TITLE OF INVENTION: Peptide-Based Immunotherapeutic Agent for Treating Allergic Disease
; FILE REFERENCE: SPO-103
; CURRENT APPLICATION NUMBER: US/09/142,524D
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: PCT/JP97/00740
; PRIOR FILING DATE: 1997-03-10
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 95
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Cryptomeria japonica
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(15)
; OTHER INFORMATION: Cryj2 peptide, Figure 2, Row 12
US-09-142-524D-95

Query Match 36.0%; Score 27; DB 4; Length 15;
Best Local Similarity 45.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 PYSAFQVDIIIV 13
|:|:|:|:
Db 5 PHFTFKVDGII 15

RESULT 11

US-08-281-193-3
; Sequence 3, Application US/08281193
; Patent No. 5466595
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 15
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/281,193
; FILING DATE:
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids

; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
US-08-281-193-3

Query Match 34.7%; Score 26; DB 1; Length 7;
Best Local Similarity 57.1%; Pred. No. 3.8e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8
|:|:|:
Db 1 NPHSGFR 7

RESULT 12

US-08-422-106-3
; Sequence 3, Application US/08422106
; Patent No. 5589170
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 15
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,106
; FILING DATE: 14-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/281,193
; FILING DATE: 27-JUL-1994
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
US-08-422-106-3

Query Match 34.7%; Score 26; DB 1; Length 7;
Best Local Similarity 57.1%; Pred. No. 3.8e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8
|:|:|:
Db 1 NPHSGFR 7

RESULT 13

US-08-735-716-3
; Sequence 3, Application US/08735716
; Patent No. 5840511
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 15
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/735,716
; FILING DATE: 23-OCT-1996

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/281,193
FILING DATE: 27-JUL-1994
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-08-735-716-3

Query Match 34.7%; Score 26; DB 2; Length 7;
Best Local Similarity 57.1%; Pred. No. 3.8e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8
DB 1 NPHSGFR 7

RESULT 14
US-08-555-568B-3
Sequence 3, Application US/08555568B
Patent No. 5976854
GENERAL INFORMATION:
APPLICANT: Jones, Simon
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/555,568B
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-08-555-568B-3

Query Match 34.7%; Score 26; DB 2; Length 7;
Best Local Similarity 57.1%; Pred. No. 3.8e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8
DB 1 NPHSGFR 7

RESULT 15
US-09-519-223-3
Sequence 3, Application US/09519223
Patent No. 6274140
GENERAL INFORMATION:
APPLICANT: Jones, Simon
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/519,223
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/555,568
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-09-519-223-3

Query Match 34.7%; Score 26; DB 3; Length 7;
Best Local Similarity 57.1%; Pred. No. 3.8e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8
DB 1 NPHSGFR 7

Search completed: November 14, 2004, 13:18:38
Job time : 24.3333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2004, 13:57:40 ; Search time 37 Seconds
(without alignments)
23.404 Million cell updates/sec

Title: US-09-831-253F-5

Perfect score: 48

Sequence: 1 TSLMIWTMM 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416_seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 791

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	52.1	7	2 PX0008	glucuronosyltransf
2	18	37.5	7	2 S09652	hypothetical prote
3	18	37.5	7	2 PH1602	Ig H chain V-D-J r
4	16	33.3	4	2 PT0661	T-cell receptor be
5	16	33.3	6	2 B34835	dnaA protein - Pse
6	16	33.3	7	4 I55382	hypothetical pepti
7	16	33.3	7	2 A43848	cell surface adhes
8	16	33.3	9	2 G85802	hypothetical prote
9	15	31.2	7	2 PT0586	T-cell receptor be
10	15	31.2	7	2 S32244	neuromodulatory pe
11	15	31.2	7	2 S32245	neuromodulatory pe
12	15	31.2	7	2 S32246	neuromodulatory pe
13	15	31.2	9	2 I52974	seminal vesicle pr
14	14	29.2	6	2 I49808	D-SP2.5 region - m
15	14	29.2	6	2 P41946	T-cell receptor ga
16	14	29.2	7	2 PN0649	pullulanase (EC 3.
17	14	29.2	8	2 A39308	glycine reductase
18	13	27.1	6	2 PT0519	T-cell receptor be
19	13	27.1	8	2 TI0952	hypothetical prote
20	13	27.1	8	2 S19288	acylase - Kluyvera
21	13	27.1	9	2 S07241	litorin - Rohde's
22	13	27.1	9	2 I58350	gene c-mpl protein
23	12	25.0	5	2 PT0281	Ig heavy chain CRD
24	12	25.0	6	2 A60986	N-formyl oligopept
25	12	25.0	6	2 I59142	platelet-derived g
26	12	25.0	8	2 PQ0012	cholecystokinin -
27	12	25.0	8	2 A43001	cholecystokinin -
28	12	25.0	8	2 A59495	Vesicle associated
29	12	25.0	8	2 JS0316	leucokinin VI - Ma

30	12	25.0	8	2 A41117	acetylcholinestera
31	12	25.0	9	2 S07205	litorin 2-Glu - Au
32	12	25.0	9	2 S07204	litorin I - Austr
33	12	25.0	9	2 A44873	caldesmon - rabbit
34	12	25.0	9	2 JS0302	xenopsin-related p
35	12	25.0	9	2 A60320	xenopsin-related p
36	11	22.9	3	3 P37196	bradykinin-potenti
37	11	22.9	4	2 A34626	RPCH-related neuro
38	11	22.9	4	2 B53284	T-cell receptor be
39	11	22.9	5	2 A32516	cholecystokinin-5
40	11	22.9	5	2 TI0954	hypothetical prote
41	11	22.9	5	2 A60803	neuropeptide - sea
42	11	22.9	5	2 JH0253	gut pentapeptide -
43	11	22.9	5	2 PT0308	Ig heavy chain CRD
44	11	22.9	5	2 PT0729	T-cell receptor be
45	11	22.9	5	2 PT0580	T-cell receptor be

ALIGNMENTS

RESULT 1

PX0008

glucuronosyltransferase (EC 2.4.1.17), hepatic - rat (fragment)

N:Alternate names: UDP-glucuronyltransferase

C:Species: Rattus norvegicus (Norway rat)

C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 07-Feb-1997

C:Accession: PX0008

R:Yokota, H.; Yuasa, A.; Sato, R.

J. Biochem. 104, 531-536, 1988

A:Title: Purification and properties of a form of UDP-glucuronyltransferase from liver m

A:Reference number: PX0008; MUID:89197852; PMID:3149280

A:Accession: PX0008

A:Molecule type: protein

A:Residues: 1-7 <YOK>

C:Keywords: glycosyltransferase; hexosyltransferase; liver

Query Match 52.1%; Score 25; DB 2; Length 7;

Best Local Similarity 50.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 TSLMIW 6

DB 1 TKLLWV 6

RESULT 2

S09652

hypothetical protein (aacC2 3' region) - Enterobacter cloacae (fragment)

C:Species: Enterobacter cloacae

C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 08-Oct-1999

C:Accession: S09652

R:Vliegenthart, J. S.; Ketelaar-van Gaalen, P. A. G.; van de Klundert, J. A. M.

Antimicrob. Agents Chemother. 33, 1153-1159, 1989

A:Title: Nucleotide sequence of the aacC2 gene, a gentamicin resistance determinant invo

A:Reference number: S09651; MUID:90024972; PMID:2552900

A:Accession: S09652

A:Molecule type: DNA

A:Residues: 1-7 <VLI>

A:Cross-references: EMBL:X51534; NID:g40878; PIDN:CAA35914.1; PID:g581034

Query Match 37.5%; Score 18; DB 2; Length 7;

Best Local Similarity 50.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 LMIW 6

DB 1 MIW 4

RESULT 3

PH1602

Ig H chain V-D-J region (wild-type clone 313) - mouse (fragment)

C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C:Accession: PH1602
R:Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A:Reference number: PH1580; MUID:93301609; PMID:8315387
A:Accession: PH1602
A:Molecule type: DNA
A:Residues: 1-7 <LEV>
A:Status: translational source: bone marrow pre-B lymphocyte
A:Experimental source: immunoglobulin
C:Keywords: immunoglobulin

Query Match 37.5%; Score 18; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 IWT 7
|:
Db 5 LWT 7

RESULT 4
PT0661
T-cell receptor beta chain V-D-J region (121-18V) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C:Accession: PT0661
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0661
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-4 <FEE>
A:Cross-references: UNIPROT:Q8BZQ7; UNIPROT:Q8CCN5
A:Experimental source: day 4 postnatal thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 33.3%; Score 16; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WT 7
||
Db 3 WT 4

RESULT 5
B34835
dnaA protein - Pseudomonas aeruginosa (fragment)
C:Species: Pseudomonas aeruginosa
C:Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 08-Oct-1999
C:Accession: B34835
R:Yee, T.W.; Smith, D.W.
Proc. Natl. Acad. Sci. U.S.A. 87, 1278-1282, 1990
A:Title: Pseudomonas chromosomal replication origins: a bacterial class distinct from Es
A:Reference number: A34835; MUID:90160310; PMID:2106132
A:Accession: B34835
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-6 <YEE>
A:Cross-references: GB:M30125; NID:g151419; PIDN:AAA25916.1; PID:g151421
C:Keywords: DNA binding

Query Match 33.3%; Score 16; DB 2; Length 6;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 SLMW 6
|:
Db 2 SVELW 6

RESULT 6
I55382
hypothetical peptide PAII promoter region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 16-Apr-1999 #sequence_revision 16-Apr-1999 #text_change 20-Apr-2000
C:Accession: I55382
R:Dawson, S.J.; Wiman, B.; Hamsten, A.; Green, F.; Humphries, S.; Henney, A.M.
J. Biol. Chem. 268, 10739-10745, 1993
A:Title: The two allele sequences of a common polymorphism in the promoter of the plasmi
A:Reference number: I55382; MUID:93266509; PMID:8388372
A:Accession: I55382
A:Status: translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-7 <DAW>
A:Cross-references: GB:M91557; NID:g190020; PIDN:AAA60110.1; PID:g190021
C:Comment: This is the hypothetical translation of a sequence from the PAII gene promoter
C:Genetics:
A:Gene: GDB:PAII
A:Cross-references: GDB:120297; OMIM:173360
A:Map position: 7q21.3-7q22

Query Match 33.3%; Score 16; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WT 7
||
Db 1 WT 2

RESULT 7
A43848
cell surface adhesin for heparan sulfate, 66K - Staphylococcus aureus (fragment)
C:Species: Staphylococcus aureus
C:Date: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A43848
R:Liang, O.D.; Ascencio, F.; Fransson, L.A.; Wadstrom, T.
Infect. Immun. 60, 899-906, 1992
A:Title: Binding of heparan sulfate to Staphylococcus aureus.
A:Reference number: A43848; MUID:92176005; PMID:1541563
A:Accession: A43848
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <LIA>
A:Cross-references: UNIPROT:Q9RSM1
A:Note: sequence extracted from NCBI backbone (NCBIP:85442)

Query Match 33.3%; Score 16; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WT 7
||
Db 2 WT 3

RESULT 8
G85802
hypothetical protein Z2947 [imported] - Escherichia coli (strain O157:H7, substrain EDL9;
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: G85802
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: G85802
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-9 <STO>

A;Cross-references: UNIPROT:Q8X4G1; GB:AE005174; NID:gl2515957; PIDN:AAG56883.1; GSPDB:D
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z2947

Query Match 33.3%; Score 16; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 MIWTMM 9
| : |
Db 1 MTYTFM 6

RESULT 9

PT0586

T-cell receptor beta chain V-D-J region (141-1CN) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C;Accession: PT0586; PT0592

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0586

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-7 <PEE>

A;Experimental source: day 19 fetal thymus, strain BALB/c (clones 141-1CN and 141-1CD)

C;Keywords: T-cell receptor

Query Match 31.2%; Score 15; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 IW 6
| : |
Db 4 IW 5

RESULT 10

S33244

neuromodulatory peptide Wwamide-1 - giant African snail

C;Species: Achatina fulica (giant African snail)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

C;Accession: S33244

R;Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.

FEBS Lett. 323, 104-108, 1993

A;Title: Wwamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of t

A;Reference number: S33244; MUID:93265912; PMID:8495720

A;Accession: S33244

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-7 <MIN>

A;Cross-references: UNIPROT:P35921

Query Match 31.2%; Score 15; DB 2; Length 7;
Best Local Similarity 25.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 LMIW 6
| : |
Db 4 MSVW 7

RESULT 11

S33245

neuromodulatory peptide Wwamide-2 - giant African snail

C;Species: Achatina fulica (giant African snail)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

C;Accession: S33245

R;Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.

FEBS Lett. 323, 104-108, 1993

A;Title: Wwamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of tl

A;Reference number: S33244; MUID:93265912; PMID:8495720

A;Accession: S33245

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-7 <MIN>

A;Cross-references: UNIPROT:P35919

Query Match 31.2%; Score 15; DB 2; Length 7;
Best Local Similarity 25.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 LMIW 6
| : |
Db 4 MSVW 7

RESULT 12

S33246

neuromodulatory peptide Wwamide-3 - giant African snail

C;Species: Achatina fulica (giant African snail)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

C;Accession: S33246

R;Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.

FEBS Lett. 323, 104-108, 1993

A;Title: Wwamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of tl

A;Reference number: S33244; MUID:93265912; PMID:8495720

A;Accession: S33246

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-7 <MIN>

A;Cross-references: UNIPROT:P35920

Query Match 31.2%; Score 15; DB 2; Length 7;
Best Local Similarity 25.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 LMIW 6
| : |
Db 4 MSVW 7

RESULT 13

152974

seminal vesicle protein IV - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999

C;Accession: 152974

R;Teng, C.T.; Harris, S.E.

DNA 2, 105-111, 1983

A;Title: The seminal vesicle secretion IV gene: detection of S1 nuclease-sensitive sites

A;Reference number: 152974; MUID:83261204; PMID:6307619

A;Accession: 152974

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-9 <RES>

A;Cross-references: GB:M27324; NID:g207124; PIDN:AAA63501.1; PID:g207125

C;Genetics:

A;Gene: SVSIV

Query Match 31.2%; Score 15; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TSLMI 5
| : |
Db 4 TSLFL 8

RESULT 14

I49808

D-SP2.5 region - mouse (fragment)

C;Species: Mus musculus (house mouse)

```

C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C:Accession: I49808
R:Kurosawa, Y.; Tonegawa, S.
J: Exp. Med. 155, 201-218, 1982
A:Title: Organization, structure, and assembly of immunoglobulin heavy chain diversity D
A:Reference number: I49808; MUID:82099938; PMID:6798155
A:Accession: I49808
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-6 <RES>
A:Cross-references: GB:J00432; NID:gl94370; PIDN:AAA37904.1; PID:9450452
C:Genetics:
A:Gene: Igh

      Query Match      29.2%; Score 14; DB 2; Length 6;
      Best Local Similarity 50.0%; Pred. No. 2.8e+05;
      Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 SLMWT 7
Db      1 STMVTT 6

RESULT 15
F41946
T-cell receptor gamma chain (1a.27) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: F41946
R:Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A:Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma ge
A:Reference number: A41946; MUID:92049316; PMID:1658619
A:Accession: F41946
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-6 <WHE>
C:Keywords: T-cell receptor

      Query Match      29.2%; Score 14; DB 2; Length 6;
      Best Local Similarity 50.0%; Pred. No. 2.8e+05;
      Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      5 IW 6
Db      4 VW 5

Search completed: November 14, 2004, 14:07:59
Job time : 49 secs

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STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/116,733
FILING DATE: 07-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1579-33
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-116-733-5

Query Match 42.7%; Score 32; DB 1; Length 22;
Best Local Similarity 54.5%; Pred. No. 27;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 SNPYSAFQVDI 11
DB 1 SSPYKWFQHDV 11

RESULT 3
US-08-819-286-20
; Sequence 20, Application US/08819286
; Patent No. 6169074
; GENERAL INFORMATION:
; APPLICANT: Montal, Mauricio
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF
; TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,286
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,599
; FILING DATE: 18-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Taylor, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07349/005001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-819-286-21

Query Match 38.7%; Score 29; DB 3; Length 20;
Best Local Similarity 75.0%; Pred. No. 86;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 QVDIIVDI 15
DB 7 QVDEVVDI 14

RESULT 5
US-08-630-052-25
; Sequence 25, Application US/08630052

SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-819-286-20

Query Match 38.7%; Score 29; DB 3; Length 16;
Best Local Similarity 75.0%; Pred. No. 66;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 QVDIIVDI 15
DB 3 QVDEVVDI 10

RESULT 4
US-08-819-286-21
; Sequence 21, Application US/08819286
; Patent No. 6169074
; GENERAL INFORMATION:
; APPLICANT: Montal, Mauricio
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF
; TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,286
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,599
; FILING DATE: 18-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Taylor, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07349/005001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-819-286-21

Query Match 38.7%; Score 29; DB 3; Length 20;
Best Local Similarity 75.0%; Pred. No. 86;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 QVDIIVDI 15
DB 7 QVDEVVDI 14

RESULT 5
US-08-630-052-25
; Sequence 25, Application US/08630052

Patent No. 639296
GENERAL INFORMATION:
APPLICANT: Brent, Roger
APPLICANT: McCoy, John M.
APPLICANT: Jensen, Timm H.
APPLICANT: Xu, Chanxing Wilson
TITLE OF INVENTION: INTERACTION TRAP SYSTEMS FOR DETECTING PROTEIN
TITLE OF INVENTION: INTERACTIONS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,052
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/504,538
FILING DATE: July 20, 1995
APPLICATION NUMBER: 08/278,082
FILING DATE: July 20, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Karen F. Lech
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00766/311001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-630-052-25

Query Match 38.7%; Score 29; DB 3; Length 20;
Best Local Similarity 62.5%; Pred. No. 86;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 PYSAFQVD 10
Db 13 PHSVFQVD 20

RESULT 6
US-08-652-877-1
Sequence 1, Application US/08652877
Patent No. 6187548
GENERAL INFORMATION:
APPLICANT: Akerstrom, Goran
APPLICANT: Juhlin, Claes
APPLICANT: Raak, Lars
APPLICANT: Crumley, Gregg R.
APPLICANT: Morse, Clarence C.
APPLICANT: Murray, Edward M.
APPLICANT: Hjalms, Goran
TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
TITLE OF INVENTION: Thereof and DNA Encoding Same
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.

Patent No. 639296
GENERAL INFORMATION:
APPLICANT: Brent, Roger
APPLICANT: McCoy, John M.
APPLICANT: Jensen, Timm H.
APPLICANT: Xu, Chanxing Wilson
TITLE OF INVENTION: INTERACTION TRAP SYSTEMS FOR DETECTING PROTEIN
TITLE OF INVENTION: INTERACTIONS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,052
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/504,538
FILING DATE: July 20, 1995
APPLICATION NUMBER: 08/278,082
FILING DATE: July 20, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Karen F. Lech
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00766/311001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-630-052-25

Query Match 38.7%; Score 29; DB 3; Length 20;
Best Local Similarity 62.5%; Pred. No. 86;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 PYSAFQVD 10
Db 13 PHSVFQVD 20

RESULT 6
US-08-652-877-1
Sequence 1, Application US/08652877
Patent No. 6187548
GENERAL INFORMATION:
APPLICANT: Akerstrom, Goran
APPLICANT: Juhlin, Claes
APPLICANT: Raak, Lars
APPLICANT: Crumley, Gregg R.
APPLICANT: Morse, Clarence C.
APPLICANT: Murray, Edward M.
APPLICANT: Hjalms, Goran
TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
TITLE OF INVENTION: Thereof and DNA Encoding Same
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.

STREET: 500 Arcola Rd., 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426-0107
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.5.1
SOFTWARE: Word 6.0 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,877
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/15203
FILING DATE: 22-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/344,836
FILING DATE: 23-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,314
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Savitzky, Martin
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: A1355E-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-454-3816
TELEFAX: 610-454-3808
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-652-877-1

Query Match 36.7%; Score 27.5; DB 3; Length 17;
Best Local Similarity 53.8%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 2 NPYSAFQVDIIVD 14
Db 4 NPYS---LDIFED 13

RESULT 7
US-08-476-515A-1
Sequence 1, Application US/08476515A
Patent No. 6239270
GENERAL INFORMATION:
APPLICANT: Akerstrom, Goran
APPLICANT: Juhlin, Claes
APPLICANT: Raak, Lars
APPLICANT: Crumley, Gregg R.
APPLICANT: Morse, Clarence C.
APPLICANT: Murray, Edward M.
APPLICANT: Hjalms, Goran
TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
TITLE OF INVENTION: Thereof and DNA Encoding Same
NUMBER OF SEQUENCES: 84
CORRESPONDENCE ADDRESS:
ADDRESSEE: Martin Savitzky
STREET: Rhone-Poulenc Rorer Inc., 500 Arcola Rd.,
STREET: 3C43,
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426-0107
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Compaq PC
OPERATING SYSTEM: Windows 95
SOFTWARE: Word 7.0 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,515A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/344,836
FILING DATE: 23-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/SE94/00483
FILING DATE: 24-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9301764-8
FILING DATE: 24-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Savitzky, Martin
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: A1355D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-454-3816
TELEFAX: 610-454-3808
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-476-515A-1

Query Match 36.7%; Score 27.5; DB 3; Length 17;
Best Local Similarity 53.8%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 2 NPYSAFQVDIIVD 14
DB 4 NPYS---LDIFED 13

RESULT 8
US-08-934-222-110
Sequence 110, Application US/08934222
Patent No. 5928896
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,222
FILING DATE: 19-SEPT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Isaacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-933-402-110

Query Match 36.0%; Score 27; DB 2; Length 14;
Best Local Similarity 57.1%; Pred. No. 1.3e+02;

APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isaacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-934-222-110

Query Match 36.0%; Score 27; DB 2; Length 14;
Best Local Similarity 57.1%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8
DB 1 NPTWTFQ 7

RESULT 9
US-08-933-402-110
Sequence 110, Application US/08933402
Patent No. 5948887
GENERAL INFORMATION:
APPLICANT: EVANS, Herbert J.
APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,402
FILING DATE: 19-SEPT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/532,818
FILING DATE: 03-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isaacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-933-402-110

Query Match 36.0%; Score 27; DB 2; Length 14;
Best Local Similarity 57.1%; Pred. No. 1.3e+02;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8
| | | | |
Db 1 NPWTVFQ 7

RESULT 10
US-09-207-621-110
; Sequence 110, Application US/09207621
; Patent No. 5952465
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/207,621
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
; APPLICATION NUMBER: PCT/US94/04294
; FILING DATE: 21-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; NAME: Isaacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-09-207-621-110

Query Match 36.0%; Score 27; DB 2; Length 14;
Best Local Similarity 57.1%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8
| | | | |
Db 1 NPWTVFQ 7

RESULT 11
US-09-532-818-110
; Sequence 110, Application US/08532818
; Patent No. 5965698
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/231,797
; FILING DATE: 03-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 21-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isaacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-09-532-818-110

Query Match 36.0%; Score 27; DB 2; Length 14;
Best Local Similarity 57.1%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8
| | | | |
Db 1 NPWTVFQ 7

RESULT 12
US-09-231-797-110
; Sequence 110, Application US/09231797
; Patent No. 6084066
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/231,797
; FILING DATE: 03-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 21-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isaacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-532-818-110

Query Match 36.0%; Score 27; DB 2; Length 14;
Best Local Similarity 57.1%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8
| | | | |
Db 1 NPWTVFQ 7

/ APPLICATION NUMBER: PCT/US94/04294
/ FILING DATE: 21-APR-1994
/ PRIOR APPLICATION NUMBER: U.S. 08/143,364
/ FILING DATE: 29-OCT-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: U.S. 08/051,741
/ FILING DATE: 23-APR-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Isaacson, John P.
/ REGISTRATION NUMBER: 33,751
/ REFERENCE/DOCKET NUMBER: 040433/0148
/ INFORMATION FOR SEQ ID NO: 110:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 14 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ US-09-231-797-110

Query Match 36.0%; Score 27; DB 3; Length 14;
Best Local Similarity 57.1%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8
|::||
Db 1 NPWTVFQ 7

RESULT 13
US-08-934-224-110
; Sequence 110, Application US/08934224
; Patent No. 6100044
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
; TITLE OF INVENTION: Site
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,224
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
; APPLICATION NUMBER: PCT/US94/04294
; FILING DATE: 21-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isaacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid

/ TOPOLOGY: linear
/ US-08-934-224-110

Query Match 36.0%; Score 27; DB 3; Length 14;
Best Local Similarity 57.1%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8
|::||
Db 1 NPWTVFQ 7

RESULT 14
US-08-933-843-110
; Sequence 110, Application US/08933843
; Patent No. 6111069
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
; TITLE OF INVENTION: Site
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/933,843
; FILING DATE: 19-SEPT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isaacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
/ US-08-933-843-110

Query Match 36.0%; Score 27; DB 3; Length 14;
Best Local Similarity 57.1%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8
|::||
Db 1 NPWTVFQ 7

RESULT 15
US-08-934-223-110
; Sequence 110, Application US/08934223
; Patent No. 6147189
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.

APPLICANT: KINI, R. Manjunatha
TITLE OF INVENTION: Polypeptides That Include Conformation-
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
TITLE OF INVENTION: Site
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/934,223
FILING DATE:
APPLICATION NUMBER: US/08/934,223
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/532,818
FILING DATE: 03-MAY-1996
APPLICATION NUMBER: PCT/US94/04294
FILING DATE: 21-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/143,364
FILING DATE: 29-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/051,741
FILING DATE: 23-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Isaacson, John P.
REGISTRATION NUMBER: 33,751
REFERENCE/DOCKET NUMBER: 040433/0148
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-934-223-110

Query Match 36.0%; Score 27; DB 3; Length 14;
Best Local Similarity 57.1%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 NPYSAPQ 8
Db 1 NPWTVFQ 7

Search completed: November 14, 2004, 12:08:47
Job time : 11.8085 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:25 ; Search time 43.4043 Seconds
(without alignments)
123.973 Million cell updates/sec

Title: US-09-831-253F-4

Perfect score: 75

Sequence: 1 SNFYSAFQVDIIVIDI 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 718658

Minimum DB seq length: 0

Maximum DB seq length: 23

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_23Sep04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	75	100.0	15	3 AAY92948	Aay92948 Transform
2	75	100.0	15	3 AAY93066	Aay93066 Transform
3	65	86.7	14	3 AAY92951	Aay92951 Transform
4	65	86.7	14	3 AAY93099	Aay93099 Transform
5	53	70.7	15	3 AAY93059	Aay93059 Transform
6	47	62.7	15	3 AAY93067	Aay93067 Transform
7	32	42.7	19	2 AAW94737	Aaw94737 Anti-Stap
8	32	42.7	19	8 ADL35119	Adl35119 CDR2 of m
9	32	42.7	21	2 AAR34228	Aar34228 HTLV-I gp
10	32	42.7	22	2 AAY17925	Aay17925 Synthetic
11	31	41.3	15	5 ABP55430	Abp55430 Human bre
12	31	41.3	15	6 ABR75594	Abr75594 Liver res
13	31	41.3	15	7 ADN07473	Adn07473 Liver res
14	30	40.0	15	8 ADL70819	Adl70819 PTP1B pho
15	30	40.0	15	8 ADL70905	Adl70905 PTP1B pho
16	30	40.0	15	8 ADL70907	Adl70907 PTP1B pho
17	30	40.0	15	8 ADL70906	Adl70906 PTP1B pho
18	30	40.0	15	8 ADL70908	Adl70908 PTP1B pho
19	30	40.0	17	2 AAR31182	Aar31182 N-termina
20	30	40.0	18	6 ABR91851	Abr91851 P. papata
21	30	40.0	19	6 ABR91858	Abr91858 P. papata
22	30	40.0	20	7 ADC60750	Adc60750 Termitomy
23	30	40.0	22	4 AAG76637	Aag76637 Human col
24	30	40.0	23	6 ABR91880	Abr91880 P. papata
25	29	38.7	15	4 AAG66403	Aag66403 Human vas

26 29 38.7 20 2 AAW32131 Interacti
27 29 38.7 21 7 ABM74026 DNA clone
28 29 38.7 22 4 AAM32954 Peptide #
29 29 38.7 22 4 AAM72723 Human bon
30 29 38.7 22 4 AAM60111 Human bra
31 29 38.7 22 4 ABG54421 Human liv
32 29 38.7 22 5 ABG42547 Human pep
33 29 38.7 23 2 AAW60840 Peptide c
34 28 37.3 10 5 ABP47086 Human Bly
35 28 37.3 10 7 ADG97913 scFV VHCD
36 28 37.3 13 3 AAB10012 H. pylori
37 28 37.3 13 4 AAB86092 H. pylori
38 28 37.3 13 4 AAB86060 H. pylori
39 28 37.3 15 3 AAY93058 Transform
40 28 37.3 20 3 AAY56754 Smooth mu
41 28 37.3 23 6 ABU03500 Angiogene
42 27.5 36.7 17 2 AAR64137 Lys-C pep
43 27.5 36.7 17 2 AAR95282 Calcium s
44 27.5 36.7 17 2 AAW43315 Human cal
45 27 36.0 9 4 AAB89867 HIV gp120

ALIGNMENTS

RESULT 1

AAV92948
ID AAY92948 standard; peptide; 15 AA.

XX AC AAY92948;

XX DT 08-NOV-2000 (first entry)

XX DE Transforming growth factor inhibitory peptide #4.

XX KW Hepatotropic; antagonist; transforming growth factor betaf; TGF-b1;
XX KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
XX KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.

XX OS Homo sapiens.

XX PN WO200031135-A1.

XX PD 02-JUN-2000.

XX PF 23-NOV-1999; 99WO-ES000375.

XX PR 24-NOV-1998; 98ES-00002465.

(CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.

Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
Borras Cuesta F;

WPI; 2000-411935/35.

Peptides that antagonize binding of transforming growth factor betaf,
useful for treatment of liver disease, especially cirrhosis, are partial
sequences of the factor or its receptors.

Claim 5; Page 81; 86pp; Spanish.

CC The invention relates to synthetic peptides that antagonise the binding
of transforming growth (TGF) factor betaf (TGF-b1) to its receptor in
vivo which have partial amino acid sequences identical, or similar, with
those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
examples of the peptides of the invention. The peptides act by
competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
they are inhibitors of stimulation of collagen synthesis in liver cells
and inhibitors of synthesis of proteolytic enzymes able to degrade the
extracellular matrix. The peptides, their mimetopes and/or DNA (or
expression systems) encoding the peptides are used for treatment of liver
disease, specifically cirrhosis

```

XX      SQ      Sequence 15 AA;
Query Match      100.0%; Score 75; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SNPYSAFQVDIIVDI 15
Db      1 SNPYSAFQVDIIVDI 15

RESULT 2
AA93066
ID      AAY93066 standard; peptide; 15 AA.
XX
AC      AAY93066;
XX
DT      08-NOV-2000 (first entry)
XX
DE      Transforming growth factor inhibitory peptide P106.
XX
KW      Hepatotrophic; antagonist; transforming growth factor betal; TGF-b1;
KW      competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW      extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX
OS      Rattus sp.
XX
PN      WO200031135-A1.
XX
PD      02-JUN-2000.
XX
PF      23-NOV-1999; 99WO-ES000375.
XX
PR      24-NOV-1998; 98ES-00002465.
XX
PA      (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
XX
PI      Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
PI      Borrás Cuesta F;
XX
DR      WPI; 2000-411935/35.
XX
PT      Peptides that antagonize binding of transforming growth factor betal,
PT      useful for treatment of liver disease, especially cirrhosis, are partial
PT      sequences of the factor or its receptors.
XX
PS      Claim 8; Page 82; 86pp; Spanish.
XX
CC      The invention relates to synthetic peptides that antagonise the binding
CC      of transforming growth (TGF) factor betal (TGF-b1) to its receptor in
CC      vivo which have partial amino acid sequences identical, or similar, with
CC      those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
CC      examples of the peptides of the invention. The peptides act by
CC      competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
CC      they are inhibitors of stimulation of collagen synthesis in liver cells
CC      and inhibitors of synthesis of proteolytic enzymes able to degrade the
CC      extracellular matrix. The peptides, their mimetopes and/or DNA (or
CC      expression systems) encoding the peptides are used for treatment of liver
CC      disease, specifically cirrhosis
XX
SQ      Sequence 14 AA;

Query Match      86.7%; Score 65; DB 3; Length 14;
Best Local Similarity 85.7%; Pred. No. 2.8e-05;
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 SNPYSAFQVDIIVD 14
Db      1 SNPYSAFQVDITID 14

RESULT 4
AA93099
ID      AAY93099 standard; peptide; 14 AA.
XX
AC      AAY93099;
XX
DT      08-NOV-2000 (first entry)
XX
DE      Transforming growth factor inhibitory peptide P145.
XX
KW      Hepatotrophic; antagonist; transforming growth factor betal; TGF-b1;
KW      competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW      extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX
XX

```


CC those of TGF- β 1 and/or its receptors. Peptides AAY92945-Y93133 represent
 CC examples of the peptides of the invention. The peptides act by
 CC competitive inhibition of the binding of TGF- β 1 to its receptors, e.g.
 CC they are inhibitors of stimulation of collagen synthesis in liver cells
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
 CC expression systems) encoding the peptides are used for treatment of liver
 CC disease, specifically cirrhosis
 XX
 SQ Sequence 15 AA;

Query Match 62.7%; Score 47; DB 3; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.078; 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AFQVDIIVDI 15
 |||||
 Db 1 AFQVDIIVDI 10

RESULT 7
 AAW94737
 ID AAW94737 standard; protein; 19 AA.

AC AAW94737;

DT 22-APR-1999 (first entry)

XX Anti-Staph (HAY) 96-110 heavy chain variable region.

XX Monoclonal antibody; MAb; lipoteichoic acid; gram positive; bacteria;
 KW immunoglobulin; phagocytosis; infection; epitope; peptide mimic;
 KW MAB 96-110.

XX Mus sp.

XX Key Location/Qualifiers

FT Region 1..19
 FT /notes "complementarity determining region (CDR) "

XX WO9857994-A2.

XX 23-DEC-1998.

XX 16-JUN-1998; 98WO-US012402.

XX 16-JUN-1997; 97US-0049871P.

XX (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.

XX Fischer GW, Schuman RF, Wong H, Stinson JL;

XX WPI; 1999-095329/08.

XX N-PSDB; AAX05581.

XX New antibodies to lipoteichoic acid of gram positive bacteria - used to
 PT develop products for the diagnosis, prevention and treatment of
 PT infections caused by gram positive bacteria.

XX Claim 21; Fig 12; 150pp; English.

XX The invention relates to a monoclonal antibody (MAB) to lipoteichoic acid
 CC of gram positive bacteria, where the MAB is a chimeric immunoglobulin
 CC comprising at least part of a human immunoglobulin constant region and at
 CC least part of a non-human immunoglobulin variable region having
 CC specificity to lipoteichoic acid of gram positive bacteria. The
 CC antibodies bind to whole bacteria and enhance phagocytosis and killing of
 CC the bacteria and enhance protection from lethal infection. The antibodies
 CC or peptides (encoded by a DNA of the variable region of anti-lipoteichoic
 CC acid antibody or characterised by amino acids corresponding to one or
 CC more of the complementarity determining regions (CDRs) of the variable
 CC region of the antibody) can be used for treating or preventing infections
 CC caused by gram positive bacteria. They can also be used for the diagnosis

CC of gram positive bacterial infections. Sequences AAW94735-39 represent
 CC heavy chain variable regions of the anti-lipoteichoic antibody 96-100
 SQ Sequence 19 AA;
 Query Match 42.7%; Score 32; DB 2; Length 19;
 Best Local Similarity 42.9%; Pred. No. 72;
 Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 SNPYSAFOVDIIVD 14
 |||:|:|
 Db 6 SNNYATFVADSVKD 19

RESULT 8

ADL35119
 ID ADL35119 standard; peptide; 19 AA.

XX ADL35119;

XX 03-JUN-2004 (first entry)

XX CDR2 of murine anti-LTA (A110) heavy chain antibody SeqID 125.

XX antibody; variable domain; framework region; FR; huFR;

XX immune system molecule; lipoteichoic acid; LTA; A110; mouse; murine.

XX Mus sp.

XX WO2004020579-A2.

XX 11-MAR-2004.

XX 06-AUG-2003; 2003WO-US024637.

XX 29-AUG-2002; 2002US-00230880.

XX (SUNO-) SUNOL MOLECULAR CORP.

XX Wong HC, Stinson JR, Mosquera LA;

XX WPI; 2004-239169/22.

XX Producing humanized antibodies for diagnostic and therapeutic purposes
 PT comprises optimizing similarity between individual antibody framework
 PT regions to help identify human framework regions suitable for making the
 PT antibodies.

XX Disclosure; SEQ ID NO 125; 137pp; English.

XX This invention relates to a novel method for producing a humanised
 CC antibody variable (V) domain or its fragment by optimising sequence
 CC similarity between individual antibody framework regions (FRs) in order
 CC to identify suitable human FRs (huFRs). Specifically, it refers to novel
 CC immune system molecules i.e. humanised monoclonal antibodies that exhibit
 CC suitable binding affinity with reduced immunogenicity in humans. The
 CC present invention describes a method of mutagenising DNA of non-human FRs
 CC to encode humanised FRs having an amino acid sequence that is
 CC substantially identical to the selected human FR previously identified
 CC through sequence similarity searching. As such, this method provides
 CC humanised light or heavy chain V domains of the sequence huFR1-huFR2
 CC -CDR2-huFR3-CDR3-huFR4, which can be used as therapeutic or diagnostic
 CC products to treat and/or diagnose diseases in humans and animals.
 CC Furthermore, the method expands the number of best fit possibilities that
 CC can be generated and provides a rational basis for assembling nearly all
 CC humanised immune system molecules of interest. This peptide sequence
 CC represents a hypervariable region (CDR) of the murine anti-LTA (A110)
 CC heavy chain antibody protein of the invention.

XX Sequence 19 AA;

Query Match 42.7%; Score 32; DB 8; Length 19;
 Best Local Similarity 42.9%; Pred. No. 72;

Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 SNPYSAFQVDIIVD 14
 |||:|:|:|:
 Db 6 SNNYATFYADSVKD 19

RESULT 9

AAR34228
 ID AAR34228 standard; peptide; 21 AA.

XX AAR34228;

XX 25-MAR-2003 (revised)

DT 04-AUG-1993 (first entry)

XX HTLV-I gp46 external envelope glycoprotein fragment 4.

XX Human T-cell leukaemia virus; hydrophilic; conjugate; aggregate;
 KW diagnosis; antibodies.

XX Synthetic.

XX WO9306843-A1.

XX 15-APR-1993.

XX 08-OCT-1992; 92WO-US008405.

XX 08-OCT-1991; 91US-00771553.

XX (UYDU-) UNIV DUKE.

XX Palker TJ, Haynes BF;

XX WPI; 1993-134125/16.

XX Antigenic determinant peptide(s) of HTLV envelope glycoprotein - useful
 PT for detecting anti-HTLV-I and -II antibodies and as vaccine against HTLV.

XX Claim 4; Page 11; 50pp; English.

XX The sequence of peptide 4 corresponds to residues 129-149 from the HTLV-I
 CC gp46 external envelope glycoprotein. When covalently linked to a carrier
 CC mol. the hydrophilic peptide can induce in a mammal the prodn. of high
 CC titres of antibodies to gp46 envelope glycoprotein from HTLV-I or -II.
 CC The peptide and carrier may be used in vaccines against HTLV-I or -II
 CC infection. The peptide may be used in a diagnostic assay to detect the
 CC presence and titre of anti-HTLV antibodies. See also AAR34225-57.
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 21 AA;

Query Match 42.7%; Score 32; DB 2; Length 21;
 Best Local Similarity 54.5%; Pred. No. 82;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 SNPYSAFQVDI 11
 |||:|:|:|:
 Db 1 SSPYWKFGHDV 11

RESULT 10

AAV17925
 ID AAV17925 standard; peptide; 22 AA.

XX AAV17925;

XX 30-JUL-1999 (first entry)

XX Synthetic peptide derived from HTLV envelope sugar protein.

XX Hydrophilic peptide; antigen determinant; envelope sugar protein; HTLV-I;

KW HTLV-II; B lymphatic corpuscle; gp46; gp63; tetanus toxoid.

XX Synthetic.

OS Human lymphotropic virus type I.

XX JP02209889-A.

XX 21-AUG-1990.

XX 08-FEB-1989; 89JP-00029551.

XX 08-FEB-1988; 88US-00153420.

PR 30-JAN-1989; 89US-00303436.

XX (UYDU-) UNIV DUKE.

XX WPI; 1990-344000/39.

XX Synthetic hydrophilic peptide - comprises 25 unit aminoacid that
 PT corresponds to at least one antigen determinant of envelope sugar
 PT protein(s) of HTLV-I and HTLV-II.

XX Claim 4; Page 1; 15pp; Japanese.

XX The invention relates to new synthetic hydrophilic peptides (AAV17922-
 CC 934) that correspond to at least one of antigen determinants of envelope
 CC sugar proteins of HTLV-I and HTLV-II identified in the B lymphatic
 CC corpuscle. When bonded covalently to a carrier molecule, the peptides can
 CC induce the production of an antibody having a high titre to the gp46 and
 CC gp63 envelope sugar proteins of HTLV-I and HTLV-II in mammals. The
 CC carrier molecule is preferably a tetanus toxoid and selected from the
 CC group of sequences shown in AAV17935-39. The carrier molecule is
 CC preferably a dipeptide-glycine-glycine). The peptides form effectively
 CC immunological response to factors causing virus HTLV-I and HTLV-II. The
 CC method also provides an effective conjugate having the peptide

XX Sequence 22 AA;

Query Match 42.7%; Score 32; DB 2; Length 22;
 Best Local Similarity 54.5%; Pred. No. 87;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 SNPYSAFQVDI 11
 |||:|:|:|:
 Db 1 SSPYWKFGHDV 11

RESULT 11

ABP55430
 ID ABP55430 standard; peptide; 15 AA.

XX ABP55430;

XX 04-FEB-2003 (first entry)

XX Human breast susceptible gene protein 10.45 N-terminal peptide SEQ:7.
 KW Human; breast susceptible gene coded protein 10.45; tumour;
 KW embryotic development deformity.

XX Homo sapiens.

XX CN1342702-A.

XX 03-APR-2002.

XX 12-SEP-2000; 2000CN-00125173.

XX 12-SEP-2000; 2000CN-00125173.

XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.

PI Mao Y, Xie Y;
XX WPI; 2002-529778/57.
XX A novel human breast susceptible gene coded protein 10.45 polypeptide,
PT and the polynucleotide encoding it, useful for treating several diseases
PT e.g. embryonic development deformity and tumors.
XX
XX Example 5; Page 20 (Disclosure); 34pp; Chinese.
XX
XX The present invention describes human breast susceptible gene coded
CC protein 10.45 (I). Also described is a process for preparing (I) using
CC DNA recombination techniques. (I) can be used for treating several
CC diseases e.g. embryonic development deformity and tumors. The present
CC sequence represents the N-terminal peptide of (I), which is used in an
CC example from the present invention
XX
SQ Sequence 15 AA;
Query Match 41.3%; Score 31; DB 5; Length 15;
Best Local Similarity 45.5%; Pred. No. 84;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 2 NPVSFAFQVDII 12
:|:|:|:|:
DB 5 SPVFKFRVNV 15
:
RESULT 12
ABR75594
ID ABR75594 standard; peptide; 15 AA.
XX
AC ABR75594;
XX
DT 28-AUG-2003 (first entry)
XX
DE Liver response-associated protein isoform (LRPI) peptide SEQ ID NO:332.
XX
KW Biomarker; liver response; liver response-associated protein isoform;
KW LRPI; liver response-associated feature; LRF.
XX
OS Synthetic.
XX
PN WO2003038444-A2.
XX
PD 08-MAY-2003.
XX
PF 31-OCT-2002; 2002WO-US034847.
XX
PR 31-OCT-2001; 2001US-0335964P.
XX
PA (PFIZ) PFIZER PROD INC.
PA (OXFO-) OXFORD GLYSCSCIENCES UK LTD.
XX
PI Amacher DE, Fasulo LM, Herath HM, Holt GD, Stiger TR;
XX
DR WPI; 2003-430566/40.
XX
PT Screening, diagnosing, staging or identifying subject at risk of
PT developing, liver response, or monitoring effect of therapy on liver
PT response, by detecting Liver Response-Associated Protein Isoforms in
PT subject sample.
XX
PS Claim 1; Page 66; 256pp; English.
XX
XX The present invention describes a method (M1) for screening or diagnosing
CC a liver response in a subject, determining the stage or severity of a
CC liver response in a subject, identifying a subject at risk of developing
CC liver response, or monitoring the effect of therapy administered to a
CC subject having liver response, involving detecting liver response-
CC associated protein isoforms (LRPIs) (see the peptides given in ABR75395
CC to ABR75806) in a test biological sample from the subject. Alternatively,
CC screening or diagnosing a liver response in a subject, or monitoring the

CC effect of a drug or therapy administered to a subject, involves
CC contacting at least one oligonucleotide probe comprising 10 or more
CC consecutive nucleotides complementary to a nucleotide sequence encoding
CC an LRPI with RNA obtained from a biological sample from the subject or
CC with cDNA copied from the RNA, where the contacting occurs under
CC conditions that permit hybridisation of the probe to the nucleotide
CC sequence if present, detecting hybridisation, if any, between the probe
CC and the nucleotide sequence, and comparing the hybridisation, if any,
CC detected in the above step, with the hybridisation detected in a control
CC sample, or with a previously determined reference range. M1 is useful for
CC screening or diagnosing a liver response in a subject, determining the
CC stage or severity of a liver response in a subject, identifying a subject
CC at risk of developing liver response, and monitoring the effect of
CC therapy administered to a subject having liver response
XX
SQ Sequence 15 AA;
Query Match 41.3%; Score 31; DB 6; Length 15;
Best Local Similarity 45.5%; Pred. No. 84;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 4 YSAFQVDIIVD 14
:|:|:|:|:
DB 2 YPQSQDLIIL 12
:
RESULT 13
ADN07473
ID ADN07473 standard; peptide; 15 AA.
XX
AC ADN07473;
XX
DT 17-JUN-2004 (first entry)
XX
DE Liver response-associated feature LRF405 #3.
XX
KW liver response; liver response-associated protein isoform; LRPI;
KW drug monitoring; therapy monitoring; liver response-associated feature;
KW LRF.
XX
OS Homo sapiens.
XX
PN US2003228583-A1.
XX
PD 11-DEC-2003.
XX
PF 31-OCT-2002; 2002US-00285394.
XX
PR 31-OCT-2001; 2001US-0335964P.
XX
PA (AMAC/) AMACHER D E.
PA (FASU/) FASULO L M.
PA (HERA/) HERATH H M A C.
PA (HOLT/) HOLT G D.
PA (STIG/) STIGER T R.
XX
PI Amacher DE, Fasulo LM, Herath HM, Holt GD, Stiger TR;
XX
DR WPI; 2003-430566/40.
XX
PT Screening, diagnosing, staging or identifying subject at risk of
PT developing, liver response, or monitoring effect of therapy on liver
PT response, by detecting Liver Response-Associated Protein Isoforms in
PT subject sample.
XX
PS Disclosure; SEQ ID NO 332; 75pp; English.
XX
XX The invention describes a method of screening (M1) or diagnosing a liver
CC response in a subject, determining the stage or severity of a liver
CC response in a subject, identifying a subject at risk of developing liver
CC response, or monitoring the effect of therapy administered to a subject
CC having liver response. The method involves detecting liver response-
CC Associated Protein Isoforms (LRPIs) in a test biological sample from the

CC subject, which has an activity or level indicative of a liver response.
CC LRP1s are selected from any one of the compounds given in the
CC specification e.g. LRPI-1.1, LRPI-2.1, LRPI-3.1 and LRPI-4.1.
CC Alternatively, screening or diagnosing a liver response in a subject, or
CC monitoring the effect of a drug or therapy administered to a subject, or
CC involves contacting at least one oligonucleotide probe comprising 10 or
CC more consecutive nucleotides complementary to a nucleotide sequence
CC encoding an LRPI with RNA obtained from a biological sample from the
CC subject or with cDNA copied from the RNA, where the contacting occurs
CC under conditions that permit hybridisation of the probe to the nucleotide
CC sequence if present, detecting hybridisation, if any, between the probe
CC and the nucleotide sequence, and comparing the hybridisation, if any,
CC detected in the above step, with the hybridisation detected in a control
CC sample, or with a previously determined reference range. The method is
CC useful for screening or diagnosing a liver response in a subject,
CC determining the stage or severity of a liver response in a subject,
CC identifying a subject at risk of developing liver response, and
CC monitoring the effect of therapy administered to a subject having liver
CC response. This is the amino acid sequence of a liver response-associated
CC feature (LRF) comprising one or more LRPI.
XX
XX Sequence 15 AA;

Query Match 41.3%; Score 31; DB 7; Length 15;
Best Local Similarity 45.5%; Pred. No. 84;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 YSAFQVDIIVD 14
| :| :| :| :|
Db 2 YPGSQLDILID 12

RESULT 14

ADL70819
ID ADL70819 standard; peptide; 15 AA.

XX AC ADL70819;

XX DT 03-JUN-2004 (first entry)

XX DE PTP1B phosphopeptide, SEQ ID 17.

XX Cytostatic; Antidiabetic; Anorectic; Antiinflammatory; Antimicrobial;
KW Cardiant; Neuroprotective; Protein tyrosine phosphatase inhibitor;
KW phosphopeptide; protein tyrosine phosphatase; cancer; diabetes; obesity;
KW inflammation; multiple sclerosis; angiogenesis-dependent disease;
KW infectious disease; appetite suppressor; congestive heart failure;
KW neurodegenerative disease; ischaemia; demyelinating disease; PTP1B;
KW protein tyrosine phosphatase 1B.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Modified-site 6 /note= "Phosphotyrosine"

XX XX WO2004020466-A1.

XX XX 11-MAR-2004.

XX PF 20-AUG-2003; 2003WO-EP050385.

XX PR 29-AUG-2002; 2002EP-00019357.

XX PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.

XX PI Hoofst Van Huijsduijn R, Walchli S, Arigoni F;

XX DR WPI; 2004-269210/25.

XX New phosphopeptides that inhibit protein tyrosine phosphatases, useful
PT for manufacturing a medicament for preventing or treating e.g. cancer,
PT diabetes, obesity, inflammation, multiple sclerosis or infectious

PT diseases.

XX Example 1; SEQ ID NO 17; 77pp; English.

XX The present invention relates to phosphopeptides that inhibit protein
CC tyrosine phosphatase. The phosphopeptides are useful as a medicament or
CC for manufacturing a medicament for the treatment and/or prevention of
CC cancer (i.e. stomach or intestinal cancer), diabetes and/or obesity,
CC inflammation, multiple sclerosis, angiogenesis-dependent disease (e.g.
CC solid cancer or metastatic cancer) or infectious disease (i.e.
CC leishmaniasis), or as a suppressor of appetite. These may also be used
CC for preventing or treating congestive heart failure, neurodegenerative
CC diseases, ischaemic events of the brain or demyelinating diseases. The
CC present sequence is one such phosphopeptide from protein tyrosine
CC phosphatase 1B (PTP1B).

XX Sequence 15 AA;

Query Match 40.0%; Score 30; DB 8; Length 15;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YSAFQVD 10
| :| :| :| :|

Db 6 YNAYQVD 12

RESULT 15

ADL70905
ID ADL70905 standard; peptide; 15 AA.

XX AC ADL70905;

XX DT 03-JUN-2004 (first entry)

XX DE PTP1B phosphopeptide #19.

XX Cytostatic; Antidiabetic; Anorectic; Antiinflammatory; Antimicrobial;
KW Cardiant; Neuroprotective; Protein tyrosine phosphatase inhibitor;
KW phosphopeptide; protein tyrosine phosphatase; cancer; diabetes; obesity;
KW inflammation; multiple sclerosis; angiogenesis-dependent disease;
KW infectious disease; appetite suppressor; congestive heart failure;
KW neurodegenerative disease; ischaemia; demyelinating disease; PTP1B;
KW protein tyrosine phosphatase 1B.

XX OS Synthetic.

XX XX WO2004020466-A1.

XX XX 11-MAR-2004.

XX XX 20-AUG-2003; 2003WO-EP050385.

XX PR 29-AUG-2002; 2002EP-00019357.

XX PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.

XX PI Hoofst Van Huijsduijn R, Walchli S, Arigoni F;

XX DR WPI; 2004-269210/25.

XX New phosphopeptides that inhibit protein tyrosine phosphatases, useful
PT for manufacturing a medicament for preventing or treating e.g. cancer,
PT diabetes, obesity, inflammation, multiple sclerosis or infectious
PT diseases.

XX Example 1; Fig 1; 77pp; English.

XX The present invention relates to phosphopeptides that inhibit protein
CC tyrosine phosphatase. The phosphopeptides are useful as a medicament or
CC for manufacturing a medicament for the treatment and/or prevention of
CC cancer (i.e. stomach or intestinal cancer), diabetes and/or obesity,
CC inflammation, multiple sclerosis, angiogenesis-dependent disease (e.g.

CC solid cancer or metastatic cancer) or infectious disease (i.e.
CC leishmaniasis), or as a suppressor of appetite. These may also be used
CC for preventing or treating congestive heart failure, neurodegenerative
CC diseases, ischaemic events of the brain or demyelinating diseases. The
CC present sequence is one such phosphopeptide from protein tyrosine
CC phosphatase 1B (PTP1B).
XX

SQ Sequence 15 AA;

Query Match 40.0%; Score 30; DB 8; Length 15;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YSAFQVD 10
|.:|||
Db 9 YNAYQVD 15

Search completed: November 14, 2004, 12:02:09
Job time : 46.4043 secs

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OM protein - protein search, using sw model

Run on: November 14, 2004, 12:03:21 ; Search time 35.4255 Seconds
(without alignments)
149.815 Million cell updates/sec

Title: US-09-831-253F-4

Perfect score: 75

Sequence: 1 SNPYSAFQVDIIVDI 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1568699 seqs, 353819137 residues

Total number of hits satisfying chosen parameters: 294451

Minimum DB seq length: 0

Maximum DB seq length: 23

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	36	48.0	17	9	US-09-071-838-173
2	36	48.0	17	14	US-10-213-512-173
3	32	42.7	19	14	US-10-230-880-125
4	31	41.3	15	14	US-10-285-394-332
5	31	41.3	19	15	US-10-424-599-201443
6	30	40.0	18	16	US-10-481-180-685
7	30	40.0	19	16	US-10-481-180-692
8	30	40.0	22	14	US-10-106-698-7411
9	30	40.0	23	16	US-10-481-180-714
10	29	38.7	20	14	US-10-162-538-25
11	29	38.7	22	9	US-09-864-761-43921
12	28	37.3	10	10	US-09-880-748-3097
13	28	37.3	10	14	US-10-293-418-3097

14	28	37.3	13	11	US-09-842-776A-30	Sequence 30, Appl
15	28	37.3	23	15	US-10-211-462-91	Sequence 91, Appl
16	27	36.0	9	14	US-10-084-813-973	Sequence 973, Appl
17	27	36.0	9	14	US-10-084-813-974	Sequence 974, Appl
18	27	36.0	9	14	US-10-084-813-975	Sequence 975, Appl
19	27	36.0	11	10	US-09-880-748-2839	Sequence 2839, Ap
20	27	36.0	11	14	US-10-293-418-2839	Sequence 2839, Ap
21	27	36.0	12	14	US-10-084-813-1019	Sequence 1019, Ap
22	27	36.0	12	14	US-10-084-813-1020	Sequence 1020, Ap
23	27	36.0	12	14	US-10-084-813-1021	Sequence 1021, Ap
24	27	36.0	12	14	US-10-084-813-1022	Sequence 1022, Ap
25	27	36.0	12	14	US-10-084-813-1023	Sequence 1023, Ap
26	27	36.0	12	14	US-10-084-813-1024	Sequence 1024, Ap
27	27	36.0	12	14	US-10-286-457-177	Sequence 177, Appl
28	27	36.0	12	16	US-10-128-520-34	Sequence 34, Appl
29	27	36.0	15	14	US-10-084-813-780	Sequence 780, Appl
30	27	36.0	15	14	US-10-084-813-781	Sequence 781, Appl
31	27	36.0	15	14	US-10-084-813-782	Sequence 782, Appl
32	27	36.0	15	14	US-10-084-813-783	Sequence 783, Appl
33	27	36.0	15	14	US-10-084-813-784	Sequence 784, Appl
34	27	36.0	15	14	US-10-084-813-785	Sequence 785, Appl
35	27	36.0	15	14	US-10-084-813-786	Sequence 786, Appl
36	27	36.0	15	14	US-10-084-813-787	Sequence 787, Appl
37	27	36.0	15	14	US-10-084-813-788	Sequence 788, Appl
38	27	36.0	15	14	US-10-354-240-95	Sequence 95, Appl
39	27	36.0	18	10	US-09-880-748-2736	Sequence 2736, Ap
40	27	36.0	18	14	US-10-084-813-826	Sequence 826, Appl
41	27	36.0	18	14	US-10-084-813-827	Sequence 827, Appl
42	27	36.0	18	14	US-10-084-813-828	Sequence 828, Appl
43	27	36.0	18	14	US-10-084-813-829	Sequence 829, Appl
44	27	36.0	18	14	US-10-084-813-830	Sequence 830, Appl
45	27	36.0	18	14	US-10-084-813-831	Sequence 831, Appl

ALIGNMENTS

RESULT 1

US-09-071-838-173
Sequence 173, Application US/09071838
Patent No. US20020152501A1
GENERAL INFORMATION:
APPLICANT: Fischer, Robert L.
APPLICANT: Ohad, Nir
APPLICANT: Kiyosue, Tomohiro
APPLICANT: Yadegari, Ramin
APPLICANT: Margossian, Linda
APPLICANT: Harada, John
APPLICANT: Goldberg, Robert B.
TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit Development in Plants
NUMBER OF SEQUENCES: 324
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,838
FILING DATE: 01-MAY-1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-086100US
TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 173:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-071-838-173

Query Match 48.0%; Score 36; DB 9; Length 17;
Best Local Similarity 46.7%; Pred. No. 16;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 SNPSAFQVDIIVDI 15
||| | : : ||
Db 3 SNPYRKFTNYTKDI 17
||| | : : ||

RESULT 2

US-10-213-512-173
; Sequence 173, Application US/10213512
; Publication No. US20030110536A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Yadegari, Ramin
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Combinations of Nucleic Acids That Control Seed and
; TITLE OF INVENTION: Fruit Development in Plants
; FILE REFERENCE: 023070-086110US
; CURRENT APPLICATION NUMBER: US/10/213,512
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: US/09/177,206
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: US 09/071,838
; PRIOR FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 173
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-10-213-512-173

Query Match 48.0%; Score 36; DB 14; Length 17;
Best Local Similarity 46.7%; Pred. No. 16;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 SNPSAFQVDIIVDI 15
||| | : : ||
Db 3 SNPYRKFTNYTKDI 17
||| | : : ||

RESULT 3

US-10-230-880-125
; Sequence 125, Application US/10230880
; Publication No. US20030190705A1
; GENERAL INFORMATION:
; APPLICANT: WONG, HING C.
; APPLICANT: STINSON, JEFFREY L.
; APPLICANT: MOSQUERA, LUIS A.
; TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
; FILE REFERENCE: 71758/58066
; CURRENT APPLICATION NUMBER: US/10/230,880
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306

; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 125
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-230-880-125

Query Match 42.7%; Score 32; DB 14; Length 19;
Best Local Similarity 42.9%; Pred. No. 96;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 SNPSAFQVDIIVD 14
||| | : : ||
Db 6 SNNYATFYADSVKD 19
||| | : : ||

RESULT 4

US-10-285-394-332
; Sequence 332, Application US/10285394
; Publication No. US20030228583A1
; GENERAL INFORMATION:
; APPLICANT: AMACHER, DAVID E.
; APPLICANT: FASULO, LISA M.
; APPLICANT: HERATH, HERATH MUDIYANSELAGE ATHULA CHANDRASIRI
; APPLICANT: HOLT, GORDON DUANE
; APPLICANT: STIGER, THOMAS R.
; TITLE OF INVENTION: BIOMARKERS OF LIVER RESPONSE
; FILE REFERENCE: POA-003,01
; CURRENT APPLICATION NUMBER: US/10/285,394
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: 60/335,964
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 412
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 332
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-285-394-332

Query Match 41.3%; Score 31; DB 14; Length 15;
Best Local Similarity 45.5%; Pred. No. 1,1e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 YSAFQVDIIVD 14
||| | : : ||
Db 2 YPGSQLDIID 12
||| | : : ||

RESULT 5

US-10-424-599-201443
; Sequence 201443, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 201443
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT3847_23928C.1.pep
US-10-424-599-201443

Query Match 41.3%; Score 31; DB 15; Length 19;
Best Local Similarity 30.8%; Pred. No. 1.5e+02;
Matches 4; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 3 PYSAFQVDIIIVDI 15
DB 2 PYATFPMTILISL 14

RESULT 6

US-10-481-180-685
; Sequence 685, Application US/10481180
; Publication No. US20040171821A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
; APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
; APPLICANT: HUMAN SERVICES
; APPLICANT: Valenzuela, Jesus G.
; APPLICANT: Belkaid, Yasmine
; APPLICANT: Kamhawi, Shaden
; APPLICANT: Sacks, David
; APPLICANT: Ribeiro, Jose M. C.
; TITLE OF INVENTION: ANTI-ARTHROPOD VECTOR VACCINES, METHODS
; TITLE OF INVENTION: OF SELECTING AND USES THEREOF
; FILE REFERENCE: 4239-67347
; CURRENT APPLICATION NUMBER: US/10/481,180
; CURRENT FILING DATE: 2003-12-17
; PRIOR APPLICATION NUMBER: PCT/US02/19663
; PRIOR FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 60/299,391
; PRIOR FILING DATE: 2001-06-19
; NUMBER OF SEQ ID NOS: 884
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 685
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; NOTE =
; OTHER INFORMATION: Synthetic Construct
US-10-481-180-685

Query Match 40.0%; Score 30; DB 16; Length 18;
Best Local Similarity 46.2%; Pred. No. 2.1e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 2 NP--YSAFQVDII 12
DB 2 NPLGYGGFAVDVV 14

RESULT 7

US-10-481-180-692
; Sequence 692, Application US/10481180
; Publication No. US20040171821A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
; APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
; APPLICANT: HUMAN SERVICES
; APPLICANT: Valenzuela, Jesus G.
; APPLICANT: Belkaid, Yasmine
; APPLICANT: Kamhawi, Shaden
; APPLICANT: Sacks, David
; APPLICANT: Ribeiro, Jose M. C.
; TITLE OF INVENTION: ANTI-ARTHROPOD VECTOR VACCINES, METHODS
; TITLE OF INVENTION: OF SELECTING AND USES THEREOF
; FILE REFERENCE: 4239-67347
; CURRENT APPLICATION NUMBER: US/10/481,180
; CURRENT FILING DATE: 2003-12-17
; PRIOR APPLICATION NUMBER: PCT/US02/19663

; PRIOR FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 60/299,391
; PRIOR FILING DATE: 2001-06-19
; NUMBER OF SEQ ID NOS: 884
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 692
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; NOTE =
; OTHER INFORMATION: Synthetic Construct
US-10-481-180-692

Query Match 40.0%; Score 30; DB 16; Length 19;
Best Local Similarity 46.2%; Pred. No. 2.2e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 2 NP--YSAFQVDII 12
DB 2 NPLGYGGFAVDVV 14

RESULT 8

US-10-106-698-7411
; Sequence 7411, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptid
; FILE REFERENCE: PA005PI
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 7411
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (20)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (22)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-7411

Query Match 40.0%; Score 30; DB 14; Length 22;
Best Local Similarity 40.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 4 YSAFQVDIIIV 13
DB 3 FGCFKIDIVV 12

RESULT 9

US-10-481-180-714
; Sequence 714, Application US/10481180
; Publication No. US20040171821A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
; APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
; APPLICANT: HUMAN SERVICES
; APPLICANT: Valenzuela, Jesus G.
; APPLICANT: Belkaid, Yasmine

; APPLICANT: Kamhawi, Shaden
; APPLICANT: Sachs, David
; APPLICANT: Ribeiro, Jose M. C.
; TITLE OF INVENTION: ANTI-ARTHOPOD VECTOR VACCINES, METHODS
; FILE REFERENCE: 4239-67347
; CURRENT APPLICATION NUMBER: US/10/481,180
; CURRENT FILING DATE: 2003-12-17
; PRIOR APPLICATION NUMBER: PCT/US02/19663
; PRIOR FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 60/299,391
; PRIOR FILING DATE: 2001-06-19
; NUMBER OF SEQ ID NOS: 884
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 714
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; NOTE =
; OTHER INFORMATION: Synthetic Construct
US-10-481-180-714

Query Match 40.0%; Score 30; DB 16; Length 23;
Best Local Similarity 46.2%; Pred. No. 2.7e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 2 NP--YSAFQVDII 12
||| |||
Db 2 NPLGYGGFAVDVV 14

RESULT 10

US-10-162-538-25
; Sequence 25, Application US/10162538
; Publication No. US20030113749A1
; GENERAL INFORMATION:
; APPLICANT: Brent, Roger
; McCoy, John M.
; Jensen, Timm H.
; Xu, Chanzing Wilson
; TITLE OF INVENTION: INTERACTION TRAP SYSTEMS FOR DETECTING
; PROTEIN INTERACTIONS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02110-2804
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/162,538
; FILING DATE: 04-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,052
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/504,538
; FILING DATE: July 20, 1995
; APPLICATION NUMBER: 08/278,082
; FILING DATE: July 20, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Karen F. Lech
; REGISTRATION NUMBER: 35,238
; REFERENCE/DOCKET NUMBER: 00786/311001
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: No. US20030113749A1 Relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-10-162-538-25

Query Match 38.7%; Score 29; DB 14; Length 20;
Best Local Similarity 62.5%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 PYSAFQVD 10
|:|:|:|
Db 13 PHSVENVD 20

RESULT 11

US-09-864-761-43921
; Sequence 43921, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wenheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecmica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117

SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 43921
LENGTH: 22
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO: AC06227.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.72
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.71
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.86
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.77
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.61
US-09-864-761-43921

Query Match 38.7%; Score 29; DB 9; Length 22;
Best Local Similarity 54.5%; Pred. No. 4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 4; Gaps 0;

Qy 1 SNPSAFQVDI 11
Db 1 STPSAFSVSL 11

RESULT 12
US-09-880-748-3097
Sequence 3097, Application US/09880748
Publication No. US2003005937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3097
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-3097

Query Match 37.3%; Score 28; DB 10; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 2; Gaps 0;

Qy 2 NPYSAFQV 9
Db 3 SPYDAFDI 10

RESULT 13
US-10-293-418-3097
Sequence 3097, Application US/10293418
Publication No. US20030223996A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523P2
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817

PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 3097
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-418-3097

Query Match 37.3%; Score 28; DB 14; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NPYSAFQV 9
Db 3 SPYDAFDI 10

RESULT 14
US-09-842-776A-30
Sequence 30, Application US/09842776A
Publication No. US20040023316A1
GENERAL INFORMATION:
APPLICANT: CONNEX GMBH
TITLE OF INVENTION: NEW METHOD FOR DETECTING ACID-RESISTANT MICROORGANISMS
FILE REFERENCE: 41735
CURRENT APPLICATION NUMBER: US/09/842,776A
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: PCT/EP99/08212
PRIOR FILING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 30
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Complementarity determining region (CDR3) of an
OTHER INFORMATION: antibody heavy chain directed to a beta-urease
OTHER INFORMATION: epitope (alternative sequence)
US-09-842-776A-30

Query Match 37.3%; Score 28; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNPYS 5
Db 6 SNEYS 10

RESULT 15
US-10-211-462-91
Sequence 91, Application US/10211462
Publication No. US20040033495A1
GENERAL INFORMATION:
APPLICANT: Murray, Richard
APPLICANT: Glynn, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Aziz, Natasha

; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and
; TITLE OF INVENTION: Methods of Screening for Angiogenesis Modulators
; FILE REFERENCE: 018501-006200US
; CURRENT APPLICATION NUMBER: US/10/211,462
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US 09/784,356
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/791,390
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: US 60/310,025
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/334,244
; PRIOR FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 230
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 91
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-211-462-91

Query Match 37.3%; Score 28; DB 15; Length 23;
Best Local Similarity 50.0%; Pred. NO. 6.3e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 SNFYSAFQVD 10
| | | | | :
Db 3 SIPYTVFQTN 12

Search completed: November 14, 2004, 12:26:59
Job time : 35.4255 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:26 ; Search time 40.0532 Seconds
(without alignments)
215.479 Million cell updates/sec

Title: US-09-831-253F-4

Perfect score: 75

Sequence: 1 SNPYSAFQVDIIVIDI 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 17482

Minimum DB seq length: 0
Maximum DB seq length: 23

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	38.7	18	2 Q9QV11	Q9qv11 rattus sp.
2	28	37.3	9	2 Q7RA82	Q7ra82 plasmodium
3	27	36.0	20	2 Q9QVB2	Q9qvb2 mus sp. . s
4	26	34.7	12	2 Q9S550	Q9s550 streptococ
5	26	34.7	16	2 Q7R3P0	Q7rsp0 plasmodium
6	26	34.7	19	2 Q9QV10	Q9qv10 rattus sp.
7	26	34.7	22	2 Q7M0L1	Q7m0l1 clostridium
8	25	33.3	10	2 Q76WM5	Q76wm5 eurypharynx
9	25	33.3	10	2 BAB87140	Bab87140 euryphary
10	25	33.3	11	2 Q7M154	Q7m154 bacillus th
11	25	33.3	12	2 Q7XB05	Q7xb05 zea mays (m
12	25	33.3	13	2 Q7X761	Q7x761 zea mays (m
13	25	33.3	13	2 Q79A22	Q79a22 borrelia bu
14	25	33.3	14	2 P81801	P81801 streptomyc
15	25	33.3	17	2 Q7XB06	Q7xb06 zea mays (m
16	25	33.3	18	2 Q7XB07	Q7xb07 zea mays (m
17	25	33.3	20	2 Q69381	Q69381 human herpe
18	25	33.3	22	2 Q68988	Q68988 human herpe
19	24.5	32.7	20	2 Q8R1Q1	Q8r1q1 mus musculu
20	24.5	32.7	21	2 Q9JK03	Q9jk03 mus musculu
21	24	32.0	8	2 Q91U19	Q91u19 influenza a
22	24	32.0	8	2 Q91U21	Q91u21 influenza a
23	24	32.0	16	2 Q7RGW0	Q7rgw0 plasmodium
24	24	32.0	16	2 Q9TQY6	Q9tgy6 oryctolagus
25	24	32.0	16	2 Q33429	Q33429 anas platyr
26	24	32.0	17	2 Q9UC43	Q9uc43 homo sapien
27	24	32.0	18	2 Q9R5G0	Q9r5g0 alcaligenes
28	24	32.0	21	2 Q7RKF7	Q7rkf7 plasmodium
29	24	32.0	22	2 Q7R7E7	Q7r7e7 plasmodium
30	24	32.0	22	2 Q7RLB6	Q7rlb6 plasmodium
31	24	32.0	22	2 Q9QV59	Q9qv59 cavia (guin

32	23.5	31.3	19	2 Q8SEP2	Q8sep2 genista tyr
33	23.5	31.3	19	2 Q8SKW8	Q8skw8 genista val
34	23.5	31.3	19	2 Q8SKX1	Q8skx1 genista gas
35	23.5	31.3	19	2 Q8SKX3	Q8skx3 genista eph
36	23.5	31.3	19	2 Q8SKX5	Q8skx5 genista dor
37	23.5	31.3	19	2 Q8SKX7	Q8skx7 genista dem
38	23.5	31.3	19	2 Q8SKX9	Q8skx9 genista cil
39	23.5	31.3	21	2 Q7SHB6	Q7shb6 neurospora
40	23	30.7	10	2 Q76WK9	Q76mk9 eurypharynx
41	23	30.7	10	2 BAB87148	Bab87148 euryphary
42	23	30.7	10	2 BAB87156	Bab87156 euryphary
43	23	30.7	10	2 BAB87164	Bab87164 euryphary
44	23	30.7	14	2 Q9R5I8	Q9r5i8 vibrio algi
45	23	30.7	15	2 Q9F5B2	Q9fab2 silene aega

ALIGNMENTS

RESULT 1

Q9QV11 PRELIMINARY; PRT; 18 AA.
AC Q9QV11;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Sucrase-alpha-dextrinase subunit beta, S-D subunit beta
DE (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP MEDLINE=920311479; PubMed=1931964;
RX Zhu J.S., Conklin K.A., Scheving L.A., Smith A.J., Gray G.M.;
RT "Structural and functional correlates of sucrase-alpha-dextrinase in
RT intact brush border membranes.";
RL Biochemistry 30:10399-10408(1991).
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 2122 MW; 68FFIABAB7B24E49 CRC64;

Query Match 38.7%; Score 29; DB 2; Length 18;
Best Local Similarity 45.5%; Pred. No. 5.1e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 SNPYSAFQVDI 11
||| |:::
Db 5 SNPISELRVEV 15

RESULT 2

Q7RA82 PRELIMINARY; PRT; 9 AA.
AC Q7RA82;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Hypothetical protein (Fragment).
GN Names=PY06620;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=17XNL;
RC PubMed=12368865;
RA Carleton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perteau M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,

```

RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., White O.R.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., Hoffman S.L., Gardner M.J.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii."
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
KW EMBL; AABL01002263; EAA18865.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1001 MW; 4687ASAB476455B7 CRC64;

Query Match 37.3%; Score 28; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNPSYS 5
DB 3 SNPSYS 7

RESULT 3
Q9QVB2 ID Q9QVB2 PRELIMINARY; PRT; 20 AA.
AC Q9QVB2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Serine protease (Fragment).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE.
RX MEDLINE=93020730; PubMed=1404084;
RA Damjanov A., Damjanov I.;
RT "Isolation of serine protease from granulated metrial gland cells of
RT mice and rats with lectin from Dolichos biflorus."
RL J. Reprod. Fertil. 95:679-684(1992).
SQ SEQUENCE 20 AA; 2290 MW; 0A304F61A22C50D CRC64;

Query Match 36.0%; Score 27; DB 2; Length 20;
Best Local Similarity 71.4%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SNPSYS 7
DB 11 SRPYNAF 17

RESULT 4
Q9S550 ID Q9S550 PRELIMINARY; PRT; 12 AA.
AC Q9S550;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE DexB (Fragment).
GN Name=dexB;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D39;
RX MEDLINE=99214122; PubMed=10198036;
RA Iannelli F., Pearce B.J., Pozzi G.,

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RT "The type 2 capsule locus of Streptococcus pneumoniae.";
RL J. Bacteriol. 181:2652-2654(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=D39;
RA Pearce B.J., Iannelli F., Pozzi G.;
RL Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF026471; AAD10169.1; -.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1405 MW; 90A979D2B2B9CDDA CRC64;

Query Match 34.7%; Score 26; DB 2; Length 12;
Best Local Similarity 40.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 PYSAFQVDII 12
DB 3 PWDAPCVELL 12

RESULT 5
Q7RSP0 ID Q7RSP0 PRELIMINARY; PRT; 16 AA.
AC Q7RSP0;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=PY00315;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=12368865;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perteau M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwily S.L.,
RA Shalom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii."
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
KW EMBL; AABL01000088; EAA22680.1; -.
SQ SEQUENCE 16 AA; 1979 MW; A87BC2C996760379 CRC64;

Query Match 34.7%; Score 26; DB 2; Length 16;
Best Local Similarity 44.4%; Pred. No. 1.6e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 YSAFOVDII 12
DB 3 YCRFSIDIL 11

RESULT 6
Q9QV10 ID Q9QV10 PRELIMINARY; PRT; 19 AA.
AC Q9QV10;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Sucrase-alpha-dextrinase subunit alpha, S-D subunit alpha

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DE (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=92031479; PubMed=1931964;
RA Zhu J.S., Conklin K.A., Scheving L.A., Smith A.J., Gray G.M.;
RT "Structural and functional correlates of sucrose-alpha-dextrinase in
RT intact brush border membranes.";
RL Biochemistry 30:10399-10408(1991).
FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 2119 MW; C84537919B7149D1 CRC64;

Query Match 34.7%; Score 26; DB 2; Length 19;
Best Local Similarity 40.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 4 YSAFQVDIIIV 13
   ||| : : |||
Db 5 FSALEISLIV 14

RESULT 7
Q7MOL1 PRELIMINARY; PRT; 22 AA.
AC Q7MOL1
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Exoenzyme C3 (Fragment).
OS Clostridium botulinum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1491;
RN [1]
RP SEQUENCE.
RX MEDLINE=89338716; PubMed=2474453;
RA Toratani S., Yokosawa N., Yokosawa H., Ishii S.I., Oguma K.;
RT "Immuno-crossreactivity between botulinum neurotoxin type C1 or D and
RT exoenzyme C3.";
RL FEBS Lett. 252:83-87(1989).
DR PIR: S05236; S05236.
FT NON_TER 1
FT NON_TER 22
FT NON_TER 22
SQ SEQUENCE 22 AA; 2449 MW; C3A42F8BE7FF41E3 CRC64;

Query Match 34.7%; Score 26; DB 2; Length 22;
Best Local Similarity 45.5%; Pred. No. 2.3e+03;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 SNPYSAFQVDI 11
   ||| : : |||
Db 3 SNTYQBFNTNI 13

RESULT 8
Q76MM5 PRELIMINARY; PRT; 10 AA.
AC Q76MM5
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE NADH dehydrogenase subunit 2 (Fragment).
GN Name=ND2;
OS Eurypharynx pelecyanoides (pelican eel).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes;
OC Eurypharyngidae; Eurypharynx.
OX NCBI_TaxID=55117;
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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22967687; PubMed=12949142;
RA Inoue J.G., Miya M., Tsukamoto K., Nishida M.;
RT "Evolution of the deep-sea gulper eel mitochondrial genomes: large-
RT scale gene rearrangements originated within the eels.";
RL Mol. Biol. Evol. 20:1917-1924(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB046477; BAB87140.1; -;
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 1261 MW; 357BFE29C682DB47 CRC64;

Query Match 33.3%; Score 25; DB 2; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 NPYSAFQV 9
   ||| : : |||
Db 2 NPYVMELV 9

RESULT 9
BAB87140 PRELIMINARY; PRT; 10 AA.
AC BAB87140
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE NADH dehydrogenase subunit 2 (Fragment).
GN ND2.
OS Eurypharynx pelecyanoides (pelican eel).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes;
OC Eurypharyngidae; Eurypharynx.
OX NCBI_TaxID=55117;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A;
RA Inoue J.G., Miya M., Tsukamoto K., Nishida M.;
RT "Evolution of the Deep-Sea Gulper Eel Mitochondrial Genomes: Large-
RT Scale Gene Rearrangements Originated Within the Eels.";
RL Mol. Biol. Evol. 20:1917-1924(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A;
RA Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB046477; BAB87140.1; -;
KW Mitochondrion.
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 1261 MW; 357BFE29C682DB47 CRC64;

Query Match 33.3%; Score 25; DB 2; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 NPYSAFQV 9
   ||| : : |||
Db 2 NPYVMELV 9

RESULT 10
Q7M154 PRELIMINARY; PRT; 11 AA.
AC Q7M154
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
```

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Parapopal crystal protein, wax moth-specific (Fragment).
 OS Bacillus thuringiensis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1428;
 RN (1)
 RP SEQUENCE
 RA Chestukhina G.G., Kostina L.I., Zalunin I.A., Khodova O.M.,
 RA Stepanov V.M.;
 RT "Bacillus thuringiensis esp. galleriae simultaneously produces two
 RT delta-endotoxins differing strongly in primary structure and
 RT entomocidal activity";
 RL FEBS Lett. 232:249-251(1988).
 DR PIR: S00616; S00616.
 FT NON_TER 1
 FT NON_TER 11
 SQ SEQUENCE 11 AA; 1237 MW; C6FF9BD6476444D CRC64;

Query Match 33.3%; Score 25; DB 2; Length 11;
 Best Local Similarity 80.0%; Pred. No. 1.7e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SNPYS 5
 Db :|||
 5 NNPYS 9

RESULT 11
 Q7XB05 PRELIMINARY; PRT; 12 AA.
 AC Q7XB05;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Phytoene synthase 2 (Fragment).
 GN Name=psy2;
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Y-14;
 RX MEDLINE=22779048; PubMed=12897253;
 RA Palaisa K.A., Morgante M., Williams M., Rafalski A.;
 RT "Contrasting effects of selection on sequence diversity and linkage
 RT disequilibrium at two phytoene synthase loci";
 RL Plant Cell 15:1795-1806(2003).
 DR EMBL: AY300568; AAP5307.1; -.
 FT NON_TER 1
 FT NON_TER 12
 SQ SEQUENCE 12 AA; 1335 MW; 9B1E0AA00869C325 CRC64;

Query Match 33.3%; Score 25; DB 2; Length 12;
 Best Local Similarity 54.5%; Pred. No. 1.8e+03;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 SNPYSAFQVDI 11
 Db :|||
 1 SDTVSKFPVDI 11

RESULT 12
 Q7X761 PRELIMINARY; PRT; 13 AA.
 AC Q7X761;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Phytoene synthase 2 (Fragment).
 GN Name=psy2;
 OS Zea mays (Maize).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=W-17, and W-50;
 RX MEDLINE=22779048; PubMed=12897253;
 RA Palaisa K.A., Morgante M., Williams M., Rafalski A.;
 RT "Contrasting effects of selection on sequence diversity and linkage
 RT disequilibrium at two phytoene synthase loci";
 RL Plant Cell 15:1795-1806(2003).
 DR EMBL: AY300592; AAP5331.1; -.
 DR EMBL: AY300599; AAP5338.1; -.
 FT NON_TER 1
 FT NON_TER 13
 SQ SEQUENCE 13 AA; 1449 MW; 9B1E0AA05615C325 CRC64;

Query Match 33.3%; Score 25; DB 2; Length 13;
 Best Local Similarity 54.5%; Pred. No. 2e+03;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 SNPYSAFQVDI 11
 Db :|||
 2 SDTVSKFPVDI 12

RESULT 13
 Q79A22 PRELIMINARY; PRT; 13 AA.
 AC Q79A22;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE MoxR protein (Fragment).
 GN Name=moxR;
 OS Borrelia burgdorferi (Lyme disease spirochete).
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
 OX NCBI_TaxID=139;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=212;
 RA Old I.G.;
 RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: X95868; CAA64970.1; -.
 FT NON_TER 13
 SQ SEQUENCE 13 AA; 1484 MW; C7C2DF4CFD83A046 CRC64;

Query Match 33.3%; Score 25; DB 2; Length 13;
 Best Local Similarity 50.0%; Pred. No. 2e+03;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 5 SAFQVDIIVD 14
 Db :|||
 3 SGFQIDSEVE 12

RESULT 14
 P81801 PRELIMINARY; PRT; 14 AA.
 ID P81801
 AC P81801;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Purpocycin-hydrolyzing enzyme (EC 3.-.-) (Fragment).
 OS Streptomyces morookaensis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1970;
 RN (1)
 RP SEQUENCE.
 RC STRAIN=JCM4673 / KCC S-0673;
 RX PubMed=9538199;

RA Nishimura M., Matsuo H., Nakamura A., Sugiyama M.;
 RT "Purification and Characterization of a puromycin-hydrolyzing enzyme
 from blastoidin S-producing Streptomyces morookaensis.";
 RL J. Biochem. 123:247-252(1998).
 RN [2]
 RP CHARACTERIZATION, AND FUNCTION.
 RA Nishimura M., Matsuo H., Sugiyama M.;
 RT "Blasticidin S-producing Streptomyces morookaensis possesses an enzyme
 activity with hydrolyzes puromycin.";
 RL FEMS Microbiol. Lett. 132:95-100(1995).
 CC -1- FUNCTION: INACTIVATES PUROMYCIN BY CATALYZING THE HYDROLYSIS OF
 CC THE AMIDE LINKAGE BETWEEN ITS AMINONUCLEOSIDE AND O-METHYL-L-
 CC TYROSINE MOETIES. THE OPTIMUM PH IS 8.0 AND THE OPTIMAL
 CC TEMPERATURE IS 45 DEGREES CELSIUS.
 CC -1- FUNCTION: MAY HAVE AMINOPEPTIDASE ACTIVITY.
 CC -1- ENZYME REGULATION: STIMULATED BY DTT. STRONGLY INHIBITED BY ZINC
 CC ION, FERROUS ION, CUPRIC ION, MERCURY ION, N-BROMOSUCCINIMIDE AND
 CC N-ETHYLMALEIMIDE. PARTIALLY INHIBITED BY COBALT ION.
 CC -1- SUBUNIT: MONOMER.
 CC -1- MISCELLANEOUS: HAS AN ISOELECTRIC POINT OF 6.4.
 DR GO; GO:0004177; F:aminopeptidase activity; IEA.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 KW Aminopeptidase; Hydrolase.
 FT NON_TER 14 14
 SQ SEQUENCE 14 AA; 1492 MW; 3F980730E45EF3D8 CRC64;

Query Match 33.3%; Score 25; DB 2; Length 14;
 Best Local Similarity 55.6%; Pred. No. 2.1e+03;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PYSAFQVDI 11
 Db 5 PYGAWQSPI 13

RESULT 15
 Q7XB06 PRELIMINARY; PRT; 17 AA.
 AC Q7XB06;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Phytoene synthase 2 (Fragment).
 GN Name=psy2;
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PI587132;
 RX MEDLINE=22779048; PubMed=12897253;
 RA Palaisa K.A., Morgante M., Williams M., Rafalski A.;
 RT "Contrasting effects of selection on sequence diversity and linkage
 RT disequilibrium at two phytoene synthase loci.";
 RL Plant Cell 15:1795-1806(2003).
 DR EMBL; AY300558; AAF55297.1; -.
 FT NON_TER 1 1
 FT NON_TER 17 17
 SQ SEQUENCE 17 AA; 1869 MW; 8EB5FAA056459674 CRC64;

Query Match 33.3%; Score 25; DB 2; Length 17;
 Best Local Similarity 54.5%; Pred. No. 2.6e+03;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 SNPYSAFQVDI 11
 Db 6 SDTVSKFPVDI 16

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OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:25 ; Search time 9.25532 Seconds
(without alignments)
155.938 Million cell updates/sec

Title: US-09-831-253F-4
Perfect score: 75
Sequence: 1 SNPYSAFQVDIIVIDI 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 4495

Minimum DB seq length: 0
Maximum DB seq length: 23

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	41.3	22	C39800	calcium-activated potassium channel
2	31	41.3	23	PS0446	potassium channel protein slo 11 - fruit fly (Drosophila melanogaster) (fragment)
3	27	36.0	16	S16376	L-serine dehydratase
4	27	36.0	21	S69371	duodenase - bovine
5	26	34.7	22	S05236	exoenzyme C3 - Clostridium
6	25	33.3	11	S00616	paraagoral crystal
7	25	33.3	17	A58946	formylmethanofuran
8	25	33.3	23	A48968	exo-poly-alpha-galacturonate oxidase I
9	24	32.0	18	A45138	arsenite oxidase I
10	23	30.7	13	A54326	glandular kallikrein
11	23	30.7	14	B44854	L-2,4-diaminobutyrate
12	22	29.3	12	A61360	vespakinin M - horseradish
13	22	29.3	15	PS0185	27K protein A 3.4/
14	22	29.3	15	A61612	allatostatin - tobacco
15	22	29.3	15	G24417	interphotoreceptor
16	22	29.3	16	A48301	glutamate-1-semialdehyde
17	22	29.3	17	A61334	trypsin (EC 3.4.21)
18	22	29.3	18	S43834	DNA topoisomerase
19	22	29.3	18	A61392	brain-associated s
20	22	29.3	19	D24417	interphotoreceptor
21	22	29.3	20	A85659	hypothetical prote
22	22	29.3	23	C24417	interphotoreceptor
23	21	28.0	11	P70229	Ig heavy chain CDR
24	21	28.0	12	S36899	ribosomal protein
25	21	28.0	13	PC2369	unidentified 85K p
26	21	28.0	15	PA0061	protein OF200039 -
27	21	28.0	15	S29174	D-galactose-bindin
28	21	28.0	19	B26930	ermG leader peptid
29	21	28.0	19	PH1313	Ig heavy chain DJ

interphotoreceptor
lysophospholipase
mast cell proteina
probable transcrip
Ig heavy chain DJ
Ig heavy chain V r
enamelin i - bovin
MUC1 enhancer bind
hypothetical prote
NADH2 dehydrogenas
methane monooxygen
MHC class II histo
pregnancy-specific
ribosomal protein
glycoprotein H-a -
tubulin alpha-chai

ALIGNMENTS

RESULT 1

C39800
calcium-activated potassium channel, alternate exon B - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 27-Mar-1992 #sequence_revision 27-Mar-1992 #text_change 09-Jul-2004
C;Accession: C39800
R;Atkinson, N.S.; Robertson, G.A.; Ganetzky, B.
Science 253, 551-555, 1991
A;Title: A component of calcium-activated potassium channels encoded by the Drosophila
A;Reference number: A39800; MUID:91313401; PMID:1857984
A;Accession: C39800
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tr
A;Molecule type: mRNA
A;Residues: 1-22 <ATK>
A;Cross-references: UNIPROT:Q03720
C;Genetics:
A;Gene: FlyBase:slo
A;Cross-references: FlyBase:FBgn0003429

Query Match 41.3%; Score 31; DB 2; Length 22;
Best Local Similarity 44.4%; Pred. No. 46;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNPYSAFQV 9
:||||:|:
DB 6 ANPYAGYQL 14

RESULT 2

PS0446
potassium channel protein slo 11 - fruit fly (Drosophila melanogaster) (fragment)
C;Species: Drosophila melanogaster
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: PS0446
R;Adelman, J.P.; Shen, K.Z.; Kavanaugh, M.P.; Warren, R.A.; Wu, Y.N.; Lagrutta, A.; Bon
Neuron 9, 209-216, 1992
A;Title: Calcium-activated potassium channels expressed from cloned complementary DNAs
A;Reference number: JH0697; MUID:92360299; PMID:1497890
A;Accession: PS0446
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-23 <ADB>
A;Cross-references: UNIPROT:Q03720
C;Genetics:
C;Comment: This potassium channel is activated by calcium.
A;Gene: FlyBase:slo
A;Cross-references: FlyBase:FBgn0003429
C;Keywords: alternative splicing; ion channel; potassium channel; transmembrane protein

Query Match 41.3%; Score 31; DB 2; Length 23;
Best Local Similarity 44.4%; Pred. No. 48;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNPYSAFQV 9
:||||: :|
Db 7 ANPYAGYQL 15

RESULT 3

S16376
L-serine dehydratase beta chain - Peptostreptococcus asaccharolyticus
C:Species: Peptostreptococcus asaccharolyticus
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S16376
R:Grabowski, R.; Buckel, W.
Eur. J. Biochem. 199, 89-94, 1991
A:Title: Purification and properties of an iron-sulfur-containing and pyridoxal-phosphat
A:Reference number: S16224; PMID:91293139; PMID:2065681
A:Accession: S16376
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-16 <EUR>
A:Cross-references: UNIPROT:P33074

Query Match 36.0%; Score 27; DB 2; Length 16;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 YSAFQV 9
:||||: :|
Db 1 YSAFEV 6

RESULT 4

S69371
duodenase - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004.
C:Accession: S69371
R:Zamolodchikova, T.S.; Vorotyntseva, T.I.; Antonov, V.K.
Eur. J. Biochem. 227, 866-872, 1995
A:Title: Duodenase, a new serine protease of unusual specificity from bovine duodenal mu
A:Reference number: S69371; PMID:7867648
A:Accession: S69371
A:Molecule type: protein
A:Residues: 1-21 <ZAM>
A:Cross-references: UNIPROT:Q9GLN2
C:Superfamily: trypsin; trypsin homology

Query Match 36.0%; Score 27; DB 2; Length 21;
Best Local Similarity 71.4%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SNPYSAF 7
:||||: :|
Db 11 SRPYMAF 17

RESULT 5

S05236.
exoenzyme C3 - Clostridium botulinum (fragment)
C:Species: Clostridium botulinum
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C:Accession: S05236
R:Toratani, S.; Yokosawa, N.; Yokosawa, H.; Ishii, S.I.; Oguma, K.
FEBS Lett. 252, 83-87, 1989
A:Title: Immuno-crossreactivity between botulinum neurotoxin type C1 or D and exoenzyme
A:Reference number: S05236; PMID:89338716; PMID:2474453
A:Accession: S05236
A:Molecule type: protein
A:Residues: 1-22 <TOR>
A:Cross-references: UNIPROT:Q7M0U1

Query Match 34.7%; Score 26; DB 2; Length 22;
Best Local Similarity 45.5%; Pred. No. 3.6e+02;

Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 1 SNPYSAFQVDI 11
:||||: :|
Db 3 SNTYQEFNTNI 13

RESULT 6

S00616
parasporal crystal protein, wax moth-specific - Bacillus thuringiensis (strain gallierae)
N:Alternate names: delta-endotoxin; parasporal crystal protein positive chain
C:Species: Bacillus thuringiensis
C>Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C:Accession: S00616
R:Cheshukhina, G.G.; Kostina, L.I.; Zalunin, I.A.; Khodova, O.M.; Stepanov, V.M.
FEBS Lett. 232, 249-251, 1988
A:Title: Bacillus thuringiensis ssp. gallierae simultaneously produces two delta-endotoxi
A:Reference number: S00615
A:Accession: S00616
A:Molecule type: protein
A:Residues: 1-11 <CHE>
A:Cross-references: UNIPROT:Q7MI54
C:Comment: This toxin is effective against the larvae of Galleria mellonella (greater wax
C:Superfamily: parasporal crystal protein
C:Keywords: delta-endotoxin

Query Match 33.3%; Score 25; DB 2; Length 11;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNPYS 5
:||||: :|
Db 5 NNPS 9

RESULT 7

AS8946
formylmethanofuran dehydrogenase (EC 1.2.99.5) (molybdenum) chain C - Methanobacterium t
N:Alternate names: formylmethanofuran dehydrogenase (molybdenum) chain B [misidentified
C:Species: Methanobacterium thermoautotrophicum
C>Date: 16-Apr-1999 #sequence_revision 16-Apr-1999 #text_change 04-Feb-2000
C:Accession: AS8946
R:Hochheimer, A.; Schmitz, R.A.; Thauer, R.K.; Hedderich, R.
Eur. J. Biochem. 234, 910-920, 1995
A:Title: The tungsten formylmethanofuran dehydrogenase from Methanobacterium thermoaut
A:Reference number: S63519; PMID:96163477; PMID:8575452
A:Accession: AS8946
A:Molecule type: protein
A:Residues: 1-17 <HOC>
A>Note: the authors identify this peptide as the amino terminus of chain B, but it appe
C:Keywords: iron-sulfur protein; metalloprotein; molybdenum; molybdopterin; oxidoreducta

Query Match 33.3%; Score 25; DB 2; Length 17;
Best Local Similarity 41.7%; Pred. No. 4e+02;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0; .

QY 3 PYSAPQVDIIIVD 14
:||||: :|
Db 6 PTSDPFQIGLEAD 17

RESULT 8

AS8968
exo-poly-alpha-galacturonosidase (EC 3.2.1.82) - Clostridium thermosaccharolyticum (fra
N:Alternate names: exo-poly-alpha-galacturonate hydrolase
C:Species: Clostridium thermosaccharolyticum, Clostridium tartarivorum
C>Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 06-Dec-1996
C:Accession: A48968
R:van Rijssel, M.; Gerwig, G.J.; Hansen, T.A.
Appl. Environ. Microbiol. 59, 828-836, 1993
A:Title: Isolation and characterization of an extracellular glycosylated protein comple
A:Reference number: A48968; PMID:93243739; PMID:8481009
A:Accession: A48968

A;Status: preliminary
A;Molecule type: protein

A;Residues: 1-23 <VAM>

A;Note: sequence extracted from NCBI backbone (NCBIP:130462)
C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 33.3%; Score 25; DB 2; Length 23;
Best Local Similarity 57.1%; Pred. No. 5.7e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 YSAFOVD 10

Db 3 YAAPEYD 9

RESULT 9

A45138
arsenite oxidase II - Alcaligenes faecalis (fragment)

C;Species: Alcaligenes faecalis

C;Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C;Accession: A45138

R;Anderson, G.L.; Williams, J.; Hille, R.

J. Biol. Chem. 267, 23674-23682, 1992

A;Title: The purification and characterization of arsenite oxidase from *Alcaligenes faecalis*
A;Reference number: A45138; MUID:93054722; PMID:1331097

A;Accession: A45138

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-18 <AND>

A;Cross-references: UNIPROT:Q7SIF3; UNIPROT:Q9R5G0

A;Note: sequence extracted from NCBI backbone (NCBIP:118544)

Query Match 32.0%; Score 24; DB 2; Length 18;
Best Local Similarity 33.3%; Pred. No. 6.5e+02;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 4 YSAFQVDIIVDI 15

Db 5 YPACQSVKVL 16

RESULT 10

A54326
glandular kallikrein-1 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 29-Aug-1994 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995

C;Accession: A54326

R;Riegman, P.H.; Vlietstra, R.J.; van der Korput, H.A.; Romijn, J.C.; Trapman, J.

Mol. Cell. Endocrinol. 76, 181-190, 1991

A;Title: Identification and androgen-regulated expression of two major human glandular kallikreins
A;Reference number: A54326; MUID:92324494; PMID:1726490

A;Accession: A54326

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-13 <RIE>

A;Experimental source: prostate

A;Note: sequence extracted from NCBI backbone (NCBIP:108060)

Query Match 30.7%; Score 23; DB 2; Length 13;
Best Local Similarity 80.0%; Pred. No. 6.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNPYS 5

Db 2 SHPYS 6

RESULT 11

B44854

L-2,4-diaminobutyrate decarboxylase (EC 4.1.1.-) - *Vibrio alginolyticus* (fragment)

C;Species: *Vibrio alginolyticus*

C;Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C;Accession: B44854; B41817

R;Yamamoto, S.; Tsuzaki, Y.; Tougou, K.; Shinoda, S.

J. Gen. Microbiol. 138, 1461-1465, 1992

A;Title: Purification and characterization of L-2,4-diaminobutyrate decarboxylase from *Vibrio alginolyticus*
A;Reference number: A44854; MUID:92381494; PMID:1512577

A;Accession: B44854

A;Molecule type: protein

A;Residues: 1-14 <YAM>

A;Cross-references: UNIPROT:Q9R518

A;Note: sequence extracted from NCBI backbone (NCBIP:112332)

C;Keywords: carbon-carbon lyase; carboxy-lyase

Query Match 30.7%; Score 23; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 7.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 SAFOVD 10

Db 2 TAPEVD 7

RESULT 12

A61360

vespakinin M - hornet (*Vespa mandarinia*)

C;Species: *Vespa mandarinia*

C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004

C;Accession: A61360

R;Kishimura, H.; Yasuhara, T.; Yoshida, H.; Nakajima, T.

Chem. Pharm. Bull. 24, 2896-2897, 1976

A;Title: Vespakinin-M, a novel bradykinin analogue containing hydroxyproline, in the

A;Reference number: A61360; MUID:77114342; PMID:1017116

A;Accession: A61360

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-12 <KIS>

A;Cross-references: UNIPROT:Q7M3T3

C;Superfamily: unassigned animal peptides

C;Keywords: hydroxyproline; venom

F;4/Modified site: 4-hydroxyproline (Pro) #status experimental

Query Match 29.3%; Score 22; DB 2; Length 12;

Best Local Similarity 42.9%; Pred. No. 9.4e+02;

Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 YSAFOVD 10

Db 6 FSPFRID 12

RESULT 13

PS0185

27K protein A 3.4/5 - rice (fragment)

C;Species: *Oryza sativa* (rice)

C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 24-Feb-1995

C;Accession: PS0185

R;Kamo, M.; Tsugita, A.

submitted to JIPID, June 1991

A;Reference number: PS0184

A;Accession: PS0185

A;Molecule type: protein

A;Residues: 1-15 <KAM>

Query Match 29.3%; Score 22; DB 2; Length 15;

Best Local Similarity 50.0%; Pred. No. 1.2e+03;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 8 QVDIIIVDI 15

Db 1 QXEYIIVDV 8

RESULT 14

A61612

allatostatin - tobacco hornworm

C/Species: Manduca sexta (tobacco hornworm)
C/Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C/Accession: A61612
R/Kramer, S.J.; Toschi, A.; Miller, C.A.; Kataoka, H.; Quistad, G.B.; Li, J.P.; Carney, Proc. Natl. Acad. Sci. U.S.A. 88, 9458-9462, 1991
A/Title: Identification of an allatostatin from the tobacco hornworm Manduca sexta.
A/Reference number: A61612; MUID:92052112; PMID:1946359

A/Accession: A61612
A/Status: Preliminary
A/Molecule type: protein
A/Residues: 1-15 <KRA>
A/Cross-references: UNIPROT:P42559
C/Keywords: neuropeptide; pyrrolidone carboxylic acid
F;/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 29.3%; Score 22; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NPYSAF 7
|||
Db 10 NPISCF 15

RESULT 15

G24417
interphotoreceptor retinoid-binding protein - hamster (fragment)
N/Alternate names: interstitial retinol-binding protein
C/Species: Cricetinae gen. sp. (hamster)
C/Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 09-Jul-2004
C/Accession: G24417
R/Fong, S.L.; Cook, R.G.; Alvarez, R.A.; Liou, G.I.; Landers, R.A.; Bridges, C.D.B. FENS Lett. 205, 309-312, 1986
A/Title: N-terminal sequence homologies in interstitial retinol-binding proteins from 10
A/Reference number: A91365; MUID:86301171; PMID:3743780
A/Accession: G24417
A/Molecule type: protein
A/Residues: 1-15 <FON>
A/Cross-references: UNIPROT:P12665

Query Match 29.3%; Score 22; DB 2; Length 15;
Best Local Similarity 33.3%; Pred. No. 1.2e+03;
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 7 FQVDIIVDI 15
|||
Db 7 FQPSLVLDM 15

Search completed: November 14, 2004, 12:03:11
Job time : 10.2553 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2004, 12:37:20 ; Search time 155 Seconds
(without alignments)
27.773 Million cell updates/sec

Title: US-09-831-253F-3

Perfect score: 63

Sequence: 1 TSLDATMIWTMM 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 497672

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- A: Geneseqp_23Sep04:*
- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	63	100.0	12	3 AAY92947	Aay92947 Transform
2	63	100.0	12	3 AAY93008	Aay93008 Transform
3	58	92.1	12	3 AAY93009	Aay93009 Transform
4	50	79.4	11	3 AAY93094	Aay93094 Transform
5	48	76.2	12	3 AAY93093	Aay93093 Transform
6	37	58.7	12	3 AAY93007	Aay93007 Transform
7	36.5	57.9	9	3 AAY93096	Aay93096 Transform
8	36.5	57.9	9	3 AAY92949	Aay92949 Transform
9	35	55.6	7	3 AAY93095	Aay93095 Transform
10	35	55.6	12	3 AAY93010	Aay93010 Transform
11	31.5	50.0	9	3 AAY93097	Aay93097 Transform
12	29	46.0	7	2 AAW46010	Aaw46010 Peptide #
13	28	44.4	12	2 AAR86068	Aar86068 Anti-ELAM
14	28	44.4	12	2 AAR86065	Aar86065 Anti-ELAM
15	28	44.4	12	2 AAW26904	Aaw26904 ELAM-1 bi
16	28	44.4	12	2 AAW26900	Aaw26900 ELAM-1 bi
17	28	44.4	12	2 AAW26865	Aaw26865 ELAM-1 bi
18	28	44.4	12	2 AAW63875	Aaw63875 ELAM-1 pe
19	28	44.4	12	2 AAW63886	Aaw63886 ELAM-1 pe
20	28	44.4	12	2 AAW63878	Aaw63878 ELAM-1 pe
21	27	42.9	9	7 ADE67540	Ade67540 Human 161
22	27	42.9	10	7 ADE66432	Ade66432 Human 161
23	27	42.9	10	7 ADE67609	Ade67609 Human 161
24	27	42.9	10	7 ADE70007	Ade70007 Human 161
25	27	42.9	10	7 ADE67387	Ade67387 Human 161

26	27	42.9	10	7	AD569708	Ad569708 Human 161
27	26	41.3	9	4	AAM22800	Aam22800 HIV pepti
28	26	41.3	9	8	ADK08459	Adk08459 Human pap
29	26	41.3	9	8	ADK08095	Adk08095 Human pap
30	26	41.3	10	5	ABG34100	Abg34100 Antigenic
31	26	41.3	10	5	ABG34094	Abg34094 Antigenic
32	26	41.3	11	2	AAW13936	Aaw13936 CDR-3 fra
33	25	39.7	8	4	ABP14228	Abp14228 HIV A02 s
34	25	39.7	8	4	ABP19690	Abp19690 HIV B62 s
35	25	39.7	8	7	ADL17639	Adl17639 ERBIN PDZ
36	25	39.7	9	4	AAM22772	Aam22772 HIV pepti
37	25	39.7	9	4	AAM22747	Aam22747 HIV pepti
38	25	39.7	9	4	ABP16598	Abp16598 HIV A24 s
39	25	39.7	9	4	ABP14239	Abp14239 HIV A02 s
40	25	39.7	9	4	ABP18424	Abp18424 HIV B58 s
41	25	39.7	9	4	ABP22273	Abp22273 HIV A03 m
42	25	39.7	9	4	ABP11937	Abp11937 HIV A01 s
43	25	39.7	9	4	ABP19680	Abp19680 HIV B62 s
44	25	39.7	10	4	ABP19688	Abp19688 HIV B62 s
45	25	39.7	10	4	ABP14253	Abp14253 HIV A02 s

ALIGNMENTS

RESULT 1
AAY92947
ID AAY92947 standard; peptide; 12 AA.
XX AAY92947;
XX
XX
DT 08-NOV-2000 (first entry)
XX
DE Transforming growth factor inhibitory peptide #3.
XX
KW Hepatotropic; antagonist; transforming growth factor betai; TGF-bi;
KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX
OS Homo sapiens.
XX
PN WO200031135-A1.
XX
PD 02-JUN-2000.
XX
PF 23-NOV-1999; 99WO-ES000375.
XX
PR 24-NOV-1998; 98ES-00002465.
(CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
Ezquerro Saenz JJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
Borras Cuesta F;
WPI; 2000-411935/35.
Peptides that antagonize binding of transforming growth factor betai,
useful for treatment of liver disease, especially cirrhosis, are partial
sequences of the factor or its receptors.
Claim 4; Page 80; 86pp; Spanish.
The invention relates to synthetic peptides that antagonise the binding
of transforming growth (TGF) factor betai (TGF-bi) to its receptor in
vivo which have partial amino acid sequences identical, or similar, with
those of TGF-bi and/or its receptors. Peptides AAY92945-Y93133 represent
examples of the peptides of the invention. The peptides act by
competitive inhibition of the binding of TGF-bi to its receptors, e.g.
they are inhibitors of stimulation of collagen synthesis in liver cells
and inhibitors of synthesis of proteolytic enzymes able to degrade the
extracellular matrix. The peptides, their mimetopes and/or DNA (or
expression systems) encoding the peptides are used for treatment of liver
disease, specifically cirrhosis

```

XX
SQ      Sequence 12 AA;
      Query Match      100.0%; Score 63; DB 3; Length 12;
      Best Local Similarity 100.0%; Pred. No. 0.00011;
      Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 TSLDATMIWTMM 12
      |||||
Db      1 TSLDATMIWTMM 12
      |||||

RESULT 2
AAY93008
ID      AAY93008 standard; peptide; 12 AA.
XX
AC      AAY93008;
XX
DT      08-NOV-2000 (first entry)
XX
XX      Transforming growth factor inhibitory peptide P54.
DE
XX      Hepatotrophic; antagonist; transforming growth factor beta1; TGF-b1;
KW      competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW      extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX
OS      Rattus sp.
XX
PN      WO200031135-A1.
XX
PD      02-JUN-2000.
XX
PP      23-NOV-1999; 99WO-ES000375.
XX
PR      24-NOV-1998; 98ES-00002465.
XX
XX      (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
PI      Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
PI      Borras Cuesta F;
XX
XX      WPI; 2000-411935/35.
XX
XX      Peptides that antagonize binding of transforming growth factor beta1,
PT      useful for treatment of liver disease, especially cirrhosis, are partial
PT      sequences of the factor or its receptors.
XX
XX      Disclosure; Page 27; 86pp; Spanish.
XX
XX      The invention relates to synthetic peptides that antagonise the binding
CC      of transforming growth (TGF) factor beta1 (TGF-b1) to its receptor in
CC      vivo which have partial amino acid sequences identical, or similar, with
CC      those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
CC      examples of the peptides of the invention. The peptides act by
CC      competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
CC      they are inhibitors of stimulation of collagen synthesis in liver cells
CC      and inhibitors of synthesis of proteolytic enzymes able to degrade the
CC      extracellular matrix. The peptides, their mimetopes and/or DNA (or
CC      expression systems) encoding the peptides are used for treatment of liver
CC      disease, specifically cirrhosis
XX
XX      Sequence 12 AA;
      Query Match      92.1%; Score 58; DB 3; Length 12;
      Best Local Similarity 100.0%; Pred. No. 0.00091;
      Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      2 SLDATMIWTMM 12
      |||||
Db      1 SLDATMIWTMM 11
      |||||

RESULT 4
AAY93094
ID      AAY93094 standard; peptide; 11 AA.
XX
AC      AAY93094;
XX
DT      08-NOV-2000 (first entry)
XX
XX      Transforming growth factor inhibitory peptide P140.
DE
XX      Hepatotrophic; antagonist; transforming growth factor beta1; TGF-b1;
KW      competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW      extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX
XX

```


OS Homo sapiens.
 XX WO200031135-A1.
 XX
 PD 02-JUN-2000.
 XX
 XX 23-NOV-1999; 99WO-ES000375.
 PF
 XX 24-NOV-1998; 98ES-00002465.
 PR
 XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
 PA
 XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
 PI Borras Cuesta F;
 XX WPI; 2000-411935/35.
 XX
 XX Peptides that antagonize binding of transforming growth factor betal,
 PT useful for treatment of liver disease, especially cirrhosis, are partial
 PT sequences of the factor or its receptors.
 XX
 XX Disclosure; Page 31; 86pp; Spanish.
 PS
 XX The invention relates to synthetic peptides that antagonise the binding
 CC of transforming growth (TGF) factor betal (TGF-b1) to its receptor in
 CC vivo which have partial amino acid sequences identical, or similar, with
 CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
 CC examples of the peptides of the invention. The peptides act by
 CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
 CC they are inhibitors of stimulation of collagen synthesis in liver cells
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
 CC expression systems) encoding the peptides are used for treatment of liver
 CC disease, specifically cirrhosis
 XX
 SQ Sequence 11 AA;
 Query Match 79.4%; Score 50; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.023;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 DATMIWTMM 12
 DB 3 DATMIWTMM 11
 |||||
 |||||
 RESULT 5
 AAY93093
 ID AAY93093 standard; peptide; 12 AA.
 XX
 AC AAY93093;
 XX
 DT 08-NOV-2000 (first entry)
 XX
 XX Transforming growth factor inhibitory peptide P139.
 DE
 XX Hepatotropic; antagonist; transforming growth factor betal; TGF-b1;
 KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
 KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
 XX
 OS Homo sapiens.
 XX
 XX WO200031135-A1.
 PN
 XX 02-JUN-2000.
 PD
 XX 23-NOV-1999; 99WO-ES000375.
 PF
 XX 24-NOV-1998; 98ES-00002465.
 PR
 XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
 PA
 XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
 PI

PI Borras Cuesta F;
 XX
 DR WPI; 2000-411935/35.
 XX
 XX Peptides that antagonize binding of transforming growth factor betal,
 PT useful for treatment of liver disease, especially cirrhosis, are partial
 PT sequences of the factor or its receptors.
 XX
 XX Disclosure; Page 31; 86pp; Spanish.
 PS
 XX The invention relates to synthetic peptides that antagonise the binding
 CC of transforming growth (TGF) factor betal (TGF-b1) to its receptor in
 CC vivo which have partial amino acid sequences identical, or similar, with
 CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
 CC examples of the peptides of the invention. The peptides act by
 CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
 CC they are inhibitors of stimulation of collagen synthesis in liver cells
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
 CC expression systems) encoding the peptides are used for treatment of liver
 CC disease, specifically cirrhosis
 XX
 SQ Sequence 12 AA;
 Query Match 76.2%; Score 48; DB 3; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.058;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TSLDAMTW 9
 DB 1 TSLDAMTW 9
 |||||
 |||||
 RESULT 6
 AAY93007
 ID AAY93007 standard; peptide; 12 AA.
 XX
 AC AAY93007;
 XX
 DT 08-NOV-2000 (first entry)
 XX
 XX Transforming growth factor inhibitory peptide P53.
 DE
 XX Hepatotropic; antagonist; transforming growth factor betal; TGF-b1;
 KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
 KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
 XX
 OS Rattus sp.
 XX
 XX WO200031135-A1.
 PN
 XX 02-JUN-2000.
 PD
 XX 23-NOV-1999; 99WO-ES000375.
 PF
 XX 24-NOV-1998; 98ES-00002465.
 PR
 XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
 PA
 XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
 PI Borras Cuesta F;
 XX WPI; 2000-411935/35.
 DR
 XX Peptides that antagonize binding of transforming growth factor betal,
 PT useful for treatment of liver disease, especially cirrhosis, are partial
 PT sequences of the factor or its receptors.
 XX
 XX Disclosure; Page 27; 86pp; Spanish.
 PS
 XX The invention relates to synthetic peptides that antagonise the binding
 CC of transforming growth (TGF) factor betal (TGF-b1) to its receptor in
 CC vivo which have partial amino acid sequences identical, or similar, with

CC those of TGF- β 1 and/or its receptors. Peptides AAY92945-Y93133 represent
 CC examples of the peptides of the invention. The peptides act by
 CC competitive inhibition of the binding of TGF- β 1 to its receptors, e.g.
 CC they are inhibitors of stimulation of collagen synthesis in liver cells
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
 CC expression systems) encoding the peptides are used for treatment of liver
 CC disease, specifically cirrhosis
 XX
 SQ Sequence 12 AA;

Query Match 58.7%; Score 37; DB 3; Length 12;
 Best Local Similarity 100.0%; Pred. No. 5,6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLDATMI 8
 DB 5 TSLDATMI 12
 |||||

RESULT 7
 AAY93096
 ID AAY93096 standard; peptide; 9 AA.
 XX
 AC AAY93096;
 XX
 DT 08-NOV-2000 (first entry)
 XX
 DE Transforming growth factor inhibitory peptide P142.
 XX
 KW Hepatotropic; antagonist; transforming growth factor beta1; TGF- β 1;
 KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
 KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
 XX
 OS Homo sapiens.
 XX
 PN WO200031135-A1.
 XX
 PD 02-JUN-2000.
 XX
 PF 23-NOV-1999; 99WO-ES000375.
 XX
 PR 24-NOV-1998; 98ES-00002465.
 XX
 PA (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
 XX
 PI Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
 PI Borrás Cuesta F;
 XX
 DR WPI; 2000-411935/35.
 XX
 XX Peptides that antagonize binding of transforming growth factor beta1,
 PT useful for treatment of liver disease, especially cirrhosis, are partial
 PT sequences of the factor or its receptors.
 XX
 PS Disclosure; Page 31; 86pp; Spanish.

XX The invention relates to synthetic peptides that antagonise the binding
 CC of transforming growth (TGF) factor beta1 (TGF- β 1) to its receptor in
 CC vivo which have partial amino acid sequences identical, or similar, with
 CC those of TGF- β 1 and/or its receptors. Peptides AAY92945-Y93133 represent
 CC examples of the peptides of the invention. The peptides act by
 CC competitive inhibition of the binding of TGF- β 1 to its receptors, e.g.
 CC they are inhibitors of stimulation of collagen synthesis in liver cells
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
 CC expression systems) encoding the peptides are used for treatment of liver
 CC disease, specifically cirrhosis
 XX
 SQ Sequence 9 AA;
 Query Match 57.9%; Score 36.5; DB 3; Length 9;
 Best Local Similarity 75.0%; Pred. No. 1.7e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 9;
 OY 1 TSLDATMIWTMM 12
 DB 1 TSL---MIWTMM 9
 |||||

Matches 9; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
 OY 1 TSLDATMIWTMM 12
 DB 1 TSL---MIWTMM 9
 |||||

RESULT 8
 AAY92949
 ID AAY92949 standard; peptide; 9 AA.
 XX
 AC AAY92949;
 XX
 DT 08-NOV-2000 (first entry)
 XX
 DE Transforming growth factor inhibitory peptide #5.
 XX
 KW Hepatotropic; antagonist; transforming growth factor beta1; TGF- β 1;
 KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
 KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
 XX
 OS Homo sapiens.
 XX
 PN WO200031135-A1.
 XX
 PD 02-JUN-2000.
 XX
 PF 23-NOV-1999; 99WO-ES000375.
 XX
 PR 24-NOV-1998; 98ES-00002465.
 XX
 PA (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
 XX
 PI Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
 PI Borrás Cuesta F;
 XX
 DR WPI; 2000-411935/35.
 XX
 XX Peptides that antagonize binding of transforming growth factor beta1,
 PT useful for treatment of liver disease, especially cirrhosis, are partial
 PT sequences of the factor or its receptors.
 XX
 PS Claim 6; Page 81; 86pp; Spanish.

XX The invention relates to synthetic peptides that antagonise the binding
 CC of transforming growth (TGF) factor beta1 (TGF- β 1) to its receptor in
 CC vivo which have partial amino acid sequences identical, or similar, with
 CC those of TGF- β 1 and/or its receptors. Peptides AAY92945-Y93133 represent
 CC examples of the peptides of the invention. The peptides act by
 CC competitive inhibition of the binding of TGF- β 1 to its receptors, e.g.
 CC they are inhibitors of stimulation of collagen synthesis in liver cells
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
 CC expression systems) encoding the peptides are used for treatment of liver
 CC disease, specifically cirrhosis
 XX
 SQ Sequence 9 AA;

Query Match 57.9%; Score 36.5; DB 3; Length 9;
 Best Local Similarity 75.0%; Pred. No. 1.7e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
 OY 1 TSLDATMIWTMM 12
 DB 1 TSL---MIWTMM 9
 |||||

RESULT 9
 AAY93095
 ID AAY93095 standard; peptide; 7 AA.
 XX
 AC AAY93095;
 XX

```

DT 08-NOV-2000 (first entry)
XX Transforming growth factor inhibitory peptide P141.
DE
XX Hepatotropic; antagonist; transforming growth factor betal; TGF-b1;
KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX
OS Homo sapiens.
XX
PN WO200031135-A1.
XX
PD
XX 02-JUN-2000.
XX
XX 23-NOV-1999; 99WO-ES000375.
XX
XX 24-NOV-1998; 98ES-00002465.
XX
XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
PA
XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
PI Borrás Cuesta F;
XX
XX WPI; 2000-411935/35.
XX
XX Peptides that antagonize binding of transforming growth factor betal,
PT useful for treatment of liver disease, especially cirrhosis, are partial
PT sequences of the factor or its receptors.
XX
XX Disclosure; Page 31; 86pp; Spanish.
XX
XX The invention relates to synthetic peptides that antagonise the binding
CC of transforming growth (TGF) factor betal (TGF-b1) to its receptor in
CC vivo which have partial amino acid sequences identical, or similar, with
CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
CC examples of the peptides of the invention. The peptides act by
CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
CC they are inhibitors of stimulation of collagen synthesis in liver cells
CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
CC expression systems) encoding the peptides are used for treatment of liver
CC disease, specifically cirrhosis
XX
XX SQ Sequence 7 AA;
XX
XX Query Match 55.6%; Score 35; DB 3; Length 7;
XX Best Local Similarity 100.0%; Pred. No. 1.7e+06;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DATMIW 9
DB 1 DATMIW 6
    |||||
    |||||

RESULT 10
AAY93010
ID AAY93010 standard; peptide; 12 AA.
XX
XX AAY93010;
XX
XX 08-NOV-2000 (first entry)
XX
XX Transforming growth factor inhibitory peptide P56.
XX
XX Hepatotropic; antagonist; transforming growth factor betal; TGF-b1;
KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX
OS Rattus sp.
XX
XX WO200031135-A1.
XX
XX 02-JUN-2000.
XX
XX Peptides that antagonize binding of transforming growth factor betal,
PT useful for treatment of liver disease, especially cirrhosis, are partial
PT sequences of the factor or its receptors.
XX
XX Disclosure; Page 31; 86pp; Spanish.
XX
XX The invention relates to synthetic peptides that antagonise the binding
CC of transforming growth (TGF) factor betal (TGF-b1) to its receptor in
CC vivo which have partial amino acid sequences identical, or similar, with
CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
CC examples of the peptides of the invention. The peptides act by
CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
CC they are inhibitors of stimulation of collagen synthesis in liver cells
CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
CC expression systems) encoding the peptides are used for treatment of liver
CC disease, specifically cirrhosis
XX
XX SQ Sequence 12 AA;
XX
XX Query Match 55.6%; Score 35; DB 3; Length 12;
XX Best Local Similarity 100.0%; Pred. No. 13;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 MIWTMM 12
DB 1 MIWTMM 6
    |||||
    |||||

RESULT 11
AAY93097
ID AAY93097 standard; peptide; 9 AA.
XX
XX AAY93097;
XX
XX 08-NOV-2000 (first entry)
XX
XX Transforming growth factor inhibitory peptide P143.
XX
XX Hepatotropic; antagonist; transforming growth factor betal; TGF-b1;
KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX
XX Homo sapiens.
XX
XX WO200031135-A1.
XX
XX 02-JUN-2000.
XX
XX 23-NOV-1999; 99WO-ES000375.
XX
XX 24-NOV-1998; 98ES-00002465.
XX
XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
PA
XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
PI Borrás Cuesta F;
XX
XX WPI; 2000-411935/35.
XX
XX Peptides that antagonize binding of transforming growth factor betal,
PT useful for treatment of liver disease, especially cirrhosis, are partial
PT sequences of the factor or its receptors.
XX
XX Disclosure; Page 27; 86pp; Spanish.
XX
XX The invention relates to synthetic peptides that antagonise the binding
CC of transforming growth (TGF) factor betal (TGF-b1) to its receptor in
CC vivo which have partial amino acid sequences identical, or similar, with
CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
CC examples of the peptides of the invention. The peptides act by
CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
CC they are inhibitors of stimulation of collagen synthesis in liver cells
CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
CC expression systems) encoding the peptides are used for treatment of liver
CC disease, specifically cirrhosis
XX
XX SQ Sequence 12 AA;
XX
XX Query Match 55.6%; Score 35; DB 3; Length 12;
XX Best Local Similarity 100.0%; Pred. No. 13;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 MIWTMM 12
DB 1 MIWTMM 6
    |||||
    |||||

```

PT useful for treatment of liver disease, especially cirrhosis, are partial
 PT sequences of the factor or its receptors.

PS Disclosure; Page 31; 86pp; Spanish.

XX The invention relates to synthetic peptides that antagonise the binding
 CC of transforming growth (TGF) factor beta1 (TGF-b1) to its receptor in
 CC vivo which have partial amino acid sequences identical or similar, with
 CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
 CC examples of the peptides of the invention. The peptides act by
 CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
 CC they are inhibitors of stimulation of collagen synthesis in liver cells
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
 CC expression systems) encoding the peptides are used for treatment of liver
 CC disease, specifically cirrhosis

XX Sequence 9 AA;

Query Match 50.0%; Score 31.5; DB 3; Length 9;
 Best Local Similarity 75.0%; Pred. No. 1.7e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 TSLDATMIWTMM 12
 |||||
 Db 1 TSLDAT---TMM 9

RESULT 12

AAW46010
 ID AAW46010 standard; peptide; 7 AA.

XX AAW46010;

XX 03-JUL-1998 (first entry)

XX Peptide #41 based on human SSTR 4 (residues 282-290).

XX Hormone; receptor; antibody; vaccine; immunogen; somatostatin; IGF;
 KW insulin-like growth factor binding protein; IIGFBP; SSTR; diabetes;
 KW somatostatin receptor; insulin-like growth factor.

XX Synthetic.

OS Homo sapiens.

XX WO9744352-A1.

XX 27-NOV-1997.

XX 22-MAY-1997; 97WO-AU000312.

XX 22-MAY-1996; 96AU-00009990.

XX (NORT-) NORTHSTAR BIOLOGICALS PTY LTD.

XX Gerraty NL, Westbrook SL, Kingston DJ;

XX WPI; 1998-018427/02.

XX New non-naturally occurring peptide(s) - which are based on portions of
 PT somatostatin, somatostatin receptors and insulin-like growth factor
 PT binding protein.

PS Disclosure; Page 9; 136pp; English.

XX Peptides AAW45983-W456025 are based on portions of somatostatin,
 CC somatostatin receptors (SSTR) and insulin-like growth factor binding
 CC proteins (IGFBP). They are capable of increasing weight gain, birth
 CC weight, growth rates, milk production, levels of circulating insulin, IGF
 CC -I and IGF-III, fibre production and muscle weight. They may be used to
 CC modulate carbohydrate metabolism and in treatment of diabetes. The oil
 CC carrier may be used for delivery of the peptides

SQ Sequence 7 AA;

Query Match 46.0%; Score 29; DB 2; Length 7;
 Best Local Similarity 85.7%; Pred. No. 1.7e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLDATM 7
 |||||
 Db 1 TSLDATV 7

RESULT 13

AAR86068

ID AAR86068 standard; peptide; 12 AA.

XX AAR86068;

XX 21-JUN-1996 (first entry)

XX Anti-ELAM-1 binding peptide #45.

XX Peptide mimetic; endothelial leukocyte adhesion molecule; ELAM; selectin;
 KW receptor; leukocyte; vascular wall; endothelium; extravasation;
 KW inflammation; sialyl Lewis; cell surface glycoprotein; HL60 cell.

XX Synthetic.

XX WO9531210-A1.

XX 23-NOV-1995.

XX 11-MAY-1995; 95WO-US006315.

XX 11-MAY-1994; 94US-00241054.

XX (AFFY-) AFFYMAX TECHNOLOGIES NV.

XX Barrett RW, Cwirila SE, Dower WJ, Koller KJ, Lee J, Martens CL;
 PI Ruhland-Fritsch B;

XX WPI; 1996-010687/01.

XX New peptide(s) that bind to endothelial leukocyte adhesion molecule 1 -
 PT useful for treating inflammation and other B-selectin mediated diseases.

XX Disclosure; Page 8; 85pp; English.

XX Peptides AAR86024-R86236 are examples of peptides and their mimetics that
 CC bind to endothelial leukocyte adhesion molecule (ELAM)-1. This molecule
 CC is a member of the selectin family of receptors and is involved in
 CC binding of leukocytes to the vascular endothelial wall prior to
 CC extravasation of the leukocyte, e.g. to a site of inflammation. The
 CC peptides bind pref. to E-selectin but may also bind L- or P-selectin, and
 CC conditions. The peptides have strong affinity for the selectin receptors
 CC and inhibit the binding of the sialyl Lewis (SLe-x) part of cell surface
 CC glycoproteins to E-selectin. The peptide are small, generally less than 2
 CC KD, have an IC50 of up to 100 micromole against binding of HL60 cells to
 CC ELAM-1, have one or more peptide linkages replaced by CH2OC(O)NR,
 CC phosphonate, CH2SO2NR, CH2NR, CON(R6), or NHCONH linkages where R = H or
 CC a lower alkyl and R6 = a lower alkyl. The peptides may also have
 CC substituted N- and C-termini e.g. succinimido, N-benzoyloxycarbonyl or N-
 CC lower alkyl cpds

XX Sequence 12 AA;

Query Match 44.4%; Score 28; DB 2; Length 12;
 Best Local Similarity 80.0%; Pred. No. 2.3e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 LWTMM 12
 :|||
 Db 7 LWTMM 11

RESULT 14
 AAR86065
 ID AAR86065 standard; peptide; 12 AA.
 XX
 AC AAR86065;
 XX
 DT 21-JUN-1996 (first entry)
 XX
 DE Anti-ELAM-1 binding peptide #42.
 XX
 KW Peptide mimetic; endothelial leukocyte adhesion molecule; ELAM; selectin;
 KW receptor; leukocyte; vascular wall; endothelium; extravasation;
 KW inflammation; sialyl Lewis; cell surface glycoprotein; HL60 cell.
 XX
 OS Synthetic.
 XX
 PN WO9531210-A1.
 XX
 PD 23-NOV-1995.
 XX
 PF 11-MAY-1995; 95WO-US006315.
 XX
 PR 11-MAY-1994; 94US-00241054.
 XX
 PA (AFFY-) AFFYMAX TECHNOLOGIES NV.
 XX
 PI Barrett RW, Cwirla SE, Dower WJ, Koller KJ, Lee J, Martens CL;
 PI Ruhland-Fritsch B;
 XX
 DR WPI; 1996-010687/01.
 XX
 PT New peptide(s) that bind to endothelial leukocyte adhesion molecule 1 -
 PT useful for treating inflammation and other E-selectin mediated diseases.
 XX
 PS Disclosure; Page 8; 85pp; English.
 XX
 CC Peptides AAR86024-R86236 are examples of peptides and their mimetics that
 CC bind to endothelial leukocyte adhesion molecule (ELAM)-1. This molecule
 CC is a member of the selectin family of receptors and is involved in
 CC binding of leukocytes to the vascular endothelial wall prior to
 CC extravasation of the leukocyte, e.g. to a site of inflammation. The
 CC peptides bind pref. to E-selectin but may also bind L- or P-selectin, and
 CC conditions. The peptides have strong affinity for the selectin receptors
 CC and inhibit the binding of the sialyl Lewis (SLe-x) part of cell surface
 CC glycoproteins to E-selectin. The peptide are small, generally less than 2
 CC kd, have an IC50 of up to 100 micromole against binding of HL60 cells to
 CC ELAM-1, have one or more peptide linkages replaced by CH2OC(O)NR,
 CC phosphonate, CH2SO2NR, CH2NR, CON(R6), or NHCONH linkages where R = H or
 CC a lower alkyl and R6 = a lower alkyl. The peptides may also have
 CC substituted N- and C-termini e.g. succinimido, N-benzoyloxycarbonyl or N-
 CC lower alkyl cpds
 XX
 SQ Sequence 12 AA;

Query Match 44.4%; Score 28; DB 2; Length 12;
 Best Local Similarity 66.7%; Pred. No. 2.3e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 MIWTMM 12
 | : | |
 Db 6 MLNWNM 11

RESULT 15
 AAW26904
 ID AAW26904 standard; peptide; 12 AA.
 XX
 AC AAW26904;
 XX
 DT 27-NOV-1997 (first entry)

XX ELAM-1 binding peptide.
 DE endothelial leukocyte adhesion molecule 1; ELAM-1; HL60 cells;
 KW selectin receptor.
 XX
 OS Synthetic.
 XX
 PN US5648458-A.
 XX
 PD 15-JUL-1997.
 XX
 PF 16-FEB-1995; 95US-00390156.
 XX
 PR 06-MAY-1992; 92US-00881395.
 PR 05-MAY-1993; 93US-00057295.
 XX
 PA (AFFY-) AFFYMAX TECHNOLOGIES NV.
 XX
 PI Dower WJ, Martens CL, Cwirla SE, Barrett RW;
 XX
 DR WPI; 1997-372109/34.
 XX
 PT Peptide(s) that bind to ELAM-1 - for research or therapeutic use.
 XX
 PS Disclosure; Col 8; 39pp; English.
 XX
 CC The invention provides compounds that bind to endothelial leukocyte
 CC adhesion molecule-1 (ELAM-1). The compounds include a lead peptide
 CC HITMDQLNWNVN ("AFFY 4"; AAW26855) discovered using random peptide
 CC diversity generating systems (e.g. "peptides on plasmids" or "peptides on
 CC phage" systems) and peptides screened from a library designed to produce
 CC peptides which differ from the lead peptide by only a few residues.
 CC Peptides which block the binding of HL60 cells to ELAM-1 are the
 CC preferred compounds of the invention. These peptides generally contain
 CC the core sequence WXXLWXXM or WXXLWXX-Nle, where X is any amino acid. The
 CC peptides are used as research tools for studying the biological role of
 CC ELAM-1 and other selectin receptors; to evaluate factors that may
 CC influence or be influenced by cell adhesion; in the development of other
 CC compounds that bind to ELAM-1; and for blocking adhesion of leukocytes to
 CC cells expressing ELAM-1 in vivo, e.g. to treat symptoms related to the
 CC overproduction of cytokines. The present sequence represents an example
 CC of a peptide of the invention
 XX
 SQ Sequence 12 AA;

Query Match 44.4%; Score 28; DB 2; Length 12;
 Best Local Similarity 80.0%; Pred. No. 2.3e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 IWTMM 12
 : | | |
 Db 7 LWTMM 11

Search completed: November 14, 2004, 12:51:26
 Job time : 157 secs

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OM protein - protein search, using sw model

Run on: November 14, 2004, 12:45:20 ; Search time 187 Seconds
(without alignments)
36.922 Million cell updates/sec

Title: US-09-831-253F-3
Perfect score: 63
Sequence: 1 TSLDATMIWTMM 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 4909

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_02:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	38.1	10	1 APE_CAPGI	P80474 capnocytoph
2	24	38.1	11	2 Q9UELO	Q9ue10 homo sapien
3	24	38.1	11	2 Q7MIU2	Q7mlu2 oryza sativ
4	20	31.7	10	1 LABA_JATMU	P13270 jatropa mu
5	20	31.7	10	2 Q7MIJ3	Q7mij3 spinacia ol
6	19	30.2	11	2 Q77896	Q77896 oreochromis
7	19	30.2	12	2 Q9UCR3	Q9ucr3 homo sapien
8	18	28.6	8	2 Q8IVK3	Q8ivk3 homo sapien
9	18	28.6	8	2 Q35835	Q35835 rattus sp.
10	18	28.6	9	2 Q9H3V3	Q9h3v3 homo sapien
11	18	28.6	9	2 Q38366	Q38366 bacterioph
12	18	28.6	9	2 Q801K0	Q801k0 illicura mil
13	18	28.6	9	2 Q801K1	Q801k1 chiroxiphia
14	18	28.6	9	2 Q801K2	Q801k2 antilophia
15	18	28.6	10	2 Q7M501	Q7m501 aspergillus
16	18	28.6	10	2 Q8WTT4	Q8wtt4 homo sapien
17	18	28.6	10	2 Q8SHB4	Q8shb4 furcifer ve
18	18	28.6	10	2 Q8SHH7	Q8shc0 furcifer ou
19	18	28.6	10	2 Q8SHC0	Q8shc0 furcifer la
20	18	28.6	10	2 Q8SHC3	Q8shc3 furcifer la
21	18	28.6	10	2 Q9ESU5	Q9esu5 mus musculu
22	18	28.6	11	2 Q78118	Q78118 oreochromis
23	18	28.6	11	2 Q78120	Q78120 oreochromis
24	18	28.6	12	2 Q6RA12	Q6ra12 homo sapien
25	18	28.6	12	2 Q9UBJ5	Q9ubj5 homo sapien
26	18	28.6	12	2 Q6RAB8	Q6rab8 pygathrix b
27	18	28.6	12	2 Q6RAB9	Q6rab9 pygathrix n
28	18	28.6	12	2 Q6RAC1	Q6rac1 erythrocebu
29	18	28.6	12	2 Q6RAC2	Q6rac2 macaca mula
30	18	28.6	12	2 Q6RAC3	Q6rac3 trachypithe
31	18	28.6	12	2 Q6RAC4	Q6rac4 trachypithe

32	18	28.6	12	2 Q6RAC5	Q6rac5 hylobates l
33	18	28.6	12	2 Q6RAC6	Q6rac6 hylobates h
34	18	28.6	12	2 Q6RAC9	Q6rac9 pongo pygma
35	18	28.6	12	2 Q6RAD3	Q6rad3 gorilla gor
36	18	28.6	12	2 Q6RAE2	Q6rae2 pan troglod
37	18	28.6	12	2 Q77889	Q77889 oreochromis
38	18	28.6	12	2 Q77890	Q77890 oreochromis
39	18	28.6	12	2 Q77891	Q77891 oreochromis
40	18	28.6	12	2 Q77920	Q77920 pseudotroph
41	18	28.6	12	2 AAS87900	Aas87900 homo sapi
42	18	28.6	12	2 AAS87901	Aas87901 homo sapi
43	18	28.6	12	2 AAS87902	Aas87902 homo sapi
44	18	28.6	12	2 AAS87903	Aas87903 homo sapi
45	18	28.6	12	2 AAS87904	Aas87904 homo sapi

ALIGNMENTS

RESULT 1
APE_CAPGI STANDARD; PRT; 10 AA.
AC P80474;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Aminopeptidase (EC 3.4.11.-) (Fragment).
OS Capnocytophaga gingivalis.
OC Bacteria; Bacteroidetes; Flavobacteriales;
OC Flavobacteriaceae; Capnocytophaga.
OX NCBI_TaxID=1017;
RN [1]
RP SEQUENCE.
RC STRAIN=ATCC 33624;
RX MEDLINE=96118234; PubMed=8574402;
RA Spratt D.A., Greenman J., Schafer A.G.;
RT "Capnocytophaga gingivalis aminopeptidase: a potential virulence factor."
RL Microbiology 141:3087-3093(1995).
CC -!- FUNCTION: Aminopeptidase which hydrolyzes substrates with free N-terminal amino acid residues but not N-terminal blocked ones.
CC Optimum activity is measured at pH 7.5. May be important in the nutrition and pathogenesis of the organism in the human oral cavity.
CC -!- COFACTOR: Requires magnesium or calcium.
CC Aminopeptidase; Calcium; Direct protein sequencing; Hydrolase;
KW Magnesium.
FT NON_TER 1 1
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1306 MW; 00C0A6DB43772694 CRC64;

Query Match 38.1%; Score 24; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 DATMIW 9
| | | | |
DB 1 DYNMLW 6

RESULT 2
Q9UELO PRELIMINARY; PRT; 11 AA.
ID Q9UELO
AC Q9UELO;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fas antigen (CD95 antigen) (Fragment).
GN Name=CD95;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.
RX TISSUE=Blood;
R MEDLINE=9535401; PubMed=7543095;
RA Wada N., Matsumura M., Ohba Y., Kobayashi N., Takizawa T.,
RA Nakanishi Y.;
RT "Transcription Stimulation of the Fas-encoding gene by nuclear factor
for interleukin-6 expression upon influenza virus infection.";
RL J. Biol. Chem. 270:18007-18012(1995).
[2]
RP SEQUENCE FROM N.A.
RA Muschen M., Re D., Brauninger A., Wolf J., Hansmann M.L., Diehl V.,
RA Kuppers R., Rajewsky K.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RA Muschen M., Re D., Jungnickel B., Diehl V., Rajewsky K., Kuppers R.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22404279; PubMed=12516573;
RA Kurth J., Pernio A., Schmitz R., Iking-Konert C., Chiorazzi N.,
RA Thompson K.M., Winkler T., Rajewsky K., Kuppers R.;
RT "Lack of deleterious somatic mutations in the CD95 gene of
plasmablasts from systemic lupus erythematosus patients and
autoantibody-producing cell lines.";
RL Eur. J. Immunol. 32:3785-3792(2002).
DR EMBL; D11968; BAA20850.1; -;
DR EMBL; AJ279011; CAC35539.1; -;
DR EMBL; AJ279012; CAC35540.1; -;
DR EMBL; AJ279013; CAC35541.1; -;
DR EMBL; AJ509179; CAD48929.1; -;
DR EMBL; AJ509180; CAD48930.1; -;
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1256 MW; 0802145E2731B370 CRC64;

Query Match 38.1%; Score 24; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 IWTMM 12
DB 4 IWTLL 8

RESULT 3
Q7M1U2
ID Q7M1U2 PRELIMINARY; PRT; 11 AA.
AC Q7M1U2;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Unidentified 5.7/35K protein (Fragment).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriarthroideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE.
RA Komatsu S., Kajiwara H., Hirano H.;
RT "A rice protein library, a data-file of rice proteins separated by
two-dimensional electrophoresis.";
RL Theor. Appl. Genet. 86:935-942(1993).
DR PIR; PQ0731; PQ0731.
FT NON_TER 11 11
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1319 MW; CBE97F0E53277362 CRC64;

Query Match 38.1%; Score 24; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 ATMIW 9
DB 1 ATVMW 5

RESULT 4
LABA_JATMU
ID LABA_JATMU STANDARD; PRT; 10 AA.
AC P13270;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Labaditin.
OS Jatropha multifida (Physic nut).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids I; Malpighiales; Euphorbiaceae; Crotonoideae; Jatrophaeae;
OC Jatropha.
OX NCBI_TaxID=3996;
RN [1]
RP SEQUENCE.
RC TISSUE=Latex;
RA Koassi S., van der Sluis W.G., Boslens R., T'Hart L.A., Labadie R.P.;
RT "Labaditin, a novel cyclic decapeptide from the latex of Jatropha
multifida L. (Euphorbiaceae): Isolation and sequence determination by
means of two-dimensional NMR.";
RL FEBS Lett. 256:91-96(1989).
CC -!- FUNCTION: Labaditin is an active peptide which inhibits the
classical pathway of complement activation in vitro. Activity
seems to be based on an interaction with C1.
CC -!- PTM: This is a cyclic peptide.
CC -!- MISCELLANEOUS: Latex of this plant is used in folkloric medicine
for treatment of infected wounds, skins infections and scabies.
KW Direct protein sequencing.
SQ SEQUENCE 10 AA; 1089 MW; D98AAD6362D1B362 CRC64;

Query Match 31.7%; Score 20; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 6.7e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 IWTM 11
DB 3 WVTV 6

RESULT 5
Q7M1J3
ID Q7M1J3 PRELIMINARY; PRT; 10 AA.
AC Q7M1J3;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cystathionine gamma-synthase (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Amaranthaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE.
RX MEDLINE=95142682; PubMed=7840669;
RA Ravanel S., Droux M., Douce R.;
RT "Methionine biosynthesis in higher plants. I. Purification and
characterization of cystathionine gamma-synthase from spinach
chloroplasts.";
RL Arch. Biochem. Biophys. 316:572-584(1995).
DR PIR; S69159; S69159.
FT NON_TER 1 1
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 873 MW; D88458DDDDAB2CD CRC64;

Query Match 31.7%; Score 20; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 6.7e+03;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TSLDATMI 8
|:|:|
Db 2 TAVDAAI 9

RESULT 6

O77896 PRELIMINARY; PRT; 11 AA.
AC O77896;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DE MHC class II B locus 12 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Labroidae;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Ruczyńska Z., McAndrew B., Vincek V.,
RA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid MHC
class II B loci."
RL Genetics 149:1527-1537(1998).
DR EMBL; AF050006; AAC41345.1; -.
FT NON_TER 1
FT NON_TER 11
SQ SEQUENCE 11 AA; 1399 MW; 3F47DB7A772685A3 CRC64;

Query Match 30.2%; Score 19; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 9 WTMM 12
|:|:
Db 4 WSML 7

RESULT 7

O9UCR3 PRELIMINARY; PRT; 12 AA.
AC O9UCR3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE AUTOTAXIN (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=92129337; PubMed=1733949;
RA Stracke M.L., Krutzsch H.C., Unsworth E.J., Arestad A., Cioce V.,
RA Schiffmann E., Liotta L.A.;
RT "Identification, purification, and partial sequence analysis of
RT autotaxin, a novel motility-stimulating protein."
RL J. Biol. Chem. 267:2524-2529(1992).
FT NON_TER 1
FT NON_TER 12
SQ SEQUENCE 12 AA; 1493 MW; 433482B3F335A1A7 CRC64;

Query Match 30.2%; Score 19; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSLD 4
|:|:|

Db 6 TSLD 9

RESULT 8

O8IVK3 PRELIMINARY; PRT; 8 AA.
AC O8IVK3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Steerin2 (Fragment).
GN Name=STEERIN2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Peeters P.J., Verhasselt P., Moechars D.W., Luyten W.H.M.L.,
RA Geysen J.J.G.H.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ488208; CAD32561.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 1030 MW; E8A7245417737726 CRC64;

Query Match 28.6%; Score 18; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MIW 9
|:|:
Db 1 MLW 3

RESULT 9

O35835 PRELIMINARY; PRT; 8 AA.
AC O35835;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ORF1 protein.
GN Name=ORF1;
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98008057; PubMed=9581555;
RA Hospital V., Prat A., Joulie C., Cherif D., Day R., Cohen P.;
RT "Human and rat testis express two mRNA species encoding variants of
RT NR1 convertase, a metalloendopeptidase of the insulinase family."
RL Biochem. J. 327:773-779(1997).
DR EMBL; X93208; CAA63695.1; -.
SQ SEQUENCE 8 AA; 886 MW; EA7EA1B1ADC5A5B6 CRC64;

Query Match 28.6%; Score 18; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 ATMW 9
|:|:
Db 4 ATCW 8

RESULT 10

O9H3Y3 PRELIMINARY; PRT; 9 AA.
AC O9H3Y3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE DJ839B11.1 (Novel protein with a Kunitz/Bovine pancreatic trypsin
DE inhibitor domain and WAP-type (Whey Acidic Protein) 'four-disulfide
DE core' domains) (Fragment).
GN Name=dJ461P17.1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lloyd D.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL121778; CAB76844.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1036 MW; 2C417B01B412D1B3 CRC64;

Query Match 28.6%; Score 18; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 IWTM 11
Db 1 MWTV 4

RESULT 11

Q38366 ID Q38366 PRELIMINARY; PRT; 9 AA.
AC Q38366;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE E gene product (Fragment).
OS Bacteriophage phi-X174.
OC Viruses; ssDNA viruses; Microviridae; Microvirus.
OX NCBI_TaxID=10847;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88118956; PubMed=2963134;
RA Buckley K.J., Hayashi M.;
RT "Role of premature translational termination in the regulation of
RT expression of the phi X174 lysis gene.";
RL J. Mol. Biol. 198; 599-607 (1987).
DR EMBL; X07809; CAA30668.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1207 MW; C093B37731B36412 CRC64;

Query Match 28.6%; Score 18; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 WTM 11
Db 4 WTL 6

RESULT 12

Q801K0 ID Q801K0 PRELIMINARY; PRT; 9 AA.
AC Q801K0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Beta fibrinogen (Fragment).
GN Name=beta fibrinogen;
OS Ilicura militaris (pin-tailed manakin).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Ilicura.
OX NCBI_TaxID=208056;
RN [1]
RP SEQUENCE FROM N.A.
RA Marini M.A., Hackett S.J.;

RT "A Multifaceted Approach to the Characterization of an Intergeneric
RT Hybrid Manakin (Pipridae) from Brazil.";
RL Auk 119:1114-1120(2002).
DR EMBL; AY136617; AAN16894.1; -.
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 992 MW; 8620B378744AB1 CRC64;

Query Match 28.6%; Score 18; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 WTM 11
Db 7 WTL 9

RESULT 13

Q801K1 ID Q801K1 PRELIMINARY; PRT; 9 AA.
AC Q801K1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Beta fibrinogen (Fragment).
GN Name=beta fibrinogen;
OS Chiroxiphia caudata.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Pipridae; Chiroxiphia.
OX NCBI_TaxID=196027;
RN [1]
RP SEQUENCE FROM N.A.
RA Marini M.A., Hackett S.J.;
RT "A Multifaceted Approach to the Characterization of an Intergeneric
RT Hybrid Manakin (Pipridae) from Brazil.";
RL Auk 119:1114-1120(2002).
DR EMBL; AY136616; AAN16893.1; -.
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 992 MW; 8620B378744AB1 CRC64;

Query Match 28.6%; Score 18; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 WTM 11
Db 7 WTL 9

RESULT 14

Q801K2 ID Q801K2 PRELIMINARY; PRT; 9 AA.
AC Q801K2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Beta fibrinogen (Fragment).
GN Name=beta fibrinogen;
OS Antilophia galeata (Helmeted manakin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Tyrannidae; Antilophia.
OX NCBI_TaxID=208054;
RN [1]
RP SEQUENCE FROM N.A.
RA Marini M.A., Hackett S.J.;
RT "A Multifaceted Approach to the Characterization of an Intergeneric
RT Hybrid Manakin (Pipridae) from Brazil.";
RL Auk 119:1114-1120(2002).
DR EMBL; AY136615; AAN16892.1; -.
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 992 MW; 8620B378744AB1 CRC64;

Query Match 28.6%; Score 18; DB 2; Length 9;
Best Local Similarity 66.7%; Pred.No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 9 WTM 11
|
Db 7 WTL 9
|

RESULT 15

Q7M501 ID Q7M501 PRELIMINARY; PRT; 10 AA.
AC Q7M501;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Polygalacturonase (EC 3.2.1.15) IV (Fragment).
OS Aspergillus sp.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5065;
RN [1]
RP SEQUENCE.
RX MEDLINE=93151962; PubMed=8427629;
RA Stratilova E., Markovic O., Skrovinova D., Rexova-Benkova L.,
RA Jorvall H.;
RT "Pectinase Aspergillus sp. polygalacturonase: multiplicity,
RT divergence, and structural patterns linking fungal, bacterial, and
RT plant polygalacturonases.";
RL J. Protein Chem. 12:15-22 (1993).
DR PIR; D61440; D61440.
DR GO; GO:0004650; F:polygalacturonase activity; IEA.
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 959 MW; 845236CSA1A9D1AE CRC64;

Query Match 28.6%; Score 18; DB 2; Length 10;
Best Local Similarity 80.0%; Pred.No. 1.6e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TSLDA 5
|
Db 6 TSADA 10
|

Search completed: November 14, 2004, 12:54:38
Job time : 188 secs

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OM protein - protein search, using sw model

Run on: November 14, 2004, 12:54:46 ; Search time 136 Seconds
(without alignments)
31.219 Million cell updates/sec

Title: US-09-831-253F-3

Perfect score: 63

Sequence: 1 TSLDATWMTMM 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1568699 seqs, 353819137 residues

Total number of hits satisfying chosen parameters: 199616

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
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- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
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- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	46.0	7	9 US-09-758-128-41	Sequence 41, Appl
2	29	46.0	7	9 US-09-758-128-44	Sequence 44, Appl
3	29	46.0	7	9 US-09-758-426-41	Sequence 41, Appl
4	29	46.0	7	9 US-09-758-426-44	Sequence 44, Appl
5	29	46.0	7	9 US-09-758-198-41	Sequence 41, Appl
6	29	46.0	7	9 US-09-758-198-44	Sequence 44, Appl
7	29	46.0	7	10 US-09-861-661-41	Sequence 41, Appl
8	29	46.0	7	10 US-09-861-661-44	Sequence 44, Appl
9	27	42.9	10	14 US-10-062-109A-642	Sequence 642, App
10	27	42.9	10	14 US-10-005-480A-642	Sequence 642, App
11	26	41.3	9	15 US-10-182-252A-685	Sequence 685, App
12	25	39.7	8	14 US-10-190-082-602	Sequence 602, App
13	25	39.7	9	14 US-10-357-935-20	Sequence 20, Appl

14	39.7	9	15	US-10-182-252A-632	Sequence 632, App
15	39.7	9	15	US-10-182-252A-657	Sequence 657, App
16	39.7	9	15	US-10-182-252A-1216	Sequence 1216, Ap
17	39.7	10	14	US-10-200-708-79	Sequence 79, Appl
18	39.7	10	14	US-10-200-708-501	Sequence 501, App
19	39.7	11	10	US-09-758-109-7	Sequence 7, Appli
20	39.7	12	9	US-09-823-829-44	Sequence 44, Appl
21	39.7	12	9	US-09-840-277-69	Sequence 69, Appl
22	39.7	12	9	US-09-823-823-44	Sequence 44, Appl
23	39.7	12	15	US-10-609-217-151	Sequence 151, App
24	39.7	12	15	US-10-632-388-151	Sequence 151, App
25	39.7	12	15	US-10-651-723-151	Sequence 151, App
26	39.7	12	15	US-10-645-761-151	Sequence 151, App
27	39.7	12	15	US-10-666-696-151	Sequence 151, App
28	39.7	12	15	US-10-653-048-151	Sequence 151, App
29	38.1	7	15	US-10-651-165-170	Sequence 170, App
30	38.1	9	10	US-09-997-209-82	Sequence 82, Appl
31	38.1	9	15	US-10-182-252A-3	Sequence 3, Appli
32	38.1	9	15	US-10-182-252A-215	Sequence 215, App
33	38.1	9	15	US-10-182-252A-617	Sequence 617, App
34	38.1	9	15	US-10-182-252A-631	Sequence 631, App
35	38.1	9	15	US-10-182-252A-656	Sequence 656, App
36	38.1	9	15	US-10-182-252A-658	Sequence 658, App
37	38.1	9	15	US-10-433-206-82	Sequence 82, Appl
38	38.1	11	10	US-09-809-391-551	Sequence 551, App
39	38.1	11	10	US-09-882-171-551	Sequence 551, App
40	38.1	11	14	US-10-092-908-38	Sequence 38, Appl
41	38.1	11	14	US-10-164-861-551	Sequence 551, App
42	36.5	9	10	US-09-845-042-27	Sequence 27, Appl
43	36.5	9	14	US-10-062-109A-13	Sequence 13, Appl
44	36.5	9	14	US-10-005-480A-13	Sequence 13, Appl
45	36.5	9	15	US-10-182-252A-630	Sequence 630, App

ALIGNMENTS

RESULT 1

US-09-758-128-41
; Sequence 41, Application US/09758128
; Patent No. US20020107187A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATY, No. US20020107187A1man L.
; APPLICANT: WESTBROOK, Simon L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,128
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-758-128-41

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Best Local Similarity 85.7%; Pred. No. 1.4e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSLDATM 7

Db 1 TSLDATV 7

RESULT 2

US-09-758-128-44


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; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758.198
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-02-05
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1997-05-22
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; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1996-05-22
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-05-22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Rat
US-09-758-198-44

Query Match          46.0%; Score 29; DB 9; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.4e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLDATM 7
DB 1 TSLDATV 7

RESULT 7
US-09-861-661-41
; Sequence 41, Application US/09861661
; Publication No. US20030045676A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, DAVID J.
; APPLICANT: GERRATY, NORMAN L.
; APPLICANT: WESTBROOK, SIMON L.
; TITLE OF INVENTION: PEPTIDES, ANTIBODIES, VACCINES & USES THEREOF
; FILE REFERENCE: 054270/0135
; CURRENT APPLICATION NUMBER: US/09/861.661
; CURRENT FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-861-661-41

Query Match          46.0%; Score 29; DB 10; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.4e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLDATM 7
DB 1 TSLDATV 7

RESULT 8
US-09-861-661-44
; Sequence 44, Application US/09861661
; Publication No. US20030045676A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, DAVID J.
; APPLICANT: GERRATY, NORMAN L.
; APPLICANT: WESTBROOK, SIMON L.
; TITLE OF INVENTION: PEPTIDES, ANTIBODIES, VACCINES & USES THEREOF
; FILE REFERENCE: 054270/0135
; CURRENT APPLICATION NUMBER: US/09/861.661
; CURRENT FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05

; FILE REFERENCE: 016786/0214
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; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
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; LENGTH: 7
; TYPE: PRT
; ORGANISM: Rat
US-09-758-198-44

Query Match          46.0%; Score 29; DB 9; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.4e+06;
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DB 1 TSLDATV 7

RESULT 9
US-10-062-109A-642
; Sequence 642, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 642
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-642

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Best Local Similarity 44.4%; Pred. No. 2.9e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 TSLDATMIW 9
DB 1 TCVESTRIW 9

RESULT 10
US-10-005-480A-642
; Sequence 642, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
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; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 642
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-642

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Best Local Similarity 44.4%; Pred. No. 2.9e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 TSLDATMIW 9
DB 1 TCVESTRIW 9

RESULT 11

US-10-182-252A-685
; Sequence 685, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUUS, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEMOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 685
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-685

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Best Local Similarity 33.3%; Pred. No. 1.4e+06;
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QY 3 LDATMIWTM 11
DB 1 IQAIVWTV 9

RESULT 12

US-10-190-082-602
; Sequence 602, Application US/10190082
; Publication No. US20030148264A1
; GENERAL INFORMATION:
; APPLICANT: Laeky, Lawrence A.
; APPLICANT: Sidhu, Sachdev S.
; APPLICANT: Held, Heike A.
; TITLE OF INVENTION: PHAGE DISPLAYED PDZ DOMAIN LIGANDS
; FILE REFERENCE: EP0905R1
; CURRENT APPLICATION NUMBER: US/10/190,082
; CURRENT FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/303,634
; PRIOR FILING DATE: 2001-07-06

; NUMBER OF SEQ ID NOS: 683
; SEQ ID NO 602
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-190-082-602

Query Match 39.7%; Score 25; DB 14; Length 8;
Best Local Similarity 37.5%; Pred. No. 1.4e+06;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 DATMIWTM 11
DB 1 DETSVWVL 8

RESULT 13

US-10-357-935-20
; Sequence 20, Application US/10357935
; Publication No. US20030165958A1
; GENERAL INFORMATION:
; APPLICANT: HARDY, John Anthony
; APPLICANT: GOATE, Alison Mary
; APPLICANT: MULLAN, Michael John
; APPLICANT: CHARTIER-HARLIN, Marie-Christine
; APPLICANT: OWEN, Michael John
; TITLE OF INVENTION: Test and Model for Alzheimer's Disease
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/357,935
; FILING DATE: 03-Feb-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,250
; FILING DATE: 05-Jun-1995
; APPLICATION NUMBER: 08/104,165
; FILING DATE: 21-JAN-1992
; APPLICATION NUMBER: 9101307.8
; FILING DATE: 21-JAN-1991
; APPLICATION NUMBER: 9118445.7
; FILING DATE: 28-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joe
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 16163-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-357-935-20

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Best Local Similarity 80.0%; Pred. No. 1.4e+06;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 ATMIW 9
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Db 2 ATVIW 6

RESULT 14
US-10-182-252A-632
; Sequence 632, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUUS, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEMOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 632
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-632

Query Match 39.7%; Score 25; DB 15; Length 9;
Best Local Similarity 42.9%; Pred. No. 1.4e+06;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATMIWTM 11
|:|:
Db 3 AIVVWTL 9

RESULT 15
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; Sequence 657, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUUS, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEMOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 657

; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-657

Query Match 39.7%; Score 25; DB 15; Length 9;
Best Local Similarity 42.9%; Pred. No. 1.4e+06;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATMIWTM 11
|:|:
Db 3 AIVVWTL 9

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Job time : 137 secs

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OM protein - protein search, using sw model

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(without alignments)
22.106 Million cell updates/sec

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Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	28	44.4	12	1	US-08-390-156A-57
6	28	44.4	12	1	US-08-390-156A-61
7	28	44.4	12	1	US-08-439-817-30
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29	25	39.7	12	1	US-08-439-817-200	Sequence 200, Appl
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31	25	39.7	12	1	US-08-485-508-95	Sequence 95, Appl
32	25	39.7	12	1	US-08-485-508-98	Sequence 98, Appl
33	25	39.7	12	4	US-09-823-823-44	Sequence 44, Appl
34	25	39.7	12	4	US-09-428-082B-151	Sequence 151, Appl
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36	24	38.1	7	4	US-08-974-690C-170	Sequence 170, Appl
37	24	38.1	7	4	US-08-974-685-170	Sequence 170, Appl
38	24	38.1	7	4	US-08-974-685-180	Sequence 180, Appl
39	24	38.1	9	4	US-08-466-601A-160	Sequence 160, Appl
40	24	38.1	11	4	US-09-149-476-551	Sequence 551, Appl
41	23	36.5	8	3	US-08-444-818-563	Sequence 563, Appl
42	23	36.5	8	3	US-08-444-818-564	Sequence 564, Appl
43	23	36.5	9	3	US-09-171-705-76	Sequence 76, Appl
44	23	36.5	10	2	US-08-617-929-24	Sequence 24, Appl
45	23	36.5	11	4	US-09-620-091-443	Sequence 443, Appl

ALIGNMENTS

RESULT 1
US-08-241-054-50
; Sequence 50, Application US/08241054
; Patent No. 5643873
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Cwirla, Steven E.
; APPLICANT: Dower, William J.
; APPLICANT: Koller, Kerry J.
; APPLICANT: Lee, Jung
; APPLICANT: Martens, Christine L.
; APPLICANT: Ruhlend-Fritsch, Beatrice
; TITLE OF INVENTION: Peptides and Compounds That Bind
; TITLE OF INVENTION: Selectins Including Endothelium Leukocyte Adhesion
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/241,054
; FILING DATE: 11-MAY-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,295
; FILING DATE: 05-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/881,395
; FILING DATE: 06-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Gerald F. Swiss
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 000324-002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-7400
; TELEFAX: 415-854-8275
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-241-054-50

Query Match 44.4%; Score 28; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 1; Gaps 0;

Qy 7 LWTMM 12
Db 6 MLWNMM 11

RESULT 2

US-08-241-054-53
; Sequence 53, Application US/08241054
; Patent No. 5643873
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Cwiria, Steven E.
; APPLICANT: Dower, William J.
; APPLICANT: Koller, Kerry J.
; APPLICANT: Lee, Jung
; APPLICANT: Martens, Christine L.
; APPLICANT: Ruhland-Fritsch, Beatrice
; TITLE OF INVENTION: Peptides and Compounds That Bind
; TITLE OF INVENTION: Selectins Including Endothelium Leukocyte Adhesion
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/241,054
; FILING DATE: 11-MAY-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,295
; FILING DATE: 05-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/881,395
; FILING DATE: 06-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Gerald F. Swiss
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 000324-002
; TELEPHONE: 415-854-7400
; TELEFAX: 415-854-8275
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-241-054-53

Query Match 44.4%; Score 28; DB 1; Length 12;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 IWTMM 12
Db :||||

Db 7 LWTMM 11

RESULT 3

US-08-241-054-61
; Sequence 61, Application US/08241054
; Patent No. 5643873
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Cwiria, Steven E.
; APPLICANT: Dower, William J.
; APPLICANT: Koller, Kerry J.
; APPLICANT: Lee, Jung
; APPLICANT: Martens, Christine L.
; APPLICANT: Ruhland-Fritsch, Beatrice
; TITLE OF INVENTION: Peptides and Compounds That Bind
; TITLE OF INVENTION: Selectins Including Endothelium Leukocyte Adhesion
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/241,054
; FILING DATE: 11-MAY-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,295
; FILING DATE: 05-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/881,395
; FILING DATE: 06-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Gerald F. Swiss
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 000324-002
; TELEPHONE: 415-854-7400
; TELEFAX: 415-854-8275
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-241-054-61

Query Match 44.4%; Score 28; DB 1; Length 12;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 IWTMM 12
Db :||||

RESULT 4

US-08-390-156A-22
; Sequence 22, Application US/08390156A
; Patent No. 5648458
; GENERAL INFORMATION:
; APPLICANT: Cwiria, Steven E.
; APPLICANT: Barrett, Ronald W.

APPLICANT: Dower, William J.
APPLICANT: Martens, Christine L.
TITLE OF INVENTION: Peptides and Compounds That Bind to
TITLE OF INVENTION: ELAM-1
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Affymax Technologies, N.V.
STREET: 4001 Miranda Ave.
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,156A
FILING DATE: 16-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,295
FILING DATE: 05-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Swiss, Gerald F.
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 1023.1A
TELEPHONE: 415-496-2300
TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO: 22:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-390-156A-22

Query Match 44.4%; Score 28; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 7 MIWTMM 12
Db 6 MLWNMM 11

RESULT 5
US-08-390-156A-57
Sequence 57, Application US/08390156A
Patent No. 5648458
GENERAL INFORMATION:
APPLICANT: Cwirla, Steven E.
APPLICANT: Barrett, Ronald W.
APPLICANT: Dower, William J.
APPLICANT: Martens, Christine L.
TITLE OF INVENTION: Peptides and Compounds That Bind to
TITLE OF INVENTION: ELAM-1
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Affymax Technologies, N.V.
STREET: 4001 Miranda Ave.
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,156A
FILING DATE: 16-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,295
FILING DATE: 05-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/881,395
FILING DATE: 06-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Swiss, Gerald F.
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 1023.1A
TELEPHONE: 415-496-2300
TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO: 57:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-390-156A-57

Query Match 44.4%; Score 28; DB 1; Length 12;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 8 IWTMM 12
Db 7 LWTMM 11

RESULT 6
US-08-390-156A-61
Sequence 61, Application US/08390156A
Patent No. 5648458
GENERAL INFORMATION:
APPLICANT: Cwirla, Steven E.
APPLICANT: Barrett, Ronald W.
APPLICANT: Dower, William J.
APPLICANT: Martens, Christine L.
TITLE OF INVENTION: Peptides and Compounds That Bind to
TITLE OF INVENTION: ELAM-1
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Affymax Technologies, N.V.
STREET: 4001 Miranda Ave.
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,156A
FILING DATE: 16-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,295
FILING DATE: 05-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/881,395
FILING DATE: 06-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Swiss, Gerald F.
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 1023.1A

```
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-496-2300
/ TELEFAX: 415-424-0832
/ INFORMATION FOR SEQ ID NO: 61:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 12 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/
US-08-390-156A-61

Query Match 44.4%; Score 28; DB 1; Length 12;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 IWTMM 12
Db 7 LWTMM 11

RESULT 7
US-08-439-817-30
; Sequence 30, Application US/08439817
; Patent No. 5728802
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Cwirla, Steven E.
; APPLICANT: Dower, William J.
; APPLICANT: Koller, Kerry J.
; APPLICANT: Lee, Jung
; APPLICANT: Martens, Christine L.
; APPLICANT: Ruhland-Fritsch, Beatrice
; TITLE OF INVENTION: Peptides and Compounds That Bind
; TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion
; TITLE OF INVENTION: Molecule I (ELAM-1)
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies, NV
; STREET: 4001 Miranda Ave.
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/439,817
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/241,054
; FILING DATE: 11-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,295
; FILING DATE: 05-MAY-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/881,395
; FILING DATE: 06-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 000324-046/1056.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
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```
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/
US-08-439-817-30

Query Match 44.4%; Score 28; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 MIWTMM 12
Db 6 MLWNMM 11

RESULT 8
US-08-439-817-33
; Sequence 33, Application US/08439817
; Patent No. 5728802
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Cwirla, Steven E.
; APPLICANT: Dower, William J.
; APPLICANT: Koller, Kerry J.
; APPLICANT: Lee, Jung
; APPLICANT: Martens, Christine L.
; APPLICANT: Ruhland-Fritsch, Beatrice
; TITLE OF INVENTION: Peptides and Compounds That Bind
; TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion
; TITLE OF INVENTION: Molecule I (ELAM-1)
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies, NV
; STREET: 4001 Miranda Ave.
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/439,817
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/241,054
; FILING DATE: 11-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,295
; FILING DATE: 05-MAY-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/881,395
; FILING DATE: 06-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 000324-046/1056.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
/
US-08-439-817-33

Query Match 44.4%; Score 28; DB 1; Length 12;
Best Local Similarity 80.0%; Pred. No. 1e+02;
```

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 IWTMM 12
:||||
Db 7 LWTMM 11

RESULT 9
US-08-439-817-41
; Sequence 41, Application US/08439817
; Patent No. 5728802
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Cwirla, Steven E.
; APPLICANT: Dower, William J.
; APPLICANT: Koller, Kerry J.
; APPLICANT: Lee, Jung
; APPLICANT: Martens, Christine L.
; APPLICANT: Ruhland-Fritsch, Beatrice
; TITLE OF INVENTION: Peptides and Compounds That Bind
; TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion
; TITLE OF INVENTION: Molecule I (ELAM-1)
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies, NV
; STREET: 4001 Miranda Ave.
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/439,817
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/241,054
; FILING DATE: 11-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,295
; FILING DATE: 05-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/881,395
; FILING DATE: 06-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 000324-046/1056.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-439-817-41

Query Match 44.4%; Score 28; DB 1; Length 12;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 IWTMM 12
:||||
Db 7 LWTMM 11

RESULT 10

US-08-485-508-50
; Sequence 50, Application US/08485508
; Patent No. 5786322
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Cwirla, Steven E.
; APPLICANT: Dower, William J.
; APPLICANT: Koller, Kerry J.
; APPLICANT: Lee, Jung
; APPLICANT: Martens, Christine L.
; APPLICANT: Ruhland-Fritsch, Beatrice
; TITLE OF INVENTION: Peptides and Compounds That Bind
; TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion
; TITLE OF INVENTION: Molecule I
; NUMBER OF SEQUENCES: 162
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies, NV
; STREET: 4001 Miranda Ave.
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,508
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/241,054
; FILING DATE: 11-MAY-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,295
; FILING DATE: 05-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/881,395
; FILING DATE: 06-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 000324-002/1056
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-485-508-50

Query Match 44.4%; Score 28; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 MIWTMM 12
:||||
Db 6 MLNMM 11

RESULT 11
US-08-485-508-53
; Sequence 53, Application US/08485508
; Patent No. 5786322
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.

APPLICANT: Cwirla, Steven E.
APPLICANT: Dower, William J.
APPLICANT: Koller, Kerry J.
APPLICANT: Lee, Jung
APPLICANT: Martens, Christine L.
APPLICANT: Ruhland-Fritsch, Beatrice
TITLE OF INVENTION: Peptides and Compounds That Bind
TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion
TITLE OF INVENTION: Molecule 1
NUMBER OF SEQUENCES: 162
CORRESPONDENCE ADDRESS:
ADDRESS: Affymax Technologies, NV
STREET: 4001 Miranda Ave.
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,508
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/241,054
FILING DATE: 11-MAY-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,295
FILING DATE: 05-MAY-1993
APPLICATION NUMBER: US 07/881,395
FILING DATE: 06-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Stevens, Lauren L.
REGISTRATION NUMBER: 36,691
REFERENCE/DOCKET NUMBER: 000324-002/1056
TELEPHONE: 415-496-2300
TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-485-508-53

Query Match 44.4%; Score 28; DB 1; Length 12;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 IWTMM 12
Db 7 LWTMM 11

RESULT 12
US-08-485-508-61
Sequence 61, Application US/08485508
Patent No. 5786322
GENERAL INFORMATION:
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Dower, William J.
APPLICANT: Koller, Kerry J.
APPLICANT: Lee, Jung
APPLICANT: Martens, Christine L.
APPLICANT: Ruhland-Fritsch, Beatrice

TITLE OF INVENTION: Peptides and Compounds That Bind
TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion
TITLE OF INVENTION: Molecule 1
NUMBER OF SEQUENCES: 162
CORRESPONDENCE ADDRESS:
ADDRESS: Affymax Technologies, NV
STREET: 4001 Miranda Ave.
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,508
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/241,054
FILING DATE: 11-MAY-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,295
FILING DATE: 05-MAY-1993
APPLICATION NUMBER: US 07/881,395
FILING DATE: 06-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Stevens, Lauren L.
REGISTRATION NUMBER: 36,691
REFERENCE/DOCKET NUMBER: 000324-002/1056
TELEPHONE: 415-496-2300
TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-485-508-61

Query Match 44.4%; Score 28; DB 1; Length 12;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 IWTMM 12
Db 7 LWTMM 11

RESULT 13
US-08-396-385-9
Sequence 9, Application US/08396385
Patent No. 6001349
GENERAL INFORMATION:
APPLICANT: Schlom, Jeffrey
APPLICANT: Panicali, Dennis
TITLE OF INVENTION: GENERATION OF HUMAN CYTOTOXIC T-CELLS
TITLE OF INVENTION: SPECIFIC FOR CARCINOMA SELF-ASSOCIATED ANTIGENS AND USES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEWALL P. BRONSTEIN; DIKE, BRONSTEIN, ROBERTS
ADDRESSEE: CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: US

ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/396,385
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 44933
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
US-08-396-385-9

Query Match 42.9%; Score 27; DB 3; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 DATMIW 9
DB 3 DATYLM 8

RESULT 14
US-09-287-221-9
Sequence 9, Application US/09287221
Patent No. 6319496
GENERAL INFORMATION:
APPLICANT: Schlom, Jeffrey
APPLICANT: Panicali, Dennis
TITLE OF INVENTION: GENERATION OF HUMAN CYTOTOXIC T-CELLS
TITLE OF INVENTION: SPECIFIC FOR CARCINOMA SELF-ASSOCIATED ANTIGENS AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEWALL P. BRONSTEIN; DIKE, BRONSTEIN, ROBERTS
ADDRESSEE: & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: US
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/287,221
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/396,385
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 44933
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440

TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
US-09-287-221-9

Query Match 42.9%; Score 27; DB 3; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 DATMIW 9
DB 3 DATYLM 8

RESULT 15
US-08-104-165-20
Sequence 20, Application US/08104165
Patent No. 5877015
GENERAL INFORMATION:
APPLICANT: HARDY, John Anthony
APPLICANT: GOATE, Alison Mary
APPLICANT: MULLAN, Michael John
APPLICANT: CHARTIER-HARLIN, Marie-Christine
APPLICANT: OWEN, Michael John
TITLE OF INVENTION: Test and Model for Alzheimer's Disease
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/104,165
FILING DATE: 21-JAN-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9101307.8
FILING DATE: 21-JAN-1991
APPLICATION NUMBER: 9118445.7
FILING DATE: 28-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16163-000100
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-104-165-20

Query Match 39.7%; Score 25; DB 2; Length 9;
Best Local Similarity 80.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 ATMIW 9
DB 2 ATYIM 6

Search completed: November 14, 2004, 12:56:03
Job time : 37 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:25 ; Search time 7.40425 seconds
(without alignments)
155.938 Million cell updates/sec

Title: US-09-831-253F-3
Perfect score: 63
Sequence: 1 TSLDATMIWTMM 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 4495

Minimum DB seq length: 0
Maximum DB seq length: 23

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	47.6	15	PH1612	Ig H chain V-D-J r
2	28	44.4	14	PH1625	Ig H chain V-D-J r
3	28	44.4	14	PH1627	Ig H chain V-D-J r
4	28	44.4	15	PH1613	Ig H chain V-D-J r
5	28	44.4	16	PH1637	Ig H chain V-D-J r
6	26	41.3	17	PH1331	Ig heavy chain DJ
7	25	39.7	17	PH1630	Ig H chain V-D-J r
8	25	39.7	22	PQ0007	killer toxin - yea
9	25	39.7	23	PC4030	rRNA endonuclease
10	24	38.1	11	PQ0731	unidentified 5.7/3
11	24	38.1	13	PH1636	Ig H chain V-D-J r
12	24	38.1	14	PH1594	Ig H chain V-D-J r
13	24	38.1	16	PH1638	Ig H chain V-D-J r
14	24	38.1	20	A44921	hydroxypyruvate re
15	24	38.1	22	S40838	Arf-43 protein - h
16	24	38.1	23	T03261	glutamate-ammonia
17	23.5	37.3	19	PH1315	Ig heavy chain DJ
18	23	36.5	13	PH1620	Ig H chain V-D-J r
19	23	36.5	14	A35105	hypothetical prote
20	23	36.5	20	PH1358	Ig heavy chain DJ
21	22	34.9	7	PH1602	Ig H chain V-D-J r
22	22	34.9	21	A44139	RNA-polymerase-ass
23	21.5	34.1	20	PH1380	alpha-amylase (EC
24	21	33.3	14	PH1327	Ig heavy chain DJ
25	21	33.3	20	PL0192	Ig lambda 2 chain
26	21	33.3	20	PH1326	Ig heavy chain DJ
27	20	31.7	10	S69159	cystathionine gamm
28	20	31.7	14	PH1626	Ig H chain V-D-J r
29	20	31.7	18	A32220	T-cell receptor de

cytochrome P450-C-
L-lactate dehydrog
probable trp opero
thrABC leader pept
T-cell receptor be
Ig heavy chain DJ
r cell receptor al
Ig heavy chain DJ
self-incompatibili
major outer membra
Ig heavy chain V r
Ig heavy chain CDR
polygalacturonase
proton-translocati
collecting duct wa
aeg-46.5 protein -

ALIGNMENTS

RESULT 1

PH1612
Ig H chain V-D-J region (wild-type clone 344) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C:Accession: PH1612

R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mic.
A;Reference number: PH1580; MUID:93301609; PMID:8315387
A;Accession: PH1612
A;Molecule type: DNA
A;Residues: 1-15 <LEV>
A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin

Query Match 47.6%; Score 30; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 13;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 DATMIWT 10
DB 9 EVTMLWT 15

RESULT 2

PH1625
Ig H chain V-D-J region (clone B-less 109) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C:Accession: PH1625

R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mic
A;Reference number: PH1580; MUID:93301609; PMID:8315387
A;Accession: PH1625
A;Molecule type: DNA
A;Residues: 1-14 <LEV>
A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin

Query Match 44.4%; Score 28; DB 2; Length 14;
Best Local Similarity 80.0%; Pred. No. 29;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 TMIWT 10
DB 10 TMLWT 14

RESULT 3

PH1627

IG H chain V-D-J region (clone B-less 120) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C:Accession: PH1627
R:Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A:Reference number: PH1580; MUID:93301609; PMID:8315387
A:Accession: PH1627
A:Molecule type: DNA
A:Residues: 1-14 <LEV>
A:Experimental source: bone marrow pre-B lymphocyte
C:Keywords: immunoglobulin

Query Match 44.4%; Score 28; DB 2; Length 14;
Best Local Similarity 80.0%; Pred. No. 29;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 TMIWT 10
||:|
Db 10 TMLWT 14

RESULT 4

PH1613
IG H chain V-D-J region (clone B-less 17) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C:Accession: PH1613
R:Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A:Reference number: PH1580; MUID:93301609; PMID:8315387
A:Accession: PH1613
A:Molecule type: DNA
A:Residues: 1-15 <LEV>
A:Experimental source: bone marrow pre-B lymphocyte
C:Keywords: immunoglobulin

Query Match 44.4%; Score 28; DB 2; Length 15;
Best Local Similarity 80.0%; Pred. No. 32;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 TMIWT 10
||:|
Db 11 TMLWT 15

RESULT 5

PH1637
IG H chain V-D-J region (clone B-less 226) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C:Accession: PH1637
R:Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A:Reference number: PH1580; MUID:93301609; PMID:8315387
A:Accession: PH1637
A:Molecule type: DNA
A:Residues: 1-16 <LEV>
A:Experimental source: bone marrow pre-B lymphocyte
C:Keywords: immunoglobulin

Query Match 44.4%; Score 28; DB 2; Length 16;
Best Local Similarity 80.0%; Pred. No. 34;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 TMIWT 10
||:|
Db 12 TMLWT 16

RESULT 6

PH1331
IG heavy chain DJ region (clone C148-106) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PH1331
R:Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymphoma
A:Reference number: PH1302; MUID:93094761; PMID:1460419
A:Accession: PH1331
A:Molecule type: DNA
A:Residues: 1-17 <WAS>
C:Keywords: heterotetramer; immunoglobulin

Query Match 41.3%; Score 26; DB 2; Length 17;
Best Local Similarity 44.4%; Pred. No. 89;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 SLDATMIWT 10
:|:|
Db 3 TLRTTWT 11

RESULT 7

PH1630
IG H chain V-D-J region (clone B-less 156) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C:Accession: PH1630
R:Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A:Reference number: PH1580; MUID:93301609; PMID:8315387
A:Accession: PH1630
A:Molecule type: DNA
A:Residues: 1-17 <LEV>
A:Experimental source: bone marrow pre-B lymphocyte
C:Keywords: immunoglobulin

Query Match 39.7%; Score 25; DB 2; Length 17;
Best Local Similarity 40.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 TSLDATMIWT 10
|:|
Db 8 TTYGRPLWT 17

RESULT 8

PQ0007
Killer toxin - yeast (Pichia farinosa) (fragment)
C:Species: Pichia farinosa
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C:Accession: PQ0007
R:Suzuki, C.; Nikkuni, S.
Agric. Biol. Chem. 53, 2599-2604, 1989
A:Title: Purification and properties of the killer toxin produced by a halotolerant yeast
A:Reference number: PQ0007
A:Accession: PQ0007
A:Molecule type: protein
A:Residues: 1-22 <SUZ>
A:Cross-references: UNIPROT:P19372
A:Experimental source: strain KK1
A:Note: the full activity of this toxin depends on NaCl or KCl

Query Match 39.7%; Score 25; DB 2; Length 22;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 DATMIW 9
:|:|
Db 2 EATTIW 7

RESULT 9
PC4030
rRNA endonuclease (EC 3.1.27.10) - shiitake mushroom (fragment)
N:Alternate names: nuclease Le3
C:Species: Lentinula edodes (shiitake mushroom)
C:Date: 21-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C:Accession: PC4030
R: Kobayashi, H.; Inokuchi, N.; Koyama, T.; Tomita, M.; Irie, M.
Biosci. Biotechnol. Biochem. 59, 1169-1171, 1995
A: Title: Purification and characterization of the 2nd 5'-nucleotide-forming nuclease from *Lentinula edodes*
A: Reference number: PC4030; MUID: 95337563; PMID: 7613009
A: Accession: PC4030
A: Molecule type: DNA
A: Residues: 1-23 <KOB>
A: Cross-references: UNIPROT: Q9UR71
C: Comment: This enzyme has 3'-nucleotidase activity.
C: Keywords: endonuclease; hydrolase

Query Match 39.7%; Score 25; DB 2; Length 23;
Best Local Similarity 37.5%; Pred. No. 1.9e+02;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 SLDATMIW 9
DB 16 ALDPSPFW 23

RESULT 10
PQ0731
unidentified 5.7/35K protein [imported] - rice (fragment)
C: Species: Oryza sativa (rice)
C: Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C: Accession: PQ0731
R: Komatsu, S.; Kajiwara, H.; Hirano, H.
Theor. Appl. Genet. 86, 935-942, 1993
A: Title: A rice protein library; a data-file of rice proteins separated by two-dimensional gel electrophoresis
A: Reference number: PQ0696
A: Accession: PQ0731
A: Status: preliminary
A: Molecule type: protein
A: Residues: 1-11 <KOM>
A: Cross-references: UNIPROT: Q7M1U2

Query Match 38.1%; Score 24; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 ATMIW 9
DB 1 ATVW 5

RESULT 11
PH1636
Ig H chain V-D-J region (clone B-less 224) - mouse (fragment)
C: Species: Mus musculus (house mouse)
C: Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C: Accession: PH1636
R: Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A: Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A: Reference number: PH1580; MUID: 93301609; PMID: 8315387
A: Accession: PH1636
A: Molecule type: DNA
A: Residues: 1-13 <LEV>
A: Experimental source: bone marrow pre-B lymphocyte
C: Keywords: immunoglobulin

Query Match 38.1%; Score 24; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 1.6e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 TMWT 10
DB 10 MVWT 13

RESULT 12
PH1594
Ig H chain V-D-J region (wild-type clone 149) - mouse (fragment)
C: Species: Mus musculus (house mouse)
C: Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C: Accession: PH1594
R: Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A: Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A: Reference number: PH1580; MUID: 93301609; PMID: 8315387
A: Accession: PH1594
A: Molecule type: DNA
A: Residues: 1-14 <LEV>
A: Experimental source: bone marrow pre-B lymphocyte
C: Keywords: immunoglobulin

Query Match 38.1%; Score 24; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATMIW 10
DB 9 ATGLWT 14

RESULT 13
PH1638
Ig H chain V-D-J region (clone B-less 228) - mouse (fragment)
C: Species: Mus musculus (house mouse)
C: Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C: Accession: PH1638
R: Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A: Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A: Reference number: PH1580; MUID: 93301609; PMID: 8315387
A: Accession: PH1638
A: Molecule type: DNA
A: Residues: 1-16 <LEV>
A: Experimental source: bone marrow pre-B lymphocyte
C: Keywords: immunoglobulin

Query Match 38.1%; Score 24; DB 2; Length 16;
Best Local Similarity 60.0%; Pred. No. 2e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 TMWT 10
DB 12 SMLWT 16

RESULT 14
A44921
hydroxypyruvate reductase (EC 1.1.1.81) - Methylobacterium extorquens (fragment)
C: Species: Methylobacterium extorquens
C: Date: 01-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C: Accession: A44921
R: Chistoserdova, L.V.; Lidstrom, M.E.
J. Bacteriol. 174, 71-77, 1992
A: Title: Cloning, mutagenesis, and physiological effect of a hydroxypyruvate reductase gene from *Methylobacterium extorquens*
A: Reference number: A44921; MUID: 92104992; PMID: 1729225
A: Accession: A44921
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-20 <CHI>
A: Cross-references: GB: M81443; NID: g150010; PID: AAA25378.1; PID: g150011
A: Note: sequence extracted from NCBI backbone (NCBI: 75202, NCBI: 75203)

C;Keywords: oxidoreductase

Query Match 38.1%; Score 24; DB 2; Length 20;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SLDATM 7
|||:
Db 12 SLDATV 17

RESULT 15

S40638
ATP-43 protein - human (fragments)
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 10-Nov-1995
C;Accession: S40638
R;Hurst, H.C.; Totty, N.F.; Jones, N.C.
Nucleic Acids Res. 19, 4601-4609, 1991
A;Title: Identification and functional characterisation of the cellular activating trans
A;Reference number: S40638; MUID:91367654; PMID:1653949
A;Accession: S40638
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-22 <HUR>

Query Match 38.1%; Score 24; DB 2; Length 22;
Best Local Similarity 50.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 TSLDATMIWT 10
||| |:
Db 12 TSLPQTIVNT 21

Search completed: November 14, 2004, 12:03:10
Job time : 9.40425 secs

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OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:26 ; Search time 32.0426 Seconds
(without alignments)
215.479 Million cell updates/sec

Title: US-09-831-253F-3
Perfect score: 63
Sequence: 1 TSLDATTMTWM 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 17482

Minimum DB seq length: 0
Maximum DB seq length: 23

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_02:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	39.7	18	2 Q9ZY81	Q9zy81 amitus sp.
2	25	39.7	18	2 Q9S817	Q9s817 oryza sativ
3	25	39.7	18	2 Q9S818	Q9s818 oryza sativ
4	25	39.7	20	2 Q9TWP7	Q9twp7 leishmania
5	25	39.7	23	2 Q9UR71	Q9ur71 leishmania
6	24	38.1	10	1 APE_CAPGI	P80474 capnocytoph
7	24	38.1	11	2 Q9UELO	Q9ue10 homo sapien
8	24	38.1	11	2 Q7MIU2	Q7miu2 oryza sativ
9	24	38.1	17	1 LPW_AZOBRR	P50871 azospirillum
10	24	38.1	17	2 Q6LDJ9	Q6ldl9 rattus norv
11	24	38.1	17	2 Q6LEA8	Q6lea8 xenopus lae
12	24	38.1	17	2 AAA49911	Aaa49911 xenopus l
13	24	38.1	17	2 AAA41680	Aaa41680 rattus no
14	24	38.1	18	2 Q9ZYV8	Q9zyv8 aspilota sp
15	24	38.1	19	2 Q9ZYW5	Q9zyw5 jarra phoro
16	24	38.1	19	2 Q8W128	Q8w128 scaevola pr
17	24	38.1	20	2 Q49132	Q49132 methylobact
18	24	38.1	23	2 C07939	Q07939 nicotiana t
19	23	36.5	16	2 Q8HUN0	Q8hun0 uncultured
20	23	36.5	16	2 Q8HUM1	Q8hum1 uncultured
21	23	36.5	17	2 Q69074	Q69074 human herpe
22	23	36.5	17	2 Q8ZS29	Q8zsz9 pyrobaculum
23	23	36.5	19	2 Q6PTX6	Q6ptx6 gallus gall
24	23	36.5	19	2 AAS90337	Aas90337 gallus ga
25	22	34.9	15	2 Q9TR62	Q9tr62 oryctolagus
26	22	34.9	19	2 Q9TRP4	Q9trp4 bos taurus
27	22	34.9	21	2 Q95N72	Q95n72 equus cabal
28	22	34.9	22	2 Q48861	Q48861 oryza sativ
29	22	34.9	22	2 Q8CI00	Q8ciq0 rattus norv
30	22	34.9	23	2 Q8HA22	Q8ha22 bacterioph
31	22	34.9	23	2 Q9R570	Q9r570 nitrosomona

Q9r5e8 bacillus sp
Q9twc0 acanthamoeb
Q9prf0 oryzias lat
Q9zyv6 bethyridae
Q6wa89 myxine glut
Q865g9 actus azara
Aaq63924 myxine gl
Q93r63 yersinia pe
P13270 jatropha mu
Q7miJ3 spinacia ol
Q6vfm5 photobacter
Aar04051 photobact
Aar04054 photobact
Aas16489 photobact

ALIGNMENTS

RESULT 1
Q9ZY81 PRELIMINARY; PRT; 18 AA.
AC Q9ZY81;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome oxidase II (Fragment).
OS Amitus sp.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Platygastridae;
OC Platygastridae; Amitus.
OX NCBI_TaxID=81080;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99152621; PubMed=10028295;
RA Downton M., Austin A.D.;
RT "Evolutionary dynamics of a mitochondrial rearrangement 'hot spot' in
RL Mol. Biol. Evol. 16:298-309(1999).
DR EMBL, AF082920; AAD17780.1; --
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 1 1
SQ SEQUENCE 18 AA; 2153 MW; 6480609B2C35EC7A CRC64;
Query Match 39.7%; Score 25; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 TSLDATTMTWT 10
DB 6 TSLNNFLKWT 15
RESULT 2
Q9S817 PRELIMINARY; PRT; 18 AA.
AC Q9S817;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE 40 kDa PI 8.5 ABCISFIC acid-induced histidine rich protein
(Fragment).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE.
RX MEDLINE=95175599; PubMed=7870812;
RA Moons A., Bauw G., Prinsen E., Van Montagu M., Van der Straeten D.;

RT "Molecular and physiological responses to abscisic acid and salts in roots of salt-sensitive and salt-tolerant Indica rice varieties.";
 RL Plant Physiol. 107:177-186(1995).
 DR Gramene; Q9S817; -.
 SQ SEQUENCE 18 AA; 2094 MW; 0CD245DB237E7520 CRC64;

Query Match 39.7%; Score 25; DB 2; Length 18;
 Best Local Similarity 42.9%; Pred. No. 1.4e+03;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 DATMIWT 10
 | : : : :
 DB 10 DESVLWT 16

RESULT 3
 ID Q9S818 PRELIMINARY; PRT; 18 AA.
 AC Q9S818;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DE 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE 40 kDa PI 8.5 ABSCESSIC acid-induced protein (Fragment).
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95175599; PubMed=7870812;
 RA Moons A., Bauw G., Prinsen E., Van Montagu M., Van der Straeten D.;
 RT "Molecular and physiological responses to abscisic acid and salts in roots of salt-sensitive and salt-tolerant Indica rice varieties.";
 RL Plant Physiol. 107:177-186(1995).
 DR Gramene; Q9S818; -.
 SQ SEQUENCE 18 AA; 2097 MW; 146450D9A97BE6D83 CRC64;

Query Match 39.7%; Score 25; DB 2; Length 18;
 Best Local Similarity 42.9%; Pred. No. 1.4e+03;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 DATMIWT 10
 | : : : :
 DB 10 DESVLWT 16

RESULT 4
 ID Q9TWP7 PRELIMINARY; PRT; 20 AA.
 AC Q9TWP7;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 DE Cathepsin B-like cysteine protease (Fragment).
 OS Leishmania mexicana.
 OC Eukaryota; Euzoenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=5665;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=94187801; PubMed=8139620;
 RA Robertson C.D., Coombs G.H.;
 RT "Cathepsin B-like cysteine proteases of Leishmania mexicana.";
 RL Mol. Biochem. Parasitol. 62:271-279(1993).
 SQ SEQUENCE 20 AA; 2203 MW; FE1A260FA1DBE41F CRC64;

Query Match 39.7%; Score 25; DB 2; Length 20;
 Best Local Similarity 50.0%; Pred. No. 1.5e+03;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 SLDATMIWTM 11
 | : : : :
 DB 5 SPDASEKMPM 14

RESULT 5
 ID Q9UR71 PRELIMINARY; PRT; 23 AA.

AC Q9UR71;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2004 (TREMBlrel. 26, Last annotation update)
 DE 5'-nucleotide-forming nuclease (Fragment).
 OS Lentinula edodes (Shiitake mushroom) (Lentinus edodes).
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Agaricales; Tricholomataceae; Lentinula.
 OX NCBI_TaxID=5353;
 RN [1]
 RP SEQUENCE.

RX MEDLINE=95337563; PubMed=7613009;
 RA Kobayashi H., Inokuchi N., Koyama T., Tomita M., Irie M.;
 RT "Purification and characterization of the 2nd 5'-nucleotide-forming RT nuclease from Lentinus edodes.";
 RL Biosci. Biotechnol. Biochem. 59:1169-1171(1995).
 DR PIR; PC4030; PC4030.
 DR InterPro; IPR008947; PLC Nuclease.
 SQ SEQUENCE 23 AA; 2535 MW; 978082B3B161FCC6 CRC64;

Query Match 39.7%; Score 25; DB 2; Length 23;
 Best Local Similarity 37.5%; Pred. No. 1.8e+03;
 Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 SLDATMIW 9
 | : : : :
 DB 16 ALDPSFVW 23

RESULT 6
 ID APE CAPGI STANDARD; PRT; 10 AA.

AC P80474;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Aminopeptidase (EC 3.4.11.-) (Fragment).
 OS Capnocytophaga gingivalis.
 OC Bacteria; Bacteroidetes; Flavobacteria; Flavobacteriales;
 OC Flavobacteriaceae; Capnocytophaga.
 OX NCBI_TaxID=1017;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=ATCC 33624;
 RX MEDLINE=96118234; PubMed=8574402;
 RA Spratt D.A., Greenman J., Schaffer A.G.;
 RT "Capnocytophaga gingivalis aminopeptidase: a potential virulence factor.";
 RL Microbiology 141:3087-3093(1995).
 CC -!- FUNCTION: Aminopeptidase which hydrolyzes substrates with free N-terminal amino acid residues but not N-terminal blocked ones.
 CC Optimum activity is measured at pH 7.5. May be important in the nutrition and pathogenesis of the organism in the human oral cavity.
 CC -!- COFACTOR: Requires magnesium or calcium.
 CC Aminopeptidase; Calcium; Direct protein sequencing; Hydrolase;
 KW Magnesium.
 FT NON_TER 1 1
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1306 MW; 00C0A6DB43772694 CRC64;

Query Match 38.1%; Score 24; DB 1; Length 10;
 Best Local Similarity 50.0%; Pred. No. 1.2e+03;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 DATMIW 9
 | : : : :
 DB 1 DYNMLW 6


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RESULT 7
Q9UELO PRELIMINARY; PRT; 11 AA.
AC Q9UELO;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fas antigen (CD95 antigen) (Fragment).
GN Name=CD95;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX Wada N., Matsumura M., Ohba Y., Kobayashi N., Takizawa T.,
MEDLINE=95355401; PubMed=7543095;
RA Nakanishi Y.;
RT "Transcription Stimulation of the Fas-encoding gene by nuclear factor
for interleukin-6 expression upon influenza virus infection.";
RL J. Biol. Chem. 270:18007-18012(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Muschen M., Re D., Brauning A., Wolf J., Hansmann M.L., Diehl V.,
Kuppers R., Rajewsky K.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Muschen M., Re D., Jungnickel B., Diehl V., Rajewsky K., Kuppers R.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22404279; PubMed=12516573;
RA Kurth J., Pernotok A., Schmitz R., Iking-Konert C., Chiorazzi N.,
Thompson K.M., Winkler T., Rajewsky K., Kueppers R.;
RT "Lack of deleterious somatic mutations in the CD95 gene of
plasmablasts from systemic lupus erythematosus patients and
autoantibody-producing cell lines.";
RL Eur. J. Immunol. 32:3785-3792(2002).
DR ENBL; D31968; BAA20850.1; -
DR ENBL; AJ279011; CAC35539.1; -
DR ENBL; AJ279012; CAC35540.1; -
DR ENBL; AJ279013; CAC35541.1; -
DR ENBL; AJ509179; CAD48929.1; -
DR ENBL; AJ509180; CAD48930.1; -
FT NON TER 11
SQ SEQUENCE 11 AA; 1256 MW; 0802145E2731B370 CRC64;

Query Match 38.1%; Score 24; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 ITWM 12
Db 4 ITWL 8

RESULT 8
Q7MIU2 PRELIMINARY; PRT; 11 AA.
AC Q7MIU2;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Unidentified 5.7/35K protein (Fragment).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;

Query Match 38.1%; Score 24; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 ITWM 12
Db 4 ITWL 8

RESULT 9
LPW_AZOBR STANDARD; PRT; 17 AA.
AC P50871;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Trp operon leader peptide.
GN Name=trpL;
OS Azospirillum brasilense.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC Rhodospirillaceae; Azospirillum.
OX NCBI_TaxID=192;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sp7;
RX MEDLINE=97094331; PubMed=8939798;
RA de Troch P., Dosselaere F., Keijers V., de Wilde P., Vanderleyden J.;
RT "Isolation and characterization of the Azospirillum brasilense trpE(G)
gene, encoding anthranilate synthase.";
RL Curr. Microbiol. 34:27-32(1997).
CC -!- FUNCTION: This protein is involved in control of the biosynthesis
of tryptophan.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
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or send an email to license@isb-sib.ch).
CC -----
DR ENBL; U44127; AAC45140.1; -
KW Leader peptide; tryptophan biosynthesis.
SQ SEQUENCE 17 AA; 2114 MW; CD42DDEC3724BC9A CRC64;

Query Match 38.1%; Score 24; DB 1; Length 17;
Best Local Similarity 41.7%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 TSLDATMIWTMM 12
Db 6 TSLSCRWMPVM 17

RESULT 10
Q6LDL9 PRELIMINARY; PRT; 17 AA.
AC Q6LDL9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Neural cell adhesion molecule (Fragment).

```

GN Name=NCAM-C;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RX NCBI_TaxID=101116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=90287121; PubMed=1694009;
RA Chen A., Reyes A., Akesson R.A.;

RT "Transcription initiation sites and structural organization of the
RT extreme 5' region of the rat neural cell adhesion molecule gene.";
RL Mol. Cell. Biol. 10:3314-3324(1990).
DR EMBL; M32612; AAA41680.1; -;
FT NON_TER 1
SQ SEQUENCE 17 AA; 2026 MW; AEA1EB5F252B94F5 CRC64;

Query Match 38.1%; Score 24; DB 2; Length 17;
Best Local Similarity 60.0%; Pred. No. 2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 MIWTM 11
Db 7 LIWTL 11

RESULT 11

Q6LEA8
ID Q6LEA8 PRELIMINARY; PRT; 17 AA.

AC Q6LEA8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Neural cell adhesion molecule (Fragment).

GN Name=NCAM;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]

RP SEQUENCE FROM N.A.
RA Johnson A.D., Ovsenek N., Tonissen K.F., Krieg P.A.;
RL Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; L26396; AAA49911.1; -;
FT NON_TER 17
SQ SEQUENCE 17 AA; 2005 MW; AEBD9B5855262107 CRC64;

Query Match 38.1%; Score 24; DB 2; Length 17;
Best Local Similarity 60.0%; Pred. No. 2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 MIWTM 11
Db 7 LIWTL 11

RESULT 12

AAA49911
ID AAA49911 PRELIMINARY; PRT; 17 AA.

AC AAA49911;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Neural cell adhesion molecule (Fragment).

GN NCAM.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.

RA Johnson A.D., Ovsenek N., Tonissen K.F., Krieg P.A.;
RT "The Xenopus NCAM promoter: Appropriate expression in response to
RT neural inducing signals and identification of a conserved sequence
RT element.";
RL Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; L26396; AAA49911.1; -;
FT NON_TER 17
SQ SEQUENCE 17 AA; 2005 MW; AEBD9B5855262107 CRC64;

Query Match 38.1%; Score 24; DB 2; Length 17;
Best Local Similarity 60.0%; Pred. No. 2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 MIWTM 11
Db 7 LIWTL 11

RESULT 13

AAA41680
ID AAA41680 PRELIMINARY; PRT; 17 AA.

AC AAA41680;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Neural cell adhesion molecule (Fragment).

GN NCAM-C.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RX NCBI_TaxID=101116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=90287121; PubMed=1694009;
RA Chen A., Reyes A., Akesson R.A.;

RT "Transcription initiation sites and structural organization of the
RT extreme 5' region of the rat neural cell adhesion molecule gene.";
RL Mol. Cell. Biol. 10:3314-3324(1990).
DR EMBL; M32612; AAA41680.1; -;
FT NON_TER 17
SQ SEQUENCE 17 AA; 2026 MW; AEA1EB5F252B94F5 CRC64;

Query Match 38.1%; Score 24; DB 2; Length 17;
Best Local Similarity 60.0%; Pred. No. 2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 MIWTM 11
Db 7 LIWTL 11

RESULT 14

Q9ZVY8
ID Q9ZVY8 PRELIMINARY; PRT; 18 AA.

AC Q9ZVY8;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome oxidase II (Fragment).

OS Aspilota sp.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonidea;
OC Braconidae; Alysiinae; Aspilota.

OX NCBI_TaxID=61200;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99152621; PubMed=10028295;
RT Dowton M., Austin A.D.;
RT "Evolutionary dynamics of a mitochondrial rearrangement 'hot spot' in
RT the hymenoptera.";
RL Mol. Biol. Evol. 16:298-309(1999).

DR EMBL; AF034603; AAC79751.1; -
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON TER 1 1
 SQ SEQUENCE 18 AA; 2181 MW; F83846FDAEB8DCD6 CRC64;

Query Match 38.1%; Score 24; DB 2; Length 18;
 Best Local Similarity 62.5%; Pred. No. 2.1e+03;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 SLDATMIW 9
 |||||
 Db 7 SLKIFMIW 14

RESULT 15

Q9ZYW5 PRELIMINARY; PRT; 19 AA.
 AC Q9ZYW5;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cytochrome oxidase II (Fragment).
 OS Jarra phorocantha.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonoides;
 OC Braconidae; Doryctinae; Jarra.
 OX NCBI_TaxID=64830;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99152621; PubMed=10028295;
 RA Downton M., Austin A.D.;
 RT "Evolutionary dynamics of a mitochondrial rearrangement 'hot spot' in
 the hymenoptera.";
 RL Mol. Biol. Evol. 16:298-309(1999).
 DR EMBL; AF034596; AAC79744.1; -
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON TER 1 1
 SQ SEQUENCE 19 AA; 2291 MW; B964CCC7FDAC36C3 CRC64;

Query Match 38.1%; Score 24; DB 2; Length 19;
 Best Local Similarity 41.7%; Pred. No. 2.2e+03;
 Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 TSLDATMIWTMM 12
 |||||
 Db 6 TSLNSFFNWLKM 17

Search completed: November 14, 2004, 12:07:29
 Job time : 35.0426 secs

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OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:26 ; Search time 9.44681 Seconds
(without alignments)
84.242 Million cell updates/sec

Title: US-09-831-253F-3
Perfect score: 63
Sequence: 1 TSLDATMWTMM 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 202416

Minimum DB seq length: 0
Maximum DB seq length: 23

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	44.4	12	1	US-08-241-054-50
2	28	44.4	12	1	US-08-241-054-53
3	28	44.4	12	1	US-08-241-054-61
4	28	44.4	12	1	US-08-390-156A-22
5	28	44.4	12	1	US-08-390-156A-57
6	28	44.4	12	1	US-08-390-156A-61
7	28	44.4	12	1	US-08-439-817-30
8	28	44.4	12	1	US-08-439-817-33
9	28	44.4	12	1	US-08-439-817-41
10	28	44.4	12	1	US-08-485-508-50
11	28	44.4	12	1	US-08-485-508-53
12	28	44.4	12	1	US-08-485-508-61
13	28	44.4	13	1	US-07-920-519-12
14	28	44.4	13	1	US-08-086-410-9
15	28	44.4	13	1	US-08-314-586-12
16	27	42.9	10	3	US-08-396-385-9
17	27	42.9	10	3	US-09-287-221-9
18	26	41.3	15	4	US-09-255-501-106
19	26	41.3	15	4	US-09-255-501-107
20	25	39.7	9	2	US-08-104-165-20
21	25	39.7	9	3	US-08-464-250-20
22	25	39.7	9	3	US-08-464-250-20
23	25	39.7	11	2	US-08-319-052-7
24	25	39.7	11	2	US-08-442-108B-7
25	25	39.7	12	1	US-08-241-054-55
26	25	39.7	12	1	US-08-241-054-95
27	25	39.7	12	1	US-08-241-054-98

28	39.7	12	1	US-08-390-156A-45	Sequence 45, Appl
29	39.7	12	1	US-08-390-156A-58	Sequence 58, Appl
30	39.7	12	1	US-08-390-156A-87	Sequence 87, Appl
31	39.7	12	1	US-08-439-817-35	Sequence 35, Appl
32	39.7	12	1	US-08-439-817-75	Sequence 75, Appl
33	39.7	12	1	US-08-439-817-78	Sequence 78, Appl
34	39.7	12	1	US-08-439-817-200	Sequence 200, Appl
35	39.7	12	1	US-08-485-508-55	Sequence 55, Appl
36	39.7	12	1	US-08-485-508-95	Sequence 95, Appl
37	39.7	12	1	US-08-485-508-98	Sequence 98, Appl
38	39.7	12	4	US-09-823-823-44	Sequence 44, Appl
39	39.7	12	4	US-09-428-082B-151	Sequence 151, App
40	39.7	15	4	US-09-255-501-108	Sequence 108, App
41	39.7	20	1	US-08-382-013A-18	Sequence 18, Appl
42	39.7	20	1	US-08-241-054-81	Sequence 81, Appl
43	39.7	20	1	US-08-390-156A-38	Sequence 38, Appl
44	39.7	20	1	US-08-439-817-61	Sequence 61, Appl
45	39.7	20	1	US-08-485-508-81	Sequence 81, Appl

ALIGNMENTS

RESULT 1
US-08-241-054-50
; Sequence 50, Application US/08241054
; Patent No. 5643873
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Cwirla, Steven E.
; APPLICANT: Dower, William J.
; APPLICANT: Koller, Kerry J.
; APPLICANT: Lee, Jung
; APPLICANT: Martens, Christine L.
; APPLICANT: Ruhland-Fritsch, Beatrice
; TITLE OF INVENTION: Peptides and Compounds That Bind
; TITLE OF INVENTION: Selectins Including Endothelium Leukocyte Adhesion
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/241,054
FILING DATE: 11-MAY-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,295
FILING DATE: 05-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/881,395
FILING DATE: 06-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gerald F. Swiss
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 000324-002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
TELEFAX: 415-854-8275
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-241-054-50

Query Match 44.4%; Score 28; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. NO. 1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 1; Gaps 0;

QY 7 LWTMM 12
Db 6 MLWNMM 11

RESULT 2

US-08-241-054-53
; Sequence 53, Application US/08241054
; Patent No. 5643873
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Cwiria, Steven E.
; APPLICANT: Dower, William J.
; APPLICANT: Koller, Kerry J.
; APPLICANT: Lee, Jung
; APPLICANT: Martens, Christine L.
; APPLICANT: Ruhland-Fritsch, Beatrice
; TITLE OF INVENTION: Peptides and Compounds That Bind
; TITLE OF INVENTION: Selectins Including Endothelium Leukocyte Adhesion
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/241,054
; FILING DATE: 11-MAY-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,295
; FILING DATE: 05-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/881,395
; FILING DATE: 06-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Gerald F. Swiss
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 000324-002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-7400
; TELEFAX: 415-854-8275
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-241-054-53

Query Match 44.4%; Score 28; DB 1; Length 12;
Best Local Similarity 80.0%; Pred. NO. 1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 IWTMM 12
:||||

Db 7 LWTMM 11

RESULT 3

US-08-241-054-61
; Sequence 61, Application US/08241054
; Patent No. 5643873
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Cwiria, Steven E.
; APPLICANT: Dower, William J.
; APPLICANT: Koller, Kerry J.
; APPLICANT: Lee, Jung
; APPLICANT: Martens, Christine L.
; APPLICANT: Ruhland-Fritsch, Beatrice
; TITLE OF INVENTION: Peptides and Compounds That Bind
; TITLE OF INVENTION: Selectins Including Endothelium Leukocyte Adhesion
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/241,054
; FILING DATE: 11-MAY-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,295
; FILING DATE: 05-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/881,395
; FILING DATE: 06-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Gerald F. Swiss
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 000324-002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-7400
; TELEFAX: 415-854-8275
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-241-054-61

Query Match 44.4%; Score 28; DB 1; Length 12;
Best Local Similarity 80.0%; Pred. NO. 1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 IWTMM 12
:||||
Db 7 LWTMM 11

RESULT 4

US-08-390-156A-22
; Sequence 22, Application US/08390156A
; Patent No. 5648458
; GENERAL INFORMATION:
; APPLICANT: Cwiria, Steven E.
; APPLICANT: Barrett, Ronald W.

APPLICANT: Dower, William J.
APPLICANT: Martens, Christine L.
TITLE OF INVENTION: Peptides and Compounds That Bind to
TITLE OF INVENTION: ELAM-1
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Affymax Technologies, N.V.
STREET: 4001 Miranda Ave.
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,156A
FILING DATE: 16-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,295
FILING DATE: 05-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Swiss, Gerald F.
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 1023.1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-424-0832
TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-390-156A-22

Query Match 44.4%; Score 28; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 7 MIWTMM 12
Db 6 MLWNMM 11

RESULT 5
US-08-390-156A-57
Sequence 57, Application US/08390156A
Patent No. 5648458
GENERAL INFORMATION:
APPLICANT: Cwirla, Steven E.
APPLICANT: Barrett, Ronald W.
APPLICANT: Dower, William J.
APPLICANT: Martens, Christine L.
TITLE OF INVENTION: Peptides and Compounds That Bind to
TITLE OF INVENTION: ELAM-1
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Affymax Technologies, N.V.
STREET: 4001 Miranda Ave.
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,156A
FILING DATE: 16-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,295
FILING DATE: 05-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/881,395
FILING DATE: 06-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Swiss, Gerald F.
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 1023.1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-496-2300
TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-390-156A-57
Query Match 44.4%; Score 28; DB 1; Length 12;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 8 IWTMM 12
Db 7 LWTMM 11
RESULT 6
US-08-390-156A-61
Sequence 61, Application US/08390156A
Patent No. 5648458
GENERAL INFORMATION:
APPLICANT: Cwirla, Steven E.
APPLICANT: Barrett, Ronald W.
APPLICANT: Dower, William J.
APPLICANT: Martens, Christine L.
TITLE OF INVENTION: Peptides and Compounds That Bind to
TITLE OF INVENTION: ELAM-1
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Affymax Technologies, N.V.
STREET: 4001 Miranda Ave.
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,156A
FILING DATE: 16-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,295
FILING DATE: 05-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/881,395
FILING DATE: 06-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Swiss, Gerald F.
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 1023.1A

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-390-156A-61

Query Match 44.4%; Score 28; DB 1; Length 12;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 IWTMM 12
Db 7 LWTMM 11

RESULT 7
US-08-439-817-30
; Sequence 30, Application US/08439817
; Patent No. 5728802
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Cwiria, Steven E.
; APPLICANT: Dower, William J.
; APPLICANT: Koller, Kerry J.
; APPLICANT: Lee, Jung
; APPLICANT: Martens, Christine L.
; APPLICANT: Ruhland-Fritsch, Beatrice
; TITLE OF INVENTION: Peptides and Compounds That Bind
; TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion
; TITLE OF INVENTION: Molecule I (ELAM-1)
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies, NV
; STREET: 4001 Miranda Ave.
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/439,817
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 530
; APPLICATION NUMBER: US 08/241,054
; FILING DATE: 11-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,295
; FILING DATE: 05-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/881,395
; FILING DATE: 06-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 000324-046/1056.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-439-817-30
Query Match 44.4%; Score 28; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 7 MIWTMM 12
Db 6 MLWNMM 11

RESULT 8
US-08-439-817-33
; Sequence 33, Application US/08439817
; Patent No. 5728802
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Cwiria, Steven E.
; APPLICANT: Dower, William J.
; APPLICANT: Koller, Kerry J.
; APPLICANT: Lee, Jung
; APPLICANT: Martens, Christine L.
; APPLICANT: Ruhland-Fritsch, Beatrice
; TITLE OF INVENTION: Peptides and Compounds That Bind
; TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion
; TITLE OF INVENTION: Molecule I (ELAM-1)
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies, NV
; STREET: 4001 Miranda Ave.
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/439,817
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 530
; APPLICATION NUMBER: US 08/241,054
; FILING DATE: 11-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,295
; FILING DATE: 05-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/881,395
; FILING DATE: 06-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 000324-046/1056.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-439-817-33

Query Match 44.4%; Score 28; DB 1; Length 12;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 IWTMM 12
Db 7 LWTMM 11

RESULT 7
US-08-439-817-30
; Sequence 30, Application US/08439817
; Patent No. 5728802
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Cwiria, Steven E.
; APPLICANT: Dower, William J.
; APPLICANT: Koller, Kerry J.
; APPLICANT: Lee, Jung
; APPLICANT: Martens, Christine L.
; APPLICANT: Ruhland-Fritsch, Beatrice
; TITLE OF INVENTION: Peptides and Compounds That Bind
; TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion
; TITLE OF INVENTION: Molecule I (ELAM-1)
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies, NV
; STREET: 4001 Miranda Ave.
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/439,817
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 530
; APPLICATION NUMBER: US 08/241,054
; FILING DATE: 11-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,295
; FILING DATE: 05-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/881,395
; FILING DATE: 06-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 000324-046/1056.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 IWTMM 12
:||||
Db 7 LWTMM 11

RESULT 9

US-08-439-817-41
; Sequence 41, Application US/08439817
; Patent No. 5728802
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Cwirla, Steven E.
; APPLICANT: Dower, William J.
; APPLICANT: Koller, Kerry J.
; APPLICANT: Lee, Jung
; APPLICANT: Martens, Christine L.
; APPLICANT: Ruhland-Fritsch, Beatrice
; TITLE OF INVENTION: Peptides and Compounds That Bind
; TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion
; TITLE OF INVENTION: Molecule I (ELAM-1)
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies, NV
; STREET: 4001 Miranda Ave.
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/439,817
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/241,054
; FILING DATE: 11-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,295
; FILING DATE: 05-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/881,395
; FILING DATE: 06-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 000324-046/1056.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-439-817-41

Query Match 44.4%; Score 28; DB 1; Length 12;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 IWTMM 12
:||||
Db 7 LWTMM 11

RESULT 10

US-08-485-508-50
; Sequence 50, Application US/08485508
; Patent No. 5786322
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Cwirla, Steven E.
; APPLICANT: Dower, William J.
; APPLICANT: Koller, Kerry J.
; APPLICANT: Lee, Jung
; APPLICANT: Martens, Christine L.
; APPLICANT: Ruhland-Fritsch, Beatrice
; TITLE OF INVENTION: Peptides and Compounds That Bind
; TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion
; TITLE OF INVENTION: Molecule I
; NUMBER OF SEQUENCES: 162
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies, NV
; STREET: 4001 Miranda Ave.
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,508
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/241,054
; FILING DATE: 11-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,295
; FILING DATE: 05-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/881,395
; FILING DATE: 06-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 000324-002/1056
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-485-508-50

Query Match 44.4%; Score 28; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 MIWTMM 12
:|:|:|
Db 6 MLWNMM 11

RESULT 11

US-08-485-508-53
; Sequence 53, Application US/08485508
; Patent No. 5786322
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.

APPLICANT: Cwirla, Steven E.
APPLICANT: Dower, William J.
APPLICANT: Koller, Kerry J.
APPLICANT: Lee, Jung
APPLICANT: Martens, Christine L.
APPLICANT: Ruhland-Fritch, Beatrice
TITLE OF INVENTION: Peptides and Compounds That Bind
TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion
TITLE OF INVENTION: Molecule 1
NUMBER OF SEQUENCES: 162
CORRESPONDENCE ADDRESS:
ADDRESSEE: Affymax Technologies, NV
STREET: 4001 Miranda Ave.
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/485,508
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,295
FILING DATE: 05-MAY-1993
PRIOR APPLICATION NUMBER: US 08/241,054
FILING DATE: 11-MAY-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/881,395
FILING DATE: 06-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Stevens, Lauren L.
REGISTRATION NUMBER: 36,691
REFERENCE/DOCKET NUMBER: 000324-002/1056
TELEPHONE: 415-496-2300
TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-485-508-53

Query Match 44.4%; Score 28; DB 1; Length 12;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 IWTMM 12
:||||
DB 7 LWTMM 11

RESULT 12
US-08-485-508-61
Sequence 61, Application US/08485508
Patent No. 5786322
GENERAL INFORMATION:
APPLICANT: Barrett, Ronald W.
APPLICANT: Cwirla, Steven E.
APPLICANT: Dower, William J.
APPLICANT: Koller, Kerry J.
APPLICANT: Lee, Jung
APPLICANT: Martens, Christine L.
APPLICANT: Ruhland-Fritch, Beatrice

TITLE OF INVENTION: Peptides and Compounds That Bind
TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion
TITLE OF INVENTION: Molecule 1
NUMBER OF SEQUENCES: 162
CORRESPONDENCE ADDRESS:
ADDRESSEE: Affymax Technologies, NV
STREET: 4001 Miranda Ave.
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/485,508
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,295
FILING DATE: 05-MAY-1993
PRIOR APPLICATION NUMBER: US 08/241,054
FILING DATE: 11-MAY-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/881,395
FILING DATE: 06-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Stevens, Lauren L.
REGISTRATION NUMBER: 36,691
REFERENCE/DOCKET NUMBER: 000324-002/1056
TELEPHONE: 415-496-2300
TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-485-508-61

Query Match 44.4%; Score 28; DB 1; Length 12;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 IWTMM 12
:||||
DB 7 LWTMM 11

RESULT 13
US-07-920-519-12
Sequence 12, Application US/07920519
Patent No. 5382518
GENERAL INFORMATION:
APPLICANT: CAPUT, DANIEL
APPLICANT: FERRARA, PASCUAL
APPLICANT: GUILLEMOT, JEAN-CLAUDE
APPLICANT: KAGHAD, MOURAD
APPLICANT: LEGOUX, RICHARD
APPLICANT: LOISON, GERARD
APPLICANT: LARBE, ELIZABETH
APPLICANT: LUPKER, JOHANNES
APPLICANT: LEPLATOIS, PASCUAL
APPLICANT: SALOME, MARK
TITLE OF INVENTION: URATE OXIDASE ACTIVITY PROTEIN,
TITLE OF INVENTION: RECOMBINANT GENE CODING THEREFOR, EXPRESSION VECTOR,
TITLE OF INVENTION: MICRO-ORGANISMS AND TRANSFORMED CELLS

```
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/920,519
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/659,408
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16781/276 BEDL
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; IMMEDIATE SOURCE:
; CLONE: Hydrolysis product T 28
; US-07-920-519-12

Query Match 44.4%; Score 28; DB 1; Length 13;
Best Local Similarity 55.6%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TSLDATMIW 9
Db 4 TDVDATWQW 12

RESULT 14
US-08-086-410-9
; Sequence 9, Application US/08086410
; Patent No. 5407822
; GENERAL INFORMATION:
; APPLICANT: LEPLATOIS, Pascal
; APPLICANT: LOISON, Gerard
; APPLICANT: PESSEGU, Bernard
; APPLICANT: SHIRE, David
; TITLE OF INVENTION: Artificial promoter for the expression
; TITLE OF INVENTION: of proteins in yeast
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: King Street Station, Suite 500, 1800 Diagonal
; STREET: Road, PO Box 299
; CITY: ALEXANDRIA
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/086,410
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/768,083
; FILING DATE: 02-OCT-1991
; APPLICATION NUMBER: FR 89 17467
; FILING DATE: 29-DEC-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 16781/318
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-9300
; TELEFAX: (703) 683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: hydrolysis product T28
; US-08-086-410-9

Query Match 44.4%; Score 28; DB 1; Length 13;
Best Local Similarity 55.8%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TSLDATMIW 9
Db 4 TDVDATWQW 12

RESULT 15
US-08-314-586-12
; Sequence 12, Application US/08314586
; Patent No. 5541098
; GENERAL INFORMATION:
; APPLICANT: CAPUT, DANIEL
; APPLICANT: FERRARA, PASCUAL
; APPLICANT: GUILLEMOT, JEAN-CLAUDE
; APPLICANT: KAGHAD, MOURAD
; APPLICANT: LEGOUX, RICHARD
; APPLICANT: LOISON, GERARD
; APPLICANT: LARBRE, ELIZABETH
; APPLICANT: LUPKER, JOHANNES
; APPLICANT: LEPLATOIS, PASCUAL
; APPLICANT: SALOME, MARK
; APPLICANT: LAURENT, PATRICK
; TITLE OF INVENTION: URATE OXIDASE ACTIVITY PROTEIN,
; TITLE OF INVENTION: RECOMBINANT GENE CODING THEREFOR, EXPRESSION VECTOR,
; TITLE OF INVENTION: MICROORGANISMS AND TRANSFORMED CELLS
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/314,586
; FILING DATE: 28-SEP-1994
; CLASSIFICATION: 435
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;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/659,408
;; FILING DATE: 25-APR-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BENT, Stephen A.
;; REGISTRATION NUMBER: 29,768
;; REFERENCE/DOCKET NUMBER: 16781/509/BDL
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703)836-9300
;; TELEFAX: (703)883-4109
;; TELEX: 899149
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 13 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL: NO
;; IMMEDIATE SOURCE:
;; CLONE: Hydrolysis product T 28
US-08-314-586-12

Query Match 44.4%; Score 28; DB 1; Length 13;
Best Local Similarity 55.6%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TSLDATMIW 9
| : || |
Db 4 TDVDTWQW 12

Search completed: November 14, 2004, 12:08:47
Job time : 10.4468 secs

This Page Intended for
(010001) (010001) (010001)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:25 ; Search time 34.7234 Seconds
(without alignments)
123.973 Million cell updates/sec

Title: US-09-831-253F-3
Perfect score: 63
Sequence: 1 TSLDATMIWTMM 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 718658

Minimum DB seq length: 0
Maximum DB seq length: 23

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	63	100.0	12	3 AAY92947	Aay92947 Transform
2	63	100.0	12	3 AAY93008	Aay93008 Transform
3	58	92.1	12	3 AAY93009	Aay93009 Transform
4	50	79.4	11	3 AAY93094	Aay93094 Transform
5	50	79.4	14	3 AAY93098	Aay93098 Transform
6	50	79.4	14	3 AAY92950	Aay92950 Transform
7	48	76.2	12	3 AAY93093	Aay93093 Transform
8	37	58.7	12	3 AAY93007	Aay93007 Transform
9	36.5	57.9	9	3 AAY93096	Aay93096 Transform
10	36.5	57.9	9	3 AAY92949	Aay92949 Transform
11	35	55.6	7	3 AAY93095	Aay93095 Transform
12	35	55.6	12	3 AAY93010	Aay93010 Transform
13	31.5	50.0	9	3 AAY93097	Aay93097 Transform
14	31	49.2	14	4 AAB88161	Aab88161 CD66 pept
15	31	49.2	20	7 ADC99257	Adc99257 Cancer-re
16	30	47.6	13	4 AAU05001	Aau05001 N-termina
17	30	47.6	13	5 AAU06061	Aau06061 Human glu
18	30	47.6	16	7 ADF69672	Adf69672 Trpzip pe
19	29	46.0	7	2 AAW46010	Aaw46010 Peptide #
20	29	46.0	16	7 ADF69670	Adf69670 Trpzip pe
21	29	46.0	18	2 AAW69116	Aaw69116 Neuronal
22	28	44.4	12	2 AAR86068	Aar86068 Anti-ELAM
23	28	44.4	12	2 AAR86065	Aar86065 Anti-ELAM
24	28	44.4	12	2 AAW26904	Aaw26904 ELAM-1 b1
25	28	44.4	12	2 AAW26900	Aaw26900 ELAM-1 b1

26	28	44.4	12	2 AAW26865	Aaw26865 ELAM-1 b1
27	28	44.4	12	2 AAW63875	Aaw63875 ELAM-1 pe
28	28	44.4	12	2 AAW63886	Aaw63886 ELAM-1 pe
29	28	44.4	12	2 AAW63878	Aaw63878 ELAM-1 pe
30	28	44.4	15	2 AAR13972	Aar13972 [Asp14]Me
31	28	44.4	15	2 AAR61463	Aar61463 [Asp-14]
32	28	44.4	17	4 AAU06698	Aau06698 Peptide r
33	28	44.4	17	6 ABJ38668	Abj38668 VH-CDR3 p
34	28	44.4	17	6 ADA89077	Ada89077 Human clo
35	28	44.4	17	7 ADG74329	Adg74329 Human VH-
36	27	42.9	9	7 ADE67540	Ade67540 Human 161
37	27	42.9	10	7 ADE66432	Ade66432 Human 161
38	27	42.9	10	7 ADE67609	Ade67609 Human 161
39	27	42.9	10	7 ADE70007	Ade70007 Human 161
40	27	42.9	10	7 ADE67387	Ade67387 Human 161
41	27	42.9	10	7 ADE69708	Ade69708 Human 161
42	27	42.9	14	4 AAB88091	Aab88091 CD66 pept
43	27	42.9	15	7 ADE70131	Ade70131 Human 161
44	27	42.9	15	7 ADE70548	Ade70548 Human 161
45	27	42.9	15	7 ADE70592	Ade70592 Human 161

ALIGNMENTS

RESULT 1
AAY92947
ID AAY92947 standard; peptide; 12 AA.
XX
AC AAY92947;
XX
DT 08-NOV-2000 (first entry)
XX
XX Transforming growth factor inhibitory peptide #3.
XX Hepatotropic; antagonist; transforming growth factor beta1; TGF-beta1;
KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX Homo sapiens.
XX
XX WO2000311135-A1.
XX
XX 02-JUN-2000.
XX
XX 23-NOV-1999; 99WO-ES000375.
XX
XX 24-NOV-1998; 98ES-00002465.
XX
XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
XX Borras Cuesta F;
XX WPI; 2000-411935/35.
XX Peptides that antagonize binding of transforming growth factor beta1,
XX useful for treatment of liver disease, especially cirrhosis, are partial
XX sequences of the factor or its receptors.
XX
XX Claim 4; Page 80; 86pp; Spanish.
XX The invention relates to synthetic peptides that antagonise the binding
XX of transforming growth (TGF) factor beta1 (TGF-beta1) to its receptor in
XX vivo which have partial amino acid sequences identical, or similar, with
XX those of TGF-beta1 and/or its receptors. Peptides AAY92945-Y93133 represent
XX examples of the peptides of the invention. The peptides act by
XX competitive inhibition of the binding of TGF-beta1 to its receptors, e.g.
XX they are inhibitors of stimulation of collagen synthesis in liver cells
XX and inhibitors of synthesis of proteolytic enzymes able to degrade the
XX extracellular matrix. The peptides, their mimetopes and/or DNA (or
XX expression systems) encoding the peptides are used for treatment of liver
XX disease, specifically cirrhosis

OS Homo sapiens.
 XX WO2000031135-A1.
 PN 02-JUN-2000.
 PD 23-NOV-1999; 99WO-ES000375.
 XX 24-NOV-1998; 98ES-00002465.
 XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
 PA Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
 PI Borrás Cuesta F;
 XX WPI; 2000-411935/35.
 XX Peptides that antagonize binding of transforming growth factor betal,
 PT useful for treatment of liver disease, especially cirrhosis, are partial
 PT sequences of the factor or its receptors.
 XX Disclosure; Page 31; 86pp; Spanish.
 XX The invention relates to synthetic peptides that antagonise the binding
 CC of transforming growth (TGF) factor betal (TGF-b1) to its receptor in
 CC vivo which have partial amino acid sequences identical, or similar, with
 CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
 CC examples of the peptides of the invention. The peptides act by
 CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
 CC they are inhibitors of stimulation of collagen synthesis in liver cells
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
 CC expression systems) encoding the peptides are used for treatment of liver
 CC disease, specifically cirrhosis
 XX Sequence 11 AA;
 SQ

Query Match 79.4%; Score 50; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.023;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 DATMIWTMM 12
 Db 3 DATMIWTMM 11
 |||||
 |||||

RESULT 5
 AAY93098
 ID AAY93098 standard; peptide; 14 AA.
 XX AC AAY93098;
 XX 08-NOV-2000 (first entry)
 DT Transforming growth factor inhibitory peptide P144.
 DE Hepatotropic; antagonist; transforming growth factor betal; TGF-b1;
 XX competitive inhibition; collagen synthesis stimulation inhibitor; liver;
 KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
 XX Homo sapiens.
 OS WO2000031135-A1.
 PN 02-JUN-2000.
 XX 23-NOV-1999; 99WO-ES000375.
 XX 24-NOV-1998; 98ES-00002465.
 XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
 PA Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
 XX

PI Borrás Cuesta F;
 XX WPI; 2000-411935/35.
 XX Peptides that antagonize binding of transforming growth factor betal,
 PT useful for treatment of liver disease, especially cirrhosis, are partial
 PT sequences of the factor or its receptors.
 XX Disclosure; Page 31; 86pp; Spanish.
 XX The invention relates to synthetic peptides that antagonise the binding
 CC of transforming growth (TGF) factor betal (TGF-b1) to its receptor in
 CC vivo which have partial amino acid sequences identical, or similar, with
 CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
 CC examples of the peptides of the invention. The peptides act by
 CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
 CC they are inhibitors of stimulation of collagen synthesis in liver cells
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
 CC expression systems) encoding the peptides are used for treatment of liver
 CC disease, specifically cirrhosis
 XX Sequence 14 AA;
 SQ

Query Match 79.4%; Score 50; DB 3; Length 14;
 Best Local Similarity 75.0%; Pred. No. 0.03;
 Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 TSLDATMIWTMM 12
 Db 1 TSLDASIIWAMM 12
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 |||||

RESULT 6
 AAY92950
 ID AAY92950 standard; peptide; 14 AA.
 XX AC AAY92950;
 XX 08-NOV-2000 (first entry)
 DT Transforming growth factor inhibitory peptide #6.
 DE Hepatotropic; antagonist; transforming growth factor betal; TGF-b1;
 XX competitive inhibition; collagen synthesis stimulation inhibitor; liver;
 KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
 XX Homo sapiens.
 OS WO2000031135-A1.
 PN 02-JUN-2000.
 XX 23-NOV-1999; 99WO-ES000375.
 XX 24-NOV-1998; 98ES-00002465.
 XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
 PA Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
 PI Borrás Cuesta F;
 XX WPI; 2000-411935/35.
 XX Peptides that antagonize binding of transforming growth factor betal,
 PT useful for treatment of liver disease, especially cirrhosis, are partial
 PT sequences of the factor or its receptors.
 XX Claim 7; Page 81; 86pp; Spanish.
 XX The invention relates to synthetic peptides that antagonise the binding
 CC of transforming growth (TGF) factor betal (TGF-b1) to its receptor in
 CC vivo which have partial amino acid sequences identical, or similar, with

CC those of TGF- β 1 and/or its receptors. Peptides AAY92945-Y93133 represent
 CC examples of the peptides of the invention. The peptides act by
 CC competitive inhibition of the binding of TGF- β 1 to its receptors, e.g.
 CC they are inhibitors of stimulation of collagen synthesis in liver cells
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
 CC expression systems) encoding the peptides are used for treatment of liver
 CC disease, specifically cirrhosis
 XX
 SQ Sequence 14 AA;

Query Match 79.4%; Score 50; DB 3; Length 14;
 Best Local Similarity 75.0%; Pred. No. 0.03;
 Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 TSLDATMIWMM 12
 DB 1 TSLDASIIWMM 12
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RESULT 7
 AAY93093
 ID AAY93093 standard; peptide; 12 AA.
 AC
 XX AAY93093;
 DT 08-NOV-2000 (first entry)
 XX
 DE Transforming growth factor inhibitory peptide P139.
 XX
 KW Hepatotrophic; antagonist; transforming growth factor betal; TGF- β 1;
 KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
 KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
 XX
 OS Homo sapiens.
 XX
 PN WO200031135-A1.
 XX
 PD 02-JUN-2000.
 XX
 PF 23-NOV-1999; 99WO-ES000375.
 XX
 PR 24-NOV-1998; 98ES-00002465.
 XX
 XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
 XX
 PI Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
 PI Borrás Cuesta F;
 XX
 WPI; 2000-411935/35.
 XX
 XX Peptides that antagonize binding of transforming growth factor betal,
 PT useful for treatment of liver disease, especially cirrhosis, are partial
 PT sequences of the factor or its receptors.
 XX
 PS Disclosure; Page 31; 86pp; Spanish.
 XX
 CC The invention relates to synthetic peptides that antagonise the binding
 CC of transforming growth (TGF) factor betal (TGF- β 1) to its receptor in
 CC vivo which have partial amino acid sequences identical, or similar, with
 CC those of TGF- β 1 and/or its receptors. Peptides AAY92945-Y93133 represent
 CC examples of the peptides of the invention. The peptides act by
 CC competitive inhibition of the binding of TGF- β 1 to its receptors, e.g.
 CC they are inhibitors of stimulation of collagen synthesis in liver cells
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
 CC expression systems) encoding the peptides are used for treatment of liver
 CC disease, specifically cirrhosis
 XX
 SQ Sequence 12 AA;

Query Match 76.2%; Score 48; DB 3; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.058;

QY 1 TSLDATMI 8
 DB 5 TSLDATMI 12
 |||||:||||||

RESULT 9
 AAY93096
 ID AAY93096 standard; peptide; 9 AA.
 XX
 AC AAY93096;
 XX

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLDATMIW 9
 DB 1 TSLDATMIW 9
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RESULT 8
 AAY93007
 ID AAY93007 standard; peptide; 12 AA.
 XX
 AC AAY93007;
 XX
 DT 08-NOV-2000 (first entry)
 XX
 DE Transforming growth factor inhibitory peptide P53.
 XX
 KW Hepatotrophic; antagonist; transforming growth factor betal; TGF- β 1;
 KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
 KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
 XX
 OS Rattus sp.
 XX
 PN WO200031135-A1.
 XX
 PD 02-JUN-2000.
 XX
 PF 23-NOV-1999; 99WO-ES000375.
 XX
 PR 24-NOV-1998; 98ES-00002465.
 XX
 XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
 XX
 PI Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
 PI Borrás Cuesta F;
 XX
 WPI; 2000-411935/35.
 XX
 XX Peptides that antagonize binding of transforming growth factor betal,
 PT useful for treatment of liver disease, especially cirrhosis, are partial
 PT sequences of the factor or its receptors.
 XX
 PS Disclosure; Page 27; 86pp; Spanish.
 XX
 CC The invention relates to synthetic peptides that antagonise the binding
 CC of transforming growth (TGF) factor betal (TGF- β 1) to its receptor in
 CC vivo which have partial amino acid sequences identical, or similar, with
 CC those of TGF- β 1 and/or its receptors. Peptides AAY92945-Y93133 represent
 CC examples of the peptides of the invention. The peptides act by
 CC competitive inhibition of the binding of TGF- β 1 to its receptors, e.g.
 CC they are inhibitors of stimulation of collagen synthesis in liver cells
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
 CC expression systems) encoding the peptides are used for treatment of liver
 CC disease, specifically cirrhosis
 XX
 SQ Sequence 12 AA;

Query Match 58.7%; Score 37; DB 3; Length 12;
 Best Local Similarity 100.0%; Pred. No. 5.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLDATMI 8
 DB 5 TSLDATMI 12
 |||||:||||||

RESULT 9
 AAY93096
 ID AAY93096 standard; peptide; 9 AA.
 XX
 AC AAY93096;
 XX

DT 08-NOV-2000 (first entry)
 XX Transforming growth factor inhibitory peptide P142.
 DE Hepatotropic; antagonist; transforming growth factor betal; TGF-b1;
 XX competitive inhibition; collagen synthesis stimulation inhibitor; liver;
 KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
 KW Homo sapiens.
 XX WO200031135-A1.
 PN 02-JUN-2000.
 XX 23-NOV-1999; 99WO-ES000375.
 XX 24-NOV-1998; 98ES-00002465.
 XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
 XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
 PI Borrás Cuesta F;
 XX WPI; 2000-411935/35.
 DR Peptides that antagonize binding of transforming growth factor betal,
 XX useful for treatment of liver disease, especially cirrhosis, are partial
 PT sequences of the factor or its receptors.
 XX Claim 6; Page 81; 86pp; Spanish.
 XX The invention relates to synthetic peptides that antagonise the binding
 CC of transforming growth (TGF) factor betal (TGF-b1) to its receptor in
 CC vivo which have partial amino acid sequences identical, or similar, with
 CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
 CC examples of the peptides of the invention. The peptides act by
 CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
 CC they are inhibitors of stimulation of collagen synthesis in liver cells
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
 CC expression systems) encoding the peptides are used for treatment of liver
 CC disease, specifically cirrhosis
 XX
 SQ Sequence 9 AA;
 Query Match 57.9%; Score 36.5; DB 3; Length 9;
 Best Local Similarity 75.0%; Pred. No. 1.7e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
 QY 1 TSLDATMIWTMM 12
 Db ||| |||||
 1 TSL---MIWTMM 9
 RESULT 10
 AAY92949
 ID AAY92949 standard; peptide; 9 AA.
 XX
 AC AAY92949;
 XX
 DT 08-NOV-2000 (first entry)
 XX Transforming growth factor inhibitory peptide #5.
 DE Hepatotropic; antagonist; transforming growth factor betal; TGF-b1;
 XX competitive inhibition; collagen synthesis stimulation inhibitor; liver;
 KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
 XX Homo sapiens.
 XX WO200031135-A1.
 PN 02-JUN-2000.
 XX 23-NOV-1999; 99WO-ES000375.
 XX 24-NOV-1998; 98ES-00002465.
 XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
 XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
 PI Borrás Cuesta F;
 XX WPI; 2000-411935/35.
 DR Peptides that antagonize binding of transforming growth factor betal,
 XX useful for treatment of liver disease, especially cirrhosis, are partial
 PT sequences of the factor or its receptors.
 XX Claim 6; Page 81; 86pp; Spanish.
 XX The invention relates to synthetic peptides that antagonise the binding
 CC of transforming growth (TGF) factor betal (TGF-b1) to its receptor in
 CC vivo which have partial amino acid sequences identical, or similar, with
 CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
 CC examples of the peptides of the invention. The peptides act by
 CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
 CC they are inhibitors of stimulation of collagen synthesis in liver cells
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
 CC expression systems) encoding the peptides are used for treatment of liver
 CC disease, specifically cirrhosis
 XX
 SQ Sequence 9 AA;
 Query Match 57.9%; Score 36.5; DB 3; Length 9;
 Best Local Similarity 75.0%; Pred. No. 1.7e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
 QY 1 TSLDATMIWTMM 12
 Db ||| |||||
 1 TSL---MIWTMM 9
 RESULT 11
 AAY93095
 ID AAY93095 standard; peptide; 7 AA.
 XX
 AC AAY93095;
 XX
 DT 08-NOV-2000 (first entry)
 XX Transforming growth factor inhibitory peptide P141.
 DE Hepatotropic; antagonist; transforming growth factor betal; TGF-b1;
 KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
 KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
 XX Homo sapiens.
 XX WO200031135-A1.
 PN 02-JUN-2000.
 XX 23-NOV-1999; 99WO-ES000375.
 XX 24-NOV-1998; 98ES-00002465.
 XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
 XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
 PI Borrás Cuesta F;
 XX WPI; 2000-411935/35.
 DR Peptides that antagonize binding of transforming growth factor betal,
 XX useful for treatment of liver disease, especially cirrhosis, are partial
 PT sequences of the factor or its receptors.
 XX Claim 6; Page 81; 86pp; Spanish.
 XX The invention relates to synthetic peptides that antagonise the binding
 CC of transforming growth (TGF) factor betal (TGF-b1) to its receptor in
 CC vivo which have partial amino acid sequences identical, or similar, with
 CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
 CC examples of the peptides of the invention. The peptides act by
 CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
 CC they are inhibitors of stimulation of collagen synthesis in liver cells
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
 CC expression systems) encoding the peptides are used for treatment of liver
 CC disease, specifically cirrhosis
 XX
 SQ Sequence 9 AA;
 Query Match 57.9%; Score 36.5; DB 3; Length 9;
 Best Local Similarity 75.0%; Pred. No. 1.7e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
 QY 1 TSLDATMIWTMM 12
 Db ||| |||||
 1 TSL---MIWTMM 9

PT useful for treatment of liver disease, especially cirrhosis, are partial
 PT sequences of the factor or its receptors.

XX Disclosure; Page 31; 86pp; Spanish.

XX The invention relates to synthetic peptides that antagonise the binding
 CC of transforming growth (TGF) factor betel (TGF-b1) to its receptor in
 CC vivo which have partial amino acid sequences identical, or similar, with
 CC those of TGF-b1 and/or its receptors. Peptides AAY2945-Y93133 represent
 CC examples of the peptides of the invention. The peptides act by
 CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
 CC they are inhibitors of stimulation of collagen synthesis in liver cells
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
 CC expression systems) encoding the peptides are used for treatment of liver
 CC disease, specifically cirrhosis

XX Sequence 7 AA;

Query Match 55.6%; Score 35; DB 3; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DATMIW 9

Db 1 DATMIW 6

RESULT 12

AAY93010

ID AAY93010 standard; peptide; 12 AA.

AC AAY93010;

DT 08-NOV-2000 (first entry)

DE Transforming growth factor inhibitory peptide P56.

XX Hepatotrophic; antagonist; transforming growth factor betel; TGF-b1;
 KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
 KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.

XX Rattus sp.

PN WO200031135-A1.

XX 02-JUN-2000.

XX 23-NOV-1999; 99WO-ES000375.

XX 24-NOV-1998; 98ES-00002465.

XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.

XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;

PI Borrás Cuesta F;

XX WPI; 2000-411935/35.

XX Peptides that antagonize binding of transforming growth factor betel,
 PT useful for treatment of liver disease, especially cirrhosis, are partial
 PT sequences of the factor or its receptors.

XX Disclosure; Page 27; 86pp; Spanish.

XX The invention relates to synthetic peptides that antagonise the binding
 CC of transforming growth (TGF) factor betel (TGF-b1) to its receptor in
 CC vivo which have partial amino acid sequences identical, or similar, with
 CC those of TGF-b1 and/or its receptors. Peptides AAY2945-Y93133 represent
 CC examples of the peptides of the invention. The peptides act by
 CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
 CC they are inhibitors of stimulation of collagen synthesis in liver cells
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the

CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
 CC expression systems) encoding the peptides are used for treatment of liver
 CC disease, specifically cirrhosis

XX Sequence 12 AA;

Query Match 55.6%; Score 35; DB 3; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 MIWTMM 12

Db 1 MIWTMM 6

RESULT 13

AAY93097

ID AAY93097 standard; peptide; 9 AA.

XX AC AAY93097;

DT 08-NOV-2000 (first entry)

XX Transforming growth factor inhibitory peptide P143.

XX Hepatotrophic; antagonist; transforming growth factor betel; TGF-b1;
 KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
 KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.

XX Homo sapiens.

PN WO200031135-A1.

XX 02-JUN-2000.

XX 23-NOV-1999; 99WO-ES000375.

XX 24-NOV-1998; 98ES-00002465.

XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.

XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;

PI Borrás Cuesta F;

XX WPI; 2000-411935/35.

XX Peptides that antagonize binding of transforming growth factor betel,
 PT useful for treatment of liver disease, especially cirrhosis, are partial
 PT sequences of the factor or its receptors.

XX Disclosure; Page 31; 86pp; Spanish.

XX The invention relates to synthetic peptides that antagonise the binding
 CC of transforming growth (TGF) factor betel (TGF-b1) to its receptor in
 CC vivo which have partial amino acid sequences identical, or similar, with
 CC those of TGF-b1 and/or its receptors. Peptides AAY2945-Y93133 represent
 CC examples of the peptides of the invention. The peptides act by
 CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
 CC they are inhibitors of stimulation of collagen synthesis in liver cells
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
 CC expression systems) encoding the peptides are used for treatment of liver
 CC disease, specifically cirrhosis

XX Sequence 9 AA;

Query Match 50.0%; Score 31.5; DB 3; Length 9;
 Best Local Similarity 75.0%; Pred. No. 1.7e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 TSLDATMIWTMM 12

Db 1 TSLDAT---TMM 9

RESULT 14

AAB88161
ID AAB88161 standard; peptide; 14 AA.

XX AAB88161;

XX 17-MAY-2001 (first entry)

XX CD66 peptide CD66f(11)-10.

XX CD66; CBACAM; adhesion molecule; antiviral; antibacterial;

XX antiinflammatory; cytostatic; neutrophil activation; proliferation;

XX differentiation; cancer; angiogenesis.

XX Unidentified.

XX WO200113937-A1.

XX 01-MAR-2001.

XX 25-AUG-2000; 2000WO-US023482.

XX 26-AUG-1999; 99US-0150791P.

XX 02-SEP-1999; 99US-0152501P.

XX (SKUB/) SKUBITZ K M.

XX (SKUB/) SKUBITZ A P N.

XX Skubitz KM, Skubitz APN;

XX WPI; 2001-234981/24.

XX Novel peptides useful for activating neutrophils or blocking activation
PT of neutrophils, modulating homotypic or heterotypic adhesion of CD66
PT polypeptides, and modulating immune cell activation.

XX Claim 1; Page 54; 102pp; English.

XX The present sequence is an isolated peptide that was tested for its
CC ability to modulate the function of CD66 family polypeptides and CD66
CC ligands. 106 sequences of 13 or 14 amino acids in length, and their
CC analogues, were identified that modulate the function of at least one
CC CD66 family polypeptide and/or at least one ligand of the polypeptide.
CC The peptides are capable of modulating activation of neutrophils,
CC activation or inhibition, proliferation and/or differentiation of T-
CC cells, B-cells, NK cells, LAK cells, dendritic cells, or other immune
CC system cells, proliferation and/or differentiation of epithelial cells,
CC homotypic and/or heterotypic adhesion among CD66 family polypeptides and
CC adhesion of CD66 family polypeptides to other ligands. The peptides are
CC useful for delivering a therapeutically active agent to a patient, for
CC modifying the metastasis of malignant cells, for altering bacterial or
CC viral binding to cells or a biomaterial, for altering cell adhesion to a
CC biomaterial, for detecting tumours, for detecting inflammation, for
CC detecting a CD66 protein or its ligand, for altering angiogenesis by
CC contacting endothelial cells, tumour cells or immune cells, for altering
CC an immune response, and for altering keratinocyte proliferation

XX SQ Sequence 14 AA;

Query Match 49.2%; Score 31; DB 4; Length 14;

Best Local Similarity 50.0%; Pred. No. 80;

Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 SLDATMIWTM 11

Db 3 TLDASYLWMM 12

RESULT 15

ADC99257

ID ADC99257 standard; peptide; 20 AA.

XX ADC99257;
XX 01-JAN-2004 (first entry)
XX Cancer-related DGI-2-binder peptide - SEQ ID 90.
XX cytostatic; cancer; gene therapy; DGI-2; DGI-5; DGI-7; DGI-9; Hras;
XX leptin; VEGF; vascular endothelial growth factor receptor; VEGF-R1;
XX VEGF-R2; VEGF-R3; FLT1; FMS-related tyrosine kinase 1; FLK1; KDR;
XX kinase insert domain protein receptor; EGFR; epidermal growth factor;
XX FGFR1; fibroblast growth factor; tie-1.
XX Unidentified.
XX OS
XX WO2003035839-A2.
XX 01-MAY-2003.
XX 24-OCT-2002; 2002WO-US034021.
XX 24-OCT-2001; 2001US-0345471P.
XX (DGI-2) DGI BIOTECHNOLOGIES INC.
XX Pillutla RC, Brissette R, Spruyt M, Dedova O, Blume A;
XX Prendergast J, Goldstein N;
XX WPI; 2003-457332/43.
XX Selecting target and target binder pairs for preparing a composition for
PT treating cancer by mixing in a reaction vessel phage expressing
PT biological targets and phage expressing target binders.
XX Claim 26; SEQ ID NO 90; 172pp; English.
XX The invention relates to a novel method of selecting target and target
CC binder pairs comprising mixing in a reaction vessel phage expressing
CC biological targets and phage expressing target binders, each having
CC distinguishable selection markers and selecting target and target binder
CC pairs based on the selection markers. The molecules of the invention
CC demonstrate cytostatic activity whilst the method may be useful for
CC selecting target and target binder pairs for preparing a composition for
CC treating cancer. Furthermore, the method may be utilised during gene
CC therapy procedures. The current sequence is that of the cancer-related
CC DGI-2-binder peptide of the invention.
XX SQ Sequence 20 AA;
Query Match 49.2%; Score 31; DB 7; Length 20;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 4 DATMIWTM 11
Db 5 DAGMIWFM 12
Search completed: November 14, 2004, 12:02:06
Job time : 35.7234 secs

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OM protein - protein search, using sw model

Run on: November 14, 2004, 12:03:21 ; Search time 28.3404 Seconds
(without alignments)
149.815 Million cell updates/sec

Title: US-09-831-253F-3
Perfect score: 63
Sequence: 1 TSLDATMIWTMM 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1568699 seqs, 353819137 residues

Total number of hits satisfying chosen parameters: 294451

Minimum DB seq length: 0
Maximum DB seq length: 23

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
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- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
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- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	49.2	20	14	US-10-280-066-90
2	31	49.2	22	16	US-10-742-379-441
3	30	47.6	13	9	US-09-753-126-97
4	30	47.6	13	10	US-09-896-896A-61
5	30	47.6	13	15	US-10-330-697-97
6	30	47.6	16	10	US-09-836-770-7
7	29	46.0	7	9	US-09-758-128-41
8	29	46.0	7	9	US-09-758-128-44
9	29	46.0	7	9	US-09-758-426-41
10	29	46.0	7	9	US-09-758-426-44
11	29	46.0	7	9	US-09-758-198-41
12	29	46.0	7	9	US-09-758-198-44
13	29	46.0	7	10	US-09-861-661-41

14	29	46.0	7	10	US-09-861-661-44	Sequence 44, Appl
15	29	46.0	16	10	US-09-836-770-5	Sequence 5, Appl
16	29	46.0	22	14	US-10-195-730-319	Sequence 319, App
17	29	46.0	22	16	US-10-799-747-319	Sequence 319, App
18	28	44.4	27	14	US-10-176-791A-76	Sequence 76, Appl
19	27	42.9	10	14	US-10-062-109A-642	Sequence 642, App
20	27	42.9	10	14	US-10-005-480A-642	Sequence 642, App
21	27	42.9	22	9	US-09-864-761-47789	Sequence 47789, A
22	27	42.9	22	16	US-10-742-379-439	Sequence 439, App
23	26	41.3	9	15	US-10-182-252A-685	Sequence 685, App
24	26	41.3	14	14	US-10-435-766-101	Sequence 101, App
25	26	41.3	17	9	US-09-864-761-39131	Sequence 39131, A
26	26	41.3	17	14	US-10-225-567A-1841	Sequence 1841, App
27	26	41.3	20	14	US-10-283-017-2023	Sequence 2023, Ap
28	26	41.3	20	14	US-10-283-017-2024	Sequence 2024, Ap
29	26	41.3	22	15	US-10-410-764-86	Sequence 86, Appl
30	25	39.7	8	14	US-10-190-082-602	Sequence 602, App
31	25	39.7	9	14	US-10-357-935-20	Sequence 20, Appl
32	25	39.7	9	15	US-10-182-252A-632	Sequence 632, App
33	25	39.7	9	15	US-10-182-252A-657	Sequence 657, App
34	25	39.7	9	15	US-10-182-252A-1216	Sequence 1216, Ap
35	25	39.7	10	14	US-10-200-708-79	Sequence 79, Appl
36	25	39.7	10	14	US-10-200-708-501	Sequence 501, App
37	25	39.7	11	10	US-09-755-109-7	Sequence 7, Appl
38	25	39.7	12	9	US-09-823-829-44	Sequence 44, Appl
39	25	39.7	12	9	US-09-840-277-69	Sequence 69, Appl
40	25	39.7	12	9	US-09-823-823-44	Sequence 44, Appl
41	25	39.7	12	15	US-10-609-217-151	Sequence 151, App
42	25	39.7	12	15	US-10-632-388-151	Sequence 151, App
43	25	39.7	12	15	US-10-651-723-151	Sequence 151, App
44	25	39.7	12	15	US-10-645-761-151	Sequence 151, App
45	25	39.7	12	15	US-10-666-696-151	Sequence 151, App

ALIGNMENTS

RESULT 1

US-10-280-066-90
; Sequence 90, Application US/102800066
; Publication No. US20030180718A1
; GENERAL INFORMATION:
; APPLICANT: Pillutla, Renuka C.
; APPLICANT: Brissette, Renee
; APPLICANT: Spruyt, Michael
; APPLICANT: Dedova, Olga
; APPLICANT: Blume, Arthur J.
; APPLICANT: Prendergast, John
; APPLICANT: Goldstein, Neil I.
; TITLE OF INVENTION: TARGET SPECIFIC SCREENING AND ITS USE FOR IDENTIFYING TARGET BIN
; FILE REFERENCE: 2598-4009US1
; CURRENT APPLICATION NUMBER: US/10/280,066
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 60/345,471
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 537
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: DGI-2-20R-4-B6
US-10-280-066-90

Query Match 49.2%; Score 31; DB 14; Length 20;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 DATMIWTM 11

Db 5 DAGMIWFM 12

```
RESULT 2
US-10-742-379-441
; Sequence 441, Application US/10742379
; Publication No. US20040181033A1
; GENERAL INFORMATION:
; APPLICANT: Han, HQ
; APPLICANT: Min, Hosung
; APPLICANT: Boone, Thomas Charles
; TITLE OF INVENTION: BINDING AGENTS WHICH INHIBIT MYOSTATIN
; FILE REFERENCE: A-828 (US)
; CURRENT APPLICATION NUMBER: US/10/742,379
; CURRENT FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: US 60/435,923
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 634
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 441
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Myostatin Binding Peptide
US-10-742-379-441

Query Match          49.2%; Score 31; DB 16; Length 22;
Best Local Similarity 33.3%; Pred. No. 1.2e+02;
Matches 4; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY      1 TSLDMSLWMTMM 12
      ||| | : : : | : :
Db      1 TSDMSLLWELL 12

RESULT 3
US-09-753-126-97
; Sequence 97, Application US/09753126
; Patent No. US20020127219A1
; GENERAL INFORMATION:
; APPLICANT: OKKELS, JENS SIGURD
; APPLICANT: JENSEN, ANNE DAM
; APPLICANT: HALKIER, TORBEN
; APPLICANT: JENSEN, RIKKE BOLDING
; TITLE OF INVENTION: IMPROVED LYSOSOMAL ENZYMES AND LYSOSOMAL ENZYME
; TITLE OF INVENTION: ACTIVATORS
; FILE REFERENCE: 31-0006000S
; CURRENT APPLICATION NUMBER: US/09/753,126
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: PA 1999 01891
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: 60/174,652
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: PA 200 00865
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: 60/210,984
; PRIOR FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: 60/211,124
; PRIOR FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: PA 2000 01027
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/217,497
; PRIOR FILING DATE: 2000-07-11
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-753-126-97

Query Match          49.2%; Score 31; DB 16; Length 22;
Best Local Similarity 33.3%; Pred. No. 1.2e+02;
Matches 4; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY      1 TSLDMSLWMTMM 12
      ||| | : : : | : :
Db      1 TSDMSLLWELL 12

RESULT 4
US-09-896-896A-61
; Sequence 61, Application US/09896896A
; Publication No. US20030036181A1
; GENERAL INFORMATION:
; APPLICANT: MAXYGEN APS
; TITLE OF INVENTION: PEPTIDE EXTENDED GLYCOSYLATED POLYPEPTIDES
; FILE REFERENCE: 0217u8210
; CURRENT APPLICATION NUMBER: US/09/896,896A
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/217,497
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: US 60/225,558
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: DK PA 2000 01027
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DK PA 2000 01092
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: PCT/DK00/00743
; PRIOR FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: PCT/DK01/00090
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 61
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-896-896A-61

Query Match          47.6%; Score 30; DB 9; Length 13;
Best Local Similarity 55.6%; Pred. No. 1.1e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      2 SLDATMIWT 10
      ::::| | | |
Db      1 AVNATMWT 9

RESULT 5
US-10-330-697-97
; Sequence 97, Application US/10330697
; Publication No. US20040009165A1
; GENERAL INFORMATION:
; APPLICANT: OKKELS, JENS SIGURD
; APPLICANT: JENSEN, ANNE DAM
; APPLICANT: HALKIER, TORBEN
; APPLICANT: JENSEN, RIKKE BOLDING
; TITLE OF INVENTION: IMPROVED LYSOSOMAL ENZYMES AND LYSOSOMAL ENZYME
; TITLE OF INVENTION: ACTIVATORS
; FILE REFERENCE: 31-0006000S
; CURRENT APPLICATION NUMBER: US/10/330,697
; CURRENT FILING DATE: 2002-12-27
; PRIOR APPLICATION NUMBER: US/09/753,126
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: PA 1999 01891
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: 60/174,652
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: PA 200 00865
; PRIOR FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: 60/210,984
; PRIOR FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: 60/211,124
; PRIOR FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: PA 2000 01027
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/217,497
; PRIOR FILING DATE: 2000-07-11
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-330-697-97
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; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: 60/210,984
; PRIOR FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: 60/211,124
; PRIOR FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: PA 2000 01027
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/217,497
; PRIOR FILING DATE: 2000-07-11
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-330-697-97.

Query Match 47.6%; Score 30; DB 15; Length 13;
Best Local Similarity 55.6%; Pred. No. 1.1e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 SLDATMIWT 10
Db :::||| ||
1 AVNATMNWT 9

RESULT 6

US-09-836-770-7
; Sequence 7, Application US/09836770
; Publication No. US20030175799A1
; GENERAL INFORMATION:
; APPLICANT: Cochran, Andrea G.
; APPLICANT: Starovaenik, Melissa A.
; APPLICANT: Skelton, Nicholas
; TITLE OF INVENTION: HAIRPIN PEPTIDES WITH A NOVEL STRUCTURAL MOTIF AND
; TITLE OF INVENTION: METHODS RELATING THERETO
; FILE REFERENCE: P1875
; CURRENT APPLICATION NUMBER: US/09/836,770
; CURRENT FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 7
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide
US-09-836-770-7

Query Match 47.6%; Score 30; DB 10; Length 16;
Best Local Similarity 52.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 DATMIWTM 11
Db :||| ||:
7 DATKTWTV 14

RESULT 7

US-09-758-128-41
; Sequence 41, Application US/09758128
; Patent No. US20020107187A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATY, No. US20020107187A1man L.
; APPLICANT: WESTBROOK, Simon L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,128
; CURRENT FILING DATE: 2001-01-12

; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-758-128-41

Query Match 46.0%; Score 29; DB 9; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.4e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLDATM 7
Db :||| ||:
1 TSLDATV 7

RESULT 8

US-09-758-128-44
; Sequence 44, Application US/09758128
; Patent No. US20020107187A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATY, No. US20020107187A1man L.
; APPLICANT: WESTBROOK, Simon L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,128
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Rat
US-09-758-128-44

Query Match 46.0%; Score 29; DB 9; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.4e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLDATM 7
Db :||| ||:
1 TSLDATV 7

RESULT 9

US-09-758-426-41
; Sequence 41, Application US/09758426
; Patent No. US20020169116A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATY, No. US20020169116A1man L.
; APPLICANT: WESTBROOK, Simon L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,426
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 58

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-758-426-41

Query Match          46.0%; Score 29; DB 9; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.4e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLDATM 7
Db 1 TSLDATV 7

RESULT 10
US-09-758-426-44
; Sequence 44, Application US/09758426
; Patent No. US20020169116A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATY, No. US20020169116A1man L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,426
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US/09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9390
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Rat
US-09-758-426-44

Query Match          46.0%; Score 29; DB 9; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.4e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLDATM 7
Db 1 TSLDATV 7

RESULT 11
US-09-758-198-41
; Sequence 41, Application US/09758198
; Publication No. US20020187925A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATY, No. US20020187925A1man L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,198
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US/09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: PCT/AU97/00312
; PRIOR FILING DATE: 1997-05-22
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-861-661-41

Query Match          46.0%; Score 29; DB 9; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.4e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLDATM 7
Db 1 TSLDATV 7

RESULT 12
US-09-758-198-44
; Sequence 44, Application US/09758198
; Publication No. US20020187925A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATY, No. US20020187925A1man L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,198
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US/09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: PCT/AU97/00312
; PRIOR FILING DATE: 1997-05-22
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Rat
US-09-758-198-44

Query Match          46.0%; Score 29; DB 9; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.4e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLDATM 7
Db 1 TSLDATV 7

RESULT 13
US-09-861-661-41
; Sequence 41, Application US/09861661
; Publication No. US20030045676A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, DAVID J.
; APPLICANT: GERRATY, NORMAN L.
; TITLE OF INVENTION: PEPTIDES, ANTIBODIES, VACCINES & USES THEREOF
; FILE REFERENCE: 054270/0135
; CURRENT APPLICATION NUMBER: US/09/861,661
; CURRENT FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-861-661-41
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Search completed: November 14, 2004, 12:26:59
Job time : 29.3404 secs

Query Match 46.0%; Score 29; DB 10; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.4e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLDATM 7
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|
|
Db 1 TSLDATV 7

RESULT 14
US-09-861-661-44
; Sequence 44, Application US/09861661
; Publication No. US20030045676A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, DAVID J.
; APPLICANT: GERRATY, NORMAN L.
; APPLICANT: WESTBROOK, SIMON L.
; TITLE OF INVENTION: PEPTIDES, ANTIBODIES, VACCINES & USES THEREOF
; FILE REFERENCE: 054270/0135
; CURRENT APPLICATION NUMBER: US/09/861,661
; CURRENT FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-861-661-44

Query Match 46.0%; Score 29; DB 10; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.4e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLDATM 7
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|
Db 1 TSLDATV 7

RESULT 15
US-09-836-770-5
; Sequence 5, Application US/09836770
; Publication No. US20030175799A1
; GENERAL INFORMATION:
; APPLICANT: Cochran, Andrea G.
; APPLICANT: Starovasnik, Melissa A.
; APPLICANT: Skelton, Nicholas
; TITLE OF INVENTION: HAIRPIN PEPTIDES WITH A NOVEL STRUCTURAL MOTIF AND
; TITLE OF INVENTION: METHODS RELATING THERETO
; FILE REFERENCE: P1875
; CURRENT APPLICATION NUMBER: US/09/836,770
; CURRENT FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 5
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide
US-09-836-770-5

Query Match 46.0%; Score 29; DB 10; Length 16;
Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 DATMTWT 10
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Db 7 DATKTWT 13

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